

Access DB# 73546

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
 Reference Librarian
 Biotechnology & Chemical Library
 CM1 1E07 - 703-308-4498
 jan.delaval@uspto.gov

STAFF USE ONLY

Searcher: <u>Jan</u>	Type of Search	Vendors and cost where applicable
Searcher Phone #: <u>4498</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Location: _____	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Date Searcher Picked Up: <u>8/19/02</u>	Structure (#) _____	Questel/Orbit _____
Date Completed: <u>8/21/02</u>	Bibliographic _____	Dr.Link _____
Searcher Prep & Review Time: _____	Litigation _____	Lexis/Nexis _____
Clerical Prep Time: <u>20</u>	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Online Time: <u>15</u>	Patent Family _____	WWW/Internet _____
	Other _____	Other (specify) _____

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On: August 19, 2002, 06:14:39 ; Search time 78.53 seconds
(without alignments)
12.236 Million cell updates/sec

Title: US-09-339-922A-34

Perfect score: 53

Sequence: 1 GFTFSSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	94	2 S14580	Ig heavy chain V r
2	49	92.5	97	2 S26890	Ig heavy chain V r
3	48	90.6	113	2 S26468	Ig heavy chain V r
4	48	90.6	117	1 HVMS34	Ig heavy chain pre
5	48	90.6	121	2 D27888	Ig heavy chain V r
6	48	90.6	124	2 C27888	Ig heavy chain V r
7	46	86.8	40	2 S33406	Ig heavy chain V r
8	46	86.8	83	2 C25913	Ig heavy chain V r
9	46	86.8	98	2 S26891	Ig heavy chain V r
10	46	86.8	108	2 PL0248	Ig heavy chain V r
11	46	86.8	108	2 PH1006	Ig heavy chain pre
12	46	86.8	117	1 HVMS84	Ig heavy chain V r
13	46	86.8	117	2 PL0249	Ig heavy chain V r
14	46	86.8	117	2 PL0252	Ig heavy chain V r
15	46	86.8	119	2 E27888	Ig heavy chain V r
16	46	86.8	122	2 E27888	Ig heavy chain V r
17	46	86.8	138	2 S02258	Ig heavy chain V r
18	45	84.9	92	2 S56009	Ig heavy chain var
19	45	84.9	92	2 S56008	Ig heavy chain var
20	45	84.9	97	1 HVMS91	Ig heavy chain V r
21	45	84.9	97	2 PH0872	Ig heavy chain V r
22	45	84.9	98	2 S26889	Ig heavy chain V r
23	45	84.9	100	2 D48223	Ig heavy chain V r
24	45	84.9	102	2 S14581	Ig heavy chain V r
25	45	84.9	108	2 PH1648	Ig heavy chain V r
26	45	84.9	108	2 PH1011	Ig heavy chain V r
27	45	84.9	109	2 PH1649	Ig heavy chain V r
28	45	84.9	111	2 PH1659	Ig heavy chain V r
29	45	84.9	111	2 S40090	Ig heavy chain - m

30	45	84.9	111	2 PH1007	Ig heavy chain V r
31	45	84.9	112	2 S26327	Ig heavy chain V r
32	45	84.9	112	2 PH1647	Ig heavy chain V r
33	45	84.9	113	2 S25571	Ig heavy chain V r
34	45	84.9	117	1 H3H026	Ig heavy chain pre
35	45	84.9	117	2 A45953	Ig heavy chain pre
36	45	84.9	117	2 B34964	Ig heavy chain pre
37	45	84.9	117	2 S34012	Ig heavy chain V r
38	45	84.9	118	2 S31121	Ig heavy chain - h
39	45	84.9	119	2 C36005	Ig heavy chain V r
40	45	84.9	119	2 D36005	Ig heavy chain V r
41	45	84.9	119	2 S31107	Ig heavy chain - h
42	45	84.9	119	2 S31108	Ig heavy chain - h
43	45	84.9	120	2 S48798	Ig heavy chain V r
44	45	84.9	120	2 S55538	Ig heavy chain V r
45	45	84.9	120	2 S55539	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S14580

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C;Accession: S14580

R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.

submitted to the EMBL Data Library, March 1991

A;Description: Natural polyclonal antibodies differ from Ag-induced antibodies in V

A;Reference number: S14484

A;Accession: S14580

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-94 <CHE>

A;Cross-references: EMBL:X58652; NID:g51293; PIDN:CAA41509.1; PID:g51294

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 53; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10

|||||

Db 18 GFTFSSYDMS 27

RESULT 2

S26890

Ig heavy chain V region (DP-48) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S26890

R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o

A;Reference number: S26885; MUID:93021117

A;Accession: S26890

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-97 <TOM>

A;Cross-references: EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PID:g32917

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 92.5%; Score 49; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 GFTFSSYDM 9
|||
Db 26 GFTFSSYDM 34

RESULT 3

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

Submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <NAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match

90.6%; Score 48; DB 2; Length 113;

Best Local Similarity 90.0%; Pred. No. 0.051;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10

|||
Db 22 GFAFSSYDM 31

RESULT 4

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: J70502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J70501; MUID:89279149

A:Accession: J70502

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: This sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match

90.6%; Score 48; DB 1; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.053;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10

|||
Db 45 GFAFSSYDM 54

RESULT 5

D27888

Ig heavy chain V region (H37-60) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: D27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: D27888

A:Molecule type: DNA

A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: This sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

90.6%; Score 48; DB 2; Length 121;

Best Local Similarity 90.0%; Pred. No. 0.055;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10

|||
Db 26 GFAFSSYDM 35

RESULT 6

C27888

Ig heavy chain V region (H37-62) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: C27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: C27888

A:Molecule type: DNA

A:Residues: 1-124 <CAT>

A:Experimental source: strain Balb/c

A:Note: This sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

90.6%; Score 48; DB 2; Length 124;

Best Local Similarity 90.0%; Pred. No. 0.056;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10

|||
Db 26 GFAFSSYDM 35

RESULT 7

S33406

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998

C:Accession: S33406

R:Kettlborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.

Eur. J. Immunol. 23, 206-211, 1993

A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes

A:Reference number: S33391; MUID:93122092

A:Accession: S33406

A:Molecule type: mRNA

A:Residues: 1-40 <KET>

A:Cross-references: EMBL:X73009

A:Experimental source: strain BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 86.8%; Score 46; DB 2; Length 40;
Best Local Similarity 90.0%; Pred. No. 0.04; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 26 GFTFSSYTHS 35
|||||

RESULT 8
C25913
Ig heavy chain V region (BFL14) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
C:Accession: C25913
R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
A:Reference number: A94148; MUID:87175892
A:Accession: C25913
A:Molecule type: DNA
A:Residues: 1-83 <LAW>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 86.8%; Score 46; DB 2; Length 83;
Best Local Similarity 90.0%; Pred. No. 0.088;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 11 GFTFSSYGMS 20
|||||

RESULT 9
S26891
Ig heavy chain V region (DP-58) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26891
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117
A:Accession: S26891
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12358; NID:g32935; PIDN:CAA78228.1; PID:g32936
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 46; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 26 GFTFSSYEMN 35
|||||

RESULT 10
PL0248
Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0248
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0248
A:Molecule type: mRNA
A:Residues: 1-108 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-24/Region: framework 1
F:9-92/Domain: immunoglobulin homology <IMM>
F:25-29/Region: complementarity-determining 1
F:30-43/Region: framework 2
F:44-60/Region: complementarity-determining 2
F:61-92/Region: framework 3
F:93-99/Region: complementarity-determining 3
F:100-108/Region: framework 4

Query Match 86.8%; Score 46; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.12; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 20 GFTFSSYTHS 29
|||||

RESULT 11
PH1006
Ig heavy chain V region (clone 202.33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1006
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1006
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <TIL>
A:Experimental source: B cell, strain [N2B x N2W]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 46; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.12; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 21 GFTFSSYGMS 30
|||||

RESULT 12
HVMS84
Ig heavy chain precursor V region (5-84) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0505
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar
A:Reference number: JT0501; MUID:89279149
A:Accession: JT0505
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 86.8%; Score 46; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
 ||||| ||
 Db 45 GFTFSSYTMS 54

RESULT 13

PL0249
 Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0249
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0249
 A:Molecule type: mRNA
 A:Residues: 1-117 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3
 F:109-117/Region: framework 4

Query Match 86.8%; Score 46; DB 2; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
 ||||| ||
 Db 26 GFTFSSYTMS 35

RESULT 14

PL0252
 Ig heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0252; PL0251
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0252
 A:Molecule type: mRNA
 A:Residues: 1-117 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3
 F:109-117/Region: framework 4

Query Match 86.8%; Score 46; DB 2; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
 ||||| ||
 Db 26 GFTFSSYTMS 35

RESULT 15

F27888
 Ig heavy chain V region (H158-89H4) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
 C:Accession: F27888
 R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
 EMBO J. 5, 1577-1587, 1986
 A:Title: Structural and functional implications of a restricted antibody response to
 A:Reference number: A91043; MUID:86300658
 A:Accession: F27888
 A:Molecule type: DNA
 A:Residues: 1-119 <CAT>
 A:Experimental source: strain Balb/c
 A:Note: this sequence was determined from the germline gene
 C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 46; DB 2; Length 119;
 Best Local Similarity 90.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GFTFSSYDMS 10
 ||||| ||
 Db 26 GFTFSSYTMS 35

Search completed: August 19, 2002, 06:36:03
 Job time: 1284 sec

{

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:15 ; Search time 51.81 Seconds
(without alignments)
7.473 Million cell updates/sec

Title: US-09-339-922A-34

Perfect score: 53

Sequence: 1 GFTFSSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	90.6	117	1 HV55_MOUSE	P18526 mus musculu
2	46	86.8	117	1 HV54_MOUSE	P18525 mus musculu
3	45	84.9	97	1 HV56_MOUSE	P18527 mus musculu
4	45	84.9	117	1 HV3C_HUMAN	P01764 homo sapien
5	44	83.0	117	1 HV53_MOUSE	P18524 mus musculu
6	43	81.1	117	1 HV59_MOUSE	P18530 mus musculu
7	41	77.4	115	1 HV3D_HUMAN	P01765 homo sapien
8	40	75.5	117	1 HV52_MOUSE	P06327 mus musculu
9	39	73.6	114	1 HV00_MOUSE	P01741 mus musculu
10	39	73.6	114	1 HV01_CANFA	P01784 canis famil
11	39	73.6	116	1 HV1A_RABIT	P01826 oryctolagus
12	39	73.6	117	1 HV2B_RABIT	P01828 oryctolagus
13	39	73.6	120	1 HV3E_HUMAN	P01766 homo sapien
14	39	73.6	121	1 HV3J_HUMAN	P01771 homo sapien
15	38	71.7	114	1 HV3B_HUMAN	P01763 homo sapien
16	38	71.7	117	1 HV58_MOUSE	P18529 mus musculu
17	38	71.7	122	1 HV3G_HUMAN	P01768 homo sapien
18	38	71.7	136	1 HV16_MOUSE	P01783 mus musculu
19	37	69.8	111	1 HV35_MOUSE	P01804 mus musculu
20	37	69.8	113	1 HV27_MOUSE	P01796 mus musculu
21	37	69.8	113	1 HV28_MOUSE	P01797 mus musculu
22	37	69.8	113	1 HV29_MOUSE	P01798 mus musculu
23	37	69.8	113	1 HV30_MOUSE	P01799 mus musculu
24	37	69.8	113	1 HV31_MOUSE	P01800 mus musculu
25	37	69.8	113	1 HV34_MOUSE	P01803 mus musculu
26	37	69.8	115	1 HV32_MOUSE	P01801 mus musculu
27	37	69.8	115	1 HV33_MOUSE	P01802 mus musculu
28	37	69.8	117	1 HV02_CANFA	P01785 canis famil
29	37	69.8	117	1 HV17_MOUSE	P01786 mus musculu
30	36	67.9	98	1 HV57_MOUSE	P18528 mus musculu
31	36	67.9	119	1 HV3M_HUMAN	P01774 homo sapien
32	35	66.0	117	1 HV02_CAICR	P03981 calman croc
33	35	66.0	117	1 HV03_CARAU	P19180 carassius a

ALIGNMENTS

RESULT 1

HV55_MOUSE 34 35 66.0 126 1 HV3K_HUMAN P01772 homo sapien
 ID HV55_MOUSE STANDARD; PRT; 117 AA.
 AC P18526;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 345 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0502; HVMS34.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 90.6%; Score 48; DB 1; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.015; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1;

QY 1 GFTFSSYDMS 10

II IIIIIII

Db 45 GFTFSSYDMS 54

RESULT 2

HV54_MOUSE 34 35 66.0 126 1 HV54_MOUSE STANDARD; PRT; 117 AA.
 ID HV54_MOUSE
 AC P18525;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5-84 precursor.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0505; HVMS84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 86.8%; Score 46; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTSSYDMS 10
DB 45 GFTSSYMS 54

RESULT 3
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 84.9%; Score 45; DB 1; Length 97;
Best Local Similarity 90.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 84.9%; Score 45; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 84.9%; Score 45; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTSSYDMS 10
DB 26 GFTSSYAMS 35

RESULT 4
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; B826733F1A3CB0F1 CRC64;

Query Match 84.9%; Score 45; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTSSYDMS 10
DB 45 GFTSSYAMS 54

RESULT 5
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;

```

RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JTO503; HVMSRF.
DR HSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RE..
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 83.0%; Score 44; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY -1 GFTFSSYDMS 10
DB 45 GFTFSSYMS 54

RESULT 6
HV59_MOUSE
ID HV59_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JTO507; HVMS39.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 81.1%; Score 43; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFTFSSYDMS 10
DB 45 GFTFSSYMS 54

RESULT 7
HV3D_HUMAN
ID HV3D_HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78005528; PubMed=409716;
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;

RT "Immunoglobulin structure and genetics. Identity between variable
regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
IDENTICAL.

PIR: A02048; H3HUTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 77.4%; Score 41; DB 1; Length 115;
Best Local Similarity 80.0%; Pred. No. 0.33;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
DB 26 GFTFSSYMS 35

RESULT 8
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 Al/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281(1985).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 CC EMBL; M13787; AAA38499.1; -.
 DR PIR; A02029; HVMSAL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/44.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 75.5%; Score 40; DB 1; Length 117;
 Best Local Similarity 60.0%; Pred. No. 0.53; Indels 0; Gaps 0;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
 I:|||||:
 Db 45 GYTFTSYDIN 54

RESULT 9
 HV00_MOUSE STANDARD; PRT; 114 AA.
 AC P01741;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Ig heavy chain V region (Anti-arsenate antibody).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=79195438; PubMed=109536;
 RA Capra J.D., Nisonoff A.;
 RT "Structural studies on induced antibodies with defined idiotypic
 RT specificities. VII. The complete amino acid sequence of the heavy
 RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
 RT mice bearing a cross-reactive idiotype.";
 RL J. Immunol. 123:279-284(1979).
 CC -!- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
 CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
 CC REGION SEQUENCE.
 DR PIR; A02022; G1MSAA.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Antiarsenate antibody.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12555 MW; 99D8F0B6A69F4BE CRC64;

Query Match 73.6%; Score 39; DB 1; Length 114;
 Best Local Similarity 66.7%; Pred. No. 0.8; Indels 0; Gaps 0;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
 I:|||||:
 Db 26 GYTFSSYEL 34

RESULT 10
 HV01_CANFA STANDARD; PRT; 114 AA.
 AC P01784;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region GOM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77242268; PubMed=407924;
 RA Wasserman R.L., Capra J.D.;
 RT "Primary structure of the variable regions of two canine
 RT immunoglobulin heavy chains.";
 RL Biochemistry 16:3160-3168(1977).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A02067; AVDGM.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12430 MW; BID4745D2C4E13C4 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 114;
 Best Local Similarity 77.8%; Pred. No. 0.8; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
 I:|||||:
 Db 26 GITFSGYDM 34

RESULT 11
 HV1A_RABIT STANDARD; PRT; 116 AA.
 AC P01826;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-A1 region BS-5.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE OF 1-69.
 RX MEDLINE=73220191; PubMed=4146279;
 RA Jaton J.-C., Braun D.G.;
 RT "Amino acid sequence of the N-terminal sixty-nine residues of heavy
 RT chain derived from a homogeneous rabbit antibody.";
 RL Biochem. J. 130:539-546(1972).
 RN [2]
 RP SEQUENCE OF 64-116.
 RX MEDLINE=75183340; PubMed=4142749;
 RA Jaton J.-C.;
 RT "Completion of the analysis of the primary structure of the variable
 RT domain of a homogeneous rabbit antibody to type III pneumococcal
 RT polysaccharide.";
 RL Biochem. J. 143:723-732(1974).
 CC -!- MISCELLANEOUS: THIS GAMMA CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE
 CC III PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE

CC RABBIT.
 DR PIR: A02102; GARB15.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12349 MW; 95C6FAC93C788C42 CRC64;

 Query Match 73.6%; Score 39; DB 1; Length 116;
 Best Local Similarity 77.8%; Pred. No. 0.82;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GFTFSSYDM 9
 DB 25 GFSLSYDM 33
 II: II:IIII

 RESULT 12
 ID HV2B_RABBIT STANDARD; PRT; 117 AA.
 AC P01828;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-A2 region K-25.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76039436; PubMed=241319;
 RA Jaton J.-C.;
 RT "Comparison of the amino acid sequences of the variable domains of
 RT two homologous rabbit antibodies to type III pneumococcal
 RT polysaccharide."
 RL Biochem. J. 147:235-247(1975).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III
 CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
 DR PIR: A02104; GARB2K.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 21 91
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12580 MW; 28DB87FDB7AEE9B8 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 0.83;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 GFTFSSYDM 10
 DB 25 GFSLSYDM 34
 II: I:IIII

 RESULT 13
 ID HV3E_HUMAN STANDARD; PRT; 120 AA.
 AC P01766;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region BRO.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77117674; PubMed=65324;
 RA Capra J.D., Hopper J.E.;
 RT "Comparative studies on monotypic IgM lambda and IgG kappa from an
 RT individual patient. III. The complete amino acid sequence of the VH
 RT region of the IgM paraprotein."
 RL Immunochimistry 13:995-999(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
 CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
 CC TYPE.
 DR PIR: A02049; M3HUBW.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;

 Query Match 73.6%; Score 39; DB 1; Length 120;
 Best Local Similarity 70.0%; Pred. No. 0.85;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 GFTFSSYDM 10
 DB 26 GFTFSSYNNM 35
 II:IIII I:I

 RESULT 14
 ID HV3J_HUMAN STANDARD; PRT; 121 AA.
 AC P01771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region HIL.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RT "Amino acid sequence of the VH region of human myeloma
 RT cryoimmunoglobulin IgG HIL."
 RL Biochemistry 18:553-560(1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 DR PIR: A02054; G1HUHL.
 DR HSSP: P01772; 2F84.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

 Query Match 73.6%; Score 39; DB 1; Length 121;
 Best Local Similarity 77.8%; Pred. No. 0.86;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 1 GFTFSSYDM 9
 DB 26 GFTFSSNYGM 34
 II:IIII I:I


```

RESULT 15
HV3B_HUMAN
ID HV3B_HUMAN STANDARD; PRT; 114 AA.
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A02046; M3HUNE.
DR HSP; P01772; 2IG2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12256 MW; . D88294FB418A07B7 CRC64;

```

```

Query Match      71.7%; Score 38; DB 1; Length 114;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSYDMS 10
DB 26 GFTFSANDMN 35

```

Search completed: August 19, 2002, 06:59:05
Job time: 1370 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:50 ; Search time 140.4 Seconds
(without alignments)
12.322 Million cell updates/sec

Title: US-09-339-922A-34

Perfect score: 53

Sequence: 1 GFTFSSYDMS 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	86.8	119	11 Q920E7	Q920E7 mus musculus
2	46	86.8	486	11 Q91Z07	Q91Z07 mus musculus
3	45	84.9	437	11 Q9R1A4	Q9R1A4 mus musculus
4	45	84.9	487	11 Q99KA4	Q99KA4 mus musculus
5	44	83.0	118	4 Q9ULB6	Q9ULB6 homo sapien
6	43	81.1	95	4 Q9ULB6	Q9ULB6 homo sapien
7	43	81.1	147	4 Q9V509	Q9V509 homo sapien
8	42	79.2	113	4 Q9UL90	Q9UL90 homo sapien
9	42	79.2	140	10 Q9ARP0	Q9ARP0 oryza sativ
10	41	77.4	116	4 Q9UL93	Q9UL93 homo sapien
11	38	71.7	112	4 Q9HCC1	Q9HCC1 homo sapien
12	38	71.7	412	10 Q9ZQR5	Q9ZQR5 arabidopsis
13	38	71.7	473	11 Q91Z05	Q91Z05 mus musculus
14	38	71.7	597	4 Q96BB9	Q96BB9 homo sapien
15	38	71.7	702	10 Q9LNL6	Q9LNL6 arabidopsis
16	38	71.7	2133	12 Q98203	Q98203 molluscum c

17	37	69.8	124	4 Q9UL92	Q9UL92 homo sapien
18	37	69.8	594	5 P91823	P91823 caenorhabdi
19	37	69.8	1436	5 Q9W159	Q9W159 drosophila
20	36	67.9	479	11 Q91WPS	Q91WPS mus musculus
21	36	67.9	690	10 Q9LIB7	Q9LIB7 arabidopsis
22	36	67.9	690	10 Q940D0	Q940D0 arabidopsis
23	36	67.9	1383	5 Q91Z07	Q91Z07 caenorhabdi
24	35	66.0	112	4 Q9UGP3	Q9UGP3 homo sapien
25	35	66.0	128	3 Q94499	Q94499 schizosacch
26	35	66.0	159	4 Q96QSO	Q96QSO homo sapien
27	35	66.0	1121	2 Q9AKN9	Q9AKN9 rickettsia
28	35	66.0	1264	12 Q89230	Q89230 variola vir
29	35	66.0	1896	12 Q89096	Q89096 variola vir
30	35	66.0	1896	12 Q89117	Q89117 variola vir
31	35	66.0	1896	12 Q89192	Q89192 variola vir
32	35	66.0	1897	12 Q85406	Q85406 variola maj
33	35	66.0	1924	12 Q9JFS2	Q9JFS2 ectromelia
34	35	66.0	1933	12 Q72759	Q72759 cowpox viru
35	35	66.0	1949	12 Q9J5C1	Q9J5C1 fowlpox vir
36	34	64.2	109	11 Q9JL75	Q9JL75 mus musculu
37	34	64.2	341	4 Q9H795	Q9H795 homo sapien
38	34	64.2	379	10 Q9SSA7	Q9SSA7 arabidopsis
39	34	64.2	397	16 Q97GF8	Q97GF8 clostridium
40	34	64.2	504	2 Q9KZF1	Q9KZF1 streptomyce
41	34	64.2	520	16 Q9PMZ7	Q9PMZ7 campylobact
42	34	64.2	573	4 Q9NWM4	Q9NWM4 homo sapien
43	34	64.2	583	4 Q9H587	Q9H587 homo sapien
44	34	64.2	643	2 Q9KJI6	Q9KJI6 desulfovibr
45	34	64.2	690	2 Q9RBG8	Q9RBG8 aeromonas p

ALIGNMENTS

RESULT 1

Q920E7 ID Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7; 2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PTERIN-MIMICKING ANTI-IDIOPOPE HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF307937; AAL09421.1; -.
FT NON_TER 119
FT SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match 86.8%; Score 46; DB 11; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10

Db 26 GFTFSSYDMS 35

RESULT 2

Q91Z07 ID Q91Z07 PRELIMINARY; PRT; 486 AA.
AC Q91Z07; 2001 (TREMBlrel. 19, Created)

```

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 52.7 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010324; AAH10324.1; -.
KW Hypothetical protein.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match      86.8%; Score 46; DB 11; Length 486;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 45 GFTFSSYDMS 54
||:|||||

RESULT 3
Q9RIA4
ID Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152372; AAD40243.1; -.
DR HSSP: P01842; 7FAB.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam: PF00047; Ig_4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 437
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match      84.9%; Score 45; DB 11; Length 437;
Best Local Similarity 90.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 25 GFTFSSYAMS 34
|||||||

RESULT 4
Q99KA4
ID Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

```

```

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 52.6 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004786; AAH04786.1; -.
DR HSSP: P01810; 2FBJ
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_Cl.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam: PF00047; Ig_4.
DR SMART; SM00409; IG_3.
DR SMART; SM00407; IGV_3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match      84.9%; Score 45; DB 11; Length 487;
Best Local Similarity 90.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 45 GFTFSSYAMS 54
|||||||

RESULT 5
Q9UL91
ID Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035023; AAD56259.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match      83.0%; Score 44; DB 4; Length 118;
Best Local Similarity 80.0%; Pred. No. 0.84;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10

```

Db 26 GFTFSSYMN 35
||||||| 1;

RESULT 6
Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; -;
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 95
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 81.1%; Score 43; DB 4; Length 95;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
||||||| 1;
Db 25 GFTFSSYWMS 34

RESULT 7
Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -;
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 81.1%; Score 43; DB 4; Length 147;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
||||||| 1;
Db 26 GFTFSSYGMS 35

RESULT 8
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -;
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 79.2%; Score 42; DB 4; Length 113;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
||||||| 1;
Db 26 GFTFSSYGM 34

RESULT 9
Q9ARPO PRELIMINARY; PRT; 140 AA.
AC Q9ARPO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE P0024G09.20 PROTEIN.
GN P0024G09.20.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0024G09.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003311; BAB40128.1; -;
SQ SEQUENCE 140 AA; 15782 MW; 222CB6E0CA6FCBDD CRC64;

```

Query Match          79.2%; Score 42; DB 10; Length 140;
Best Local Similarity 77.6%; Pred. No. 2.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
DB 131 GFTFSSYEL 139

RESULT 10
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match          77.4%; Score 41; DB 4; Length 116;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
DB 25 GFTFSSYAM 33

RESULT 11
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SINGLE CHAIN FV (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme : Isolation from a
RT human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003599; Ig.

```

```

DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match          71.7%; Score 38; DB 4; Length 112;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
DB 26 GFTFDDYGMS 35

RESULT 12
Q9ZQR5 PRELIMINARY; PRT; 412 AA.
AC Q9ZQR5;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AT2G14530 PROTEIN.
GN AT2G14530.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006067; AAD15463.1; -.
DR InterPro; IPR004253; DUF231.
DR Pfam; PF03005; DUF231; 1.
SQ SEQUENCE 412 AA; 46462 MW; 1155D765FAD34CCE CRC64;

Query Match          71.7%; Score 38; DB 10; Length 412;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
DB 170 GFTFSQYNLT 179

RESULT 13
Q91Z05 PRELIMINARY; PRT; 473 AA.
ID Q91Z05
AC Q91Z05;

```

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 51.9 KDA PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010327; AAH10327.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

 Query Match 71.7%; Score 38; DB 11; Length 473;
 Best Local Similarity 77.8%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 GFTFSYDM 9
 DB 45 GFTFSYGM 53
 |||||
 |||||

 RESULT 14
 Q96BB9 PRELIMINARY; PRT; 597 AA.
 AC Q96BB9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 65.0 KDA PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015760; AAH15760.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

 Query Match 71.7%; Score 38; DB 4; Length 597;
 Best Local Similarity 70.0%; Pred. No. 61;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 GFTFSYDMS 10
 DB 45 GFTFSYAMN 54
 ||:||||
 ||:||||

 RESULT 15
 Q9LNL6 PRELIMINARY; PRT; 702 AA.
 AC Q9LNL6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE FLK21.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,

RA Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC Fl2K21 from chromosome
 RT I.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC032279; AAF9257.1; -
 SQ SEQUENCE 702 AA; 80578 MW; 425B0F22B76EC786 CRC64;

Query Match 71.7%; Score 38; DB 10; Length 702;
 Best Local Similarity 75.0%; Pred. No. 72;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSYD 8
 DB 143 GFTYNSYD 150
 |||:||||
 |||:||||

Search completed: August 19, 2002, 06:58:08
 Job time: 1398 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:14:39 ; Search time 180.34 Seconds
(without alignments)
6.159 Million cell updates/sec

Title: US-09-339-922a-34

Perfect score: 53

Sequence: 1 GFTSSYDMS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

1:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	19	AAW76007
2	53	100.0	10	22	AAW76007
3	53	100.0	117	19	AAW76001
4	53	100.0	117	22	AAW76001
5	53	100.0	117	22	AAW76001
6	50	94.3	117	20	AAW76001
7	50	94.3	128	19	AAW54000
8	50	94.3	134	13	AAW24713
9	50	94.3	466	13	AAW24812
10	49	92.5	97	21	AAW40112
11	49	92.5	102	22	AAW39276

12	49	92.5	102	22	AAW59940
13	49	92.5	102	22	AAW72535
14	49	92.5	102	22	AAW32779
15	49	92.5	139	18	AAW21652
16	48	90.6	10	19	AAW76015
17	48	90.6	10	22	AAW61373
18	48	90.6	117	19	AAW76003
19	48	90.6	117	20	AAW06381
20	48	90.6	117	22	AAW63589
21	48	90.6	117	22	AAW61361
22	48	90.6	130	20	AAW06379
23	48	90.6	239	14	AAW34511
24	48	90.6	247	16	AAW11917
25	47	88.7	10	19	AAW76016
26	47	88.7	10	22	AAW61374
27	47	88.7	115	22	AAW69601
28	47	88.7	117	20	AAW86141
29	47	88.7	119	16	AAW11919
30	47	88.7	123	19	AAW53998
31	47	88.7	239	22	AAW69603
32	46	86.8	10	22	AAU07457
33	46	86.8	87	22	AAE06990
34	46	86.8	89	22	AAE06985
35	46	86.8	97	21	AAW40089
36	46	86.8	98	19	AAW59614
37	46	86.8	98	21	AAW40113
38	46	86.8	98	22	AAE06975
39	46	86.8	98	22	AAE06976
40	46	86.8	98	22	AAE06981
41	46	86.8	98	22	AAE06982
42	46	86.8	98	22	AAW48022
43	46	86.8	116	16	AAW66307
44	46	86.8	116	18	AAW13529
45	46	86.8	116	22	AAU07483

ALIGNMENTS

RESULT 1

AAW76007
ID AAW76007 standard; Protein; 10 AA.

AC AAW76007;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR1 protein fragment #1.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-H region; CDR;
XX complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI: 1998-437472/37.

DR N-PSDB; AAW49844.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX
XX Disclosure; Page 40; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFTFSSYDMS 10
DB 1 gftfssydsms 10
|||||
RESULT 2
AAB61365
ID AAB61365 standard; peptide; 10 AA.
AC AAB61365;
XX
XX
XX 03-APR-2001 (first entry)
DE LM609 VH CDR1 peptide.
XX
XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX Unidentified.
OS
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.
XX
XX Claim 4; Page 39; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 53; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFTFSSYDMS 10
DB 1 gftfssydsms 10
|||||
RESULT 3
AAW76001
ID AAW76001 standard; Protein; 117 AA.
XX
XX AAW76001;
XX
XX 02-NOV-1998 (first entry)
DT
XX
XX Vitaxin antibody heavy chain variable region protein fragment.
XX
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; AAV49820.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 1; Fig 1a; 129pp; English.
XX
XX This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 117 AA;
SQ

{

Query Match 100.0%; Score 53; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.019; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
 DB 26 gftfssyds 35

RESULT 4

AAG63587
 ID AAG63587 standard; Protein; 117 AA.

XX

AC AAG63587;

XX

DT 15-OCT-2001 (first entry)

XX

DE A heavy chain variable region of LM609 grafted antibody.
 XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.

XX

OS Synthetic.

OS Mus sp.

XX

PN US2001011125-A1.

XX

PD 02-AUG-2001.

XX

PF 30-JAN-1997; 97US-0790540.

XX

PR 30-JAN-1997; 97US-0790540.

XX

PA (HUSE/) HUSE W D.

XX

PI Huse WD;

XX

WPI; 2001-496171/54.

XX

N-PSDB; AAH74623.

XX

New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer.

XX

PS Claim 1; Fig 1A; 25pp; English.

XX

CC The present sequence represents the heavy chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 53; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFTFSSYDMS 10
 DB 26 gftfssyds 35

RESULT 5

AAB61359
 ID AAB61359 standard; protein; 117 AA.

XX

AC AAB61359;

XX

DT 03-APR-2001 (first entry)

XX

DE Vitaxin heavy chain variable region protein.

XX

KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX Unidentified.

OS

PN WO200078815-A1.

XX

XX 28-DEC-2000.

PD

XX

PF 23-JUN-2000; 2000WO-US17454.

XX

XX 24-JUN-1999; 99US-0339922.

XX

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX

PI Huse WD, Wu H;

XX

XX WPI; 2001-050110/06.

XX

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX

XX Disclosure; Fig 1; 132pp; English.

XX

CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 53; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.019; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
 DB 26 gftfssyds 35

RESULT 6

AAW86137
 ID AAW86137 standard; Protein; 117 AA.

XX

XX AAW86137;

XX

DT 03-MAR-1999 (first entry)
 DE Protein sequence of de-immunised humanised A33 Vh.
 XX
 KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW immunogl bulin; therapeutic; streptokinase; humanised; de-immunised.
 XX
 OS Homo sapiens.
 XX
 PN WO9852976-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 21-MAY-1998; 98WO-GB01473.
 XX
 PR 14-APR-1998; 98GB-0007751.
 PR 21-MAY-1997; 97GB-0010480.
 PR 31-JUL-1997; 97GB-0016197.
 PR 28-NOV-1997; 97GB-0025270.
 PR 02-DEC-1997; 97US-0067235.
 XX
 PA (BIOV-) BIOVATION LTD.
 XX
 PI Carr FJ;
 XX
 DR WPI; 1999-045301/04.
 XX
 PT Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species
 XX
 PS Example 5; Fig 25; 77pp; English.
 XX
 CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised humanised A33 Vh.
 XX
 SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.067;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
 |||||:
 Db 26 gftfstydm 35

RESULT 7
 AAW54000
 ID AAW54000 standard; Protein; 128 AA.
 XX
 AC AAW54000;
 XX
 DT 29-JUL-1998 (first entry)
 XX
 DE Anti-CD4 antibody VH3 monkey clone 3-40.
 XX
 KW Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
 KW Old World monkey; constant domain; eczema; immuno-modulated disease;
 KW rheumatoid arthritis.
 XX
 OS Mus musculus.

OS Primate sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..128
 XX /note= "Xaa= unspecified amino acid"
 PN US5750105-A.
 XX
 PD 12-MAY-1998.
 XX
 PF 07-JUN-1995; 95US-0476349.
 XX
 PR 10-JUL-1992; 92US-0912292.
 PR 23-JUL-1991; 91US-0735084.
 PR 23-MAR-1992; 92US-0856281.
 PR 05-DEC-1995; 95US-0379072.
 PR 07-JUN-1995; 95US-0476349.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Hanna N, Newman RA, Raab RW;
 XX WPI; 1998-296690/26.
 XX
 DR Improved method for antibody treatment - uses an antibody comprising
 PT an Old World monkey variable region and a human constant domain
 PT
 XX Example 1; Fig 9c; 84pp; English.
 XX
 CC This sequence represents the VH3 domain of an anti-CD4 antibody
 CC (Ab). This sequence can be used in the method of the invention for
 CC treating a subject, where the treatment comprises administration of an
 CC Ab. The method comprises the administration of an antibody which binds to
 CC Old World monkey (e.g. baboon or macaque) variable region which binds to
 CC an antigen (Ag) (or Ag binding portion), and a human constant domain. The
 CC method is useful for the treatment of eczema and immuno-modulated
 CC diseases and especially rheumatoid arthritis. The recombinant antibodies
 CC used are sufficiently different from native monkey antibodies to allow
 CC human antigens to raise these antibodies, but similar enough to human
 CC antibody so there is no immune response to the antibodies in humans.
 CC Compared to antibodies used in therapy in prior art, these antibodies do
 CC not induce human anti-antibodies on repeated administration. They also
 CC have longer half-lives and do not have a lack of effector function with
 CC human cells.
 XX
 SQ Sequence 128 AA;

Query Match 94.3%; Score 50; DB 19; Length 128;
 Best Local Similarity 90.0%; Pred. No. 0.074;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
 |||||:
 Db 26 gftfstydm 35

RESULT 8
 AAR24713
 ID AAR24713 standard; Protein; 134 AA.
 XX
 AC AAR24713;
 XX
 DT 28-DEC-1992 (first entry).
 XX
 DE Sequence encoded by the genomic chimeric heavy chain variable region
 DE (VH) gene.
 XX
 KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
 KW antithrombotic agent; myocardial infarction therapy.
 XX
 OS Mus musculus.

```

FH Key      Location/Qualifiers
FT Peptide  1..19
FT          /label= leader
FT Region   23..49
FT          /label= Framework Region (FR) 1
FT Region   50..54
FT          /label= Complementarity determining region(CDR)1
FT Region   55..68
FT          /label= FR-2
FT Region   69..84
FT          /label= CDR-2
FT Region   85..114
FT          /label= FR-3
FT Region   115..123
FT          /label= CDR-3
FT Region   124..134
FT          /label= FR-4
XX EP491351-A.
XX
XX 24-JUN-1992.
XX
XX 17-DEC-1991; 91EP-0121591.
XX
XX 18-DEC-1990; 90JP-0413829.
XX 11-NOV-1991; 91JP-0294464.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Iwasa S, Taka H, Watanabe T, Tada H;
XX WPI; 1992-209528/26.
XX N-PSDB; AAQ25666.
XX
XX Chimeric monoclonal antibodies - contain anti-human fibrin
XX antibody light and heavy chain variable and constant for treating
XX thrombotic conditions e.g. myocardial infarction
XX
XX Example; Figure 4; 87pp; English.
XX
XX PCR primers 5'mvh and 3'mvh were used to produce a VH gene-contg.
XX fragment of about 330bp. The fragment was isolated and subcloned in
XX pUC119. The fragment was found to be a functional VH structural
XX gene, referred to as VFH, comprising a VH gene belonging to the
XX subgroup III (VHIII) and the DSP2 and JH4 genes. Northern blot
XX analysis using the whole RNA of FIB1-11 cells confirmed that VFH
XX was the gene expressed in FIB1-11 cells. The sequence is given in
XX AAQ25666.
XX
XX Sequence 134 AA;

Query Match      94.3%; Score 50; DB 13; Length 134;
Best Local Similarity 90.0%; Pred. No. 0.077;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 45 gftfsnydms 54

RESULT 9
AAR24812
ID AAR24812 standard; Protein; 466 AA.
XX
AC AAR24812;
XX
XX 28-DEC-1992 (first entry)
XX
XX Sequence encoded by the chimeric H chain cDNA contained in pTB1373.
XX Chimeric monoclonal antibody; anti-fibrin antibody; primer;
XX antithrombotic agent; myocardial infarction therapy.
KW

```

```

XX Synthetic.
OS
XX Key      Location/Qualifiers
FH Peptide  13..19
FT          /label= Leader
FT Region   20..134
FT          /label= VH
FT Region   135..232
FT          /label= CH1
FT Region   233..247
FT          /label= hinge
FT Region   248..357
FT          /label= CH2
FT Region   358..464
FT          /label= CH3
FT Misc-difference 465
FT          /note= "translated stop codon"
XX
XX EP491351-A.
XX
XX 24-JUN-1992.
XX
XX 17-DEC-1991; 91EP-0121591.
XX
XX 18-DEC-1990; 90JP-0413829.
XX 11-NOV-1991; 91JP-0294464.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Iwasa S, Taka H, Watanabe T, Tada H;
XX WPI; 1992-209528/26.
XX N-PSDB; AAQ25692.
XX
XX Chimeric monoclonal antibodies - contain anti-human fibrin
XX antibody light and heavy chain variable and constant for treating
XX thrombotic conditions e.g. myocardial infarction
XX
XX Example; Figure 11; 87pp; English.
XX
XX Plasmid pTB1373 contains the whole length of a mouse-human
XX chimeric anti-human fibrin heavy chain cDNA open reading
XX frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin
XX chimeric Ab-producing transfectant FIB1-H01/X63 as a template
XX to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
XX a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
XX primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
XX cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
XX encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
XX peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CLH
XX respectively as a primer for first strand cDNA synthesis and the
XX primer combination of 5'CLH and 3'C2H, of 5' LH and 3'CLH and of
XX 5'SH and 3' LH respectively as primers for PCR. The amplified gene
XX products were isolated and used to produce plasmids. After
XX confirmation of the cDNA sequence of each plasmid, the cDNA
XX encoding LH, VH, CH1 and CH2CH3 were joined together to give
XX plasmid pTB1373 contg. the whole length chimeric H chain
XX (LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIB,
XX
XX Sequence 466 AA;

```

```

Query Match      94.3%; Score 50; DB 13; Length 466;
Best Local Similarity 90.0%; Pred. No. 0.29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 45 gftfsnydms 54

RESULT 10

```

AAB40112
 ID AAB40112 standard; Protein; 97 AA.
 XX
 AC AAB40112;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 638.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US07946.
 XX
 PR 25-MAR-1999; 99US-0126603.
 XX
 PA (BADI) BASF AG.
 XX
 PA (GEM) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Wildom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX
 PS Claim 75; Page 121; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 XX
 SQ Sequence 97 AA;
 Query Match 92.5%; Score 49; DB 21; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.084;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFTFSSYDM 9
 Db 26 gftfssydm 34

RESULT 11
 ABB39276
 ID ABB39276 standard; Peptide; 102 AA.
 XX
 AC ABB39276;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #6782 encoded by human foetal liver single exon probe.
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00669.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver -
 XX
 PS Claim 27; SEQ ID NO 31911; 639pp + sequence listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 102 AA;
 Query Match 92.5%; Score 49; DB 22; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFTFSSYDM 9
 Db 17 gftfssydm 25

RESULT 12
 AAM59940
 ID AAM59940 standard; Protein; 102 AA.
 XX
 AC AAM59940;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32045.
 KW Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX Homo sapiens.

OS WO200157275-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US00667.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human brains -

PS Example 4; SEQ ID NO: 32045; 650pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.

XX Sequence 102 AA;

Query Match 92.5%; Score 49; DB 22; Length 102;

Best Local Similarity 100.0%; Pred. No. 0.089;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDM 9

Db 17 gftfssydm 25

RESULT 13

AAW72535

ID AAW72535 standard; Protein; 102 AA.

XX AAW72535;

AC 06-NOV-2001 (first entry)

DT Human bone marrow expressed probe encoded protein SEQ ID NO: 32841.

DE Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -

PS Example 4; SEQ ID NO: 32841; 658pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.

XX Sequence 102 AA;

Qy 1 GFTFSSYDM 9

Db 17 gftfssydm 25

RESULT 14

AAM32779

ID AAM32779 standard; Protein; 102 AA.

XX AAM32779;

XX 17-OCT-2001 (first entry)

DT Peptide #6816 encoded by probe for measuring placental gene expression.

DE Probe; microarray; human; placenta; antenatal diagnosis;

KW genetic disorder.

XX Homo sapiens.

XX WO200157272-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US00663.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-48897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -

```

XX Claim 27; SEQ ID No 33048; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AA131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
SQ Sequence 102 AA;

Query Match          92.5%; Score 49; DB 22; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
Db 17 gftfssydm 25
|||||

RESULT 15
AAW21652
ID AAW21652 standard; Protein; 139 AA.
XX
AC AAW21652;
XX
DT 03-JAN-1998 (first entry)
XX
DE Humanised reshaped Mab 15 heavy chain variable region.
XX
KW Humanised antibody; monoclonal antibody; Mab 15; tumour;
KW lung cancer; therapy.
XX
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.
OS Chimeric synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Protein 20..139
FT /label= Mat_protein
FT Region 20..49
FT /label= Framework-1
FT Region 50..54
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT Region 55..68
FT /label= Framework-2
FT Region 69..85
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 86..117
FT /label= Framework-3
FT Region 118..128
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT Region 129..138
FT /label= Framework-4
XX
PN EP781847-A1.
XX
PD 02-JUL-1997.
XX
PF 25-OCT-1996; 96EP-0117154.
XX
PR 06-NOV-1995; 95EP-0117407.
XX
PA (MÈRE ) MERCK PATENT GMBH.
XX
PI Bendig; M, Jones T, Saidana J;

```

```

XX WPI; 1997-334904/31.
DR N-PSDB; AAT72237.
XX
FT Humanised form of murine monoclonal antibody Mab 15 - useful for
FT treating lung cancer
XX
PS Claim 2; Fig 12; 71pp; English.
XX
CC This polypeptide comprises the heavy chain variable region VH
CC of humanised reshaped monoclonal antibody (Mab) 15 comprising
CC complementarity determining regions of murine Mab 15 (DSM ACC2117),
CC and reshaped human 30pI framework regions. It is expressed by a
CC cDNA clone (see AAT72237) prepared using PCR mutagenesis methods. A
CC claimed process for preparation of humanised reshaped Mab 15
CC involves: cloning and sequencing murine Mab 15 VL and VH regions
CC (see AAW21653 and AAW21654); constructing, expressing and analysing
CC of murine Mab 15 antibody (see AAW21655-56); modelling the structure
CC of variable regions; preparing an oligonucleotide sequence which codes
CC for the constant regions of the light and heavy chain of a human
CC immunoglobulin; and constructing, expressing and analysing the
CC complete reshaped human Mab 15. The humanised Mab can be used for
CC treating tumours, especially lung cancer, and for the manufacture
CC of a drug related to tumours, especially lung cancer.
XX
SQ Sequence 139 AA;

Query Match          92.5%; Score 49; DB 18; Length 139;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
Db 45 gftfssydm 54
|||||

Search completed: August 19, 2002, 06:39:10
Job time: 1471 sec

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:14:39 ; Search time 61.75 seconds
(without alignments)
3.956 Million cell updates/sec

Title: US-09-339-922A-34

Perfect score: 53

Sequence: 1 GFTFSSYDMS 10

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	94.3	128	1	US-08-478-039-73
2	50	94.3	128	1	US-08-478-039-102
3	50	94.3	128	1	US-08-476-349A-73
4	50	94.3	128	1	US-08-476-349A-102
5	48	90.6	239	2	US-07-956-399-4
6	48	90.6	247	5	PCT-US94-07659-2
7	47	88.7	119	5	PCT-US94-07659-6
8	47	88.7	123	1	US-08-478-039-71
9	47	88.7	123	1	US-08-478-039-104
10	47	88.7	123	1	US-08-476-349A-71
11	47	88.7	123	1	US-08-476-349A-104
12	46	86.8	98	2	US-08-665-202-31
13	46	86.8	116	3	US-08-545-809A-101
14	46	86.8	116	4	US-08-983-607-36
15	46	86.8	122	1	US-08-276-852-80
16	46	86.8	122	1	US-08-899-575-80
17	46	86.8	122	1	US-08-899-575-80
18	46	86.8	122	5	PCT-US95-08743-80
19	46	86.8	123	2	US-08-665-202-30
20	46	86.8	239	2	US-08-553-497A-18
21	45	84.9	35	2	US-08-765-179B-1
22	45	84.9	98	2	US-08-428-197-48
23	45	84.9	98	5	PCT-US93-10535-48
24	45	84.9	102	2	US-08-273-146-65
25	45	84.9	110	1	US-08-211-202-117
26	45	84.9	113	3	US-08-974-899-6
27	45	84.9	116	2	US-08-428-197-2

28 45 84.9 116 5 PCT-US93-10555-2 Sequence 2, Appli
29 45 84.9 117 3 US-08-545-809A-109 Sequence 109, App
30 45 84.9 117 4 US-08-983-607-46 Sequence 46, Appl
31 45 84.9 117 4 US-08-752-693A-3 Sequence 3, Appli
32 45 84.9 117 4 US-08-752-693A-4 Sequence 4, Appli
33 45 84.9 117 4 US-09-157-370-1 Sequence 1, Appli
34 45 84.9 118 2 US-08-652-816A-12 Sequence 12, Appli
35 45 84.9 118 4 US-08-487-761-15 Sequence 15, Appli
36 45 84.9 118 5 PCT-US93-08435-10 Sequence 10, Appli
37 45 84.9 120 4 US-09-025-769B-38 Sequence 38, Appli
38 45 84.9 120 1 US-09-025-769B-63 Sequence 63, Appli
39 45 84.9 121 1 US-08-339-582-2 Sequence 2, Appli
40 45 84.9 122 2 US-07-934-373C-21 Sequence 21, Appli
41 45 84.9 122 3 US-08-437-642B-21 Sequence 21, Appli
42 45 84.9 122 5 PCT-US93-07832-21 Sequence 21, Appli
43 45 84.9 122 5 PCT-US93-08435-12 Sequence 12, Appli
44 45 84.9 122 5 PCT-US93-08435-14 Sequence 14, Appli
45 45 84.9 122 5 PCT-US93-08435-43 Sequence 43, Appli

ALIGNMENTS

RESULT 1
US-08-478-039-73
; Sequence 73, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-478-039-73

Query Match 94.3%; Score 50; DB 1; Length 128;
Best Local Similarity 90.0%; Pred. No. 0.028;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTSSYDMS 10
Db 26 GFTSSYDMN 35

RESULT 2
US-08-478-039-102
; Sequence 102, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:

; CHROMOSOME/SEGMENT: #40
US-08-478-039-102

Query Match 94.3%; Score 50; DB 1; Length 128;
Best Local Similarity 90.0%; Pred. No. 0.028;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTSSYDMS 10
Db 26 GFTSSYDMN 35

RESULT 3
US-08-476-349A-73
; Sequence 73, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-476-349A-73

Query Match

94.3%; Score 50; DB 1; Length 128;

Best Local Similarity 90.0%; Pred. No. 0.028; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
|||||

Db 26 GFTFSSYDMS 35

RESULT 4
US-08-476-349A-102
; Sequence 102, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
US-08-476-349A-102

Query Match 94.3%; Score 50; DB 1; Length 128;
Best Local Similarity 90.0%; Pred. No. 0.028;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
|||||

Db 26 GFTFSSYDMS 35

RESULT 5
US-07-956-399-4
; Sequence 4, Application US/07956399
; Patent No. 5876717
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: TAKI, SHINSUKE
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
; TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,399
; FILING DATE: 19921005
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5876717man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-956-399-4

Query Match 90.6%; Score 48; DB 2; Length 239;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
|||||

Db 148 GFTFSSYDMS 157

RESULT 6
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurie, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.

ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 90.6%; Score 48; DB 5; Length 247;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
|| |||||
Db 45 GFAFSSYDMS 54

RESULT 7
PCT-US94-07659-6
Sequence 6, Application PC/TUS9407659
GENERAL INFORMATION:
APPLICANT: Young, Peter
APPLICANT: Gross, Mitchell
APPLICANT: Jonak, Zdenka L.
APPLICANT: Theisen, Timothy
APPLICANT: Hurle, Mark
APPLICANT: Jackson, Jeffrey R.
TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithline Beecham Corporation - Corp.
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-6
Query Match 88.7%; Score 47; DB 5; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GFTFSSYDMS 10
|| |||||
Db 26 GTFSSYDMS 35
RESULT 8
US-08-478-039-71
Sequence 71, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-34
US-08-478-039-71

Query Match 88.7%; Score 47; DB 1; Length 123;
Best Local Similarity 80.0%; Pred. No. 0.094;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTFSSYDMS 10
Db 26 GTFSTYDMT 35

RESULT 9
US-08-478-039-104
; Sequence 104, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid

; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #34
US-08-478-039-104

Query Match 88.7%; Score 47; DB 1; Length 123;
Best Local Similarity 80.0%; Pred. No. 0.094;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTFSSYDMS 10
Db 26 GTFSTYDMT 35

RESULT 10
US-08-476-349A-71
; Sequence 71, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey

; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-34
US-08-476-349A-71

Query Match 88.7%; Score 47; DB 1; Length 123;
Best Local Similarity 80.0%; Pred. No. 0.094;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
Db 26 GFTFSTYDMT 35
|||||:||||

RESULT 11
US-08-476-349A-104
; Sequence 104, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
-CHROMOSOME/SEGMENT: #34
US-08-476-349A-104

Query Match 88.7%; Score 47; DB 1; Length 123;
Best Local Similarity 80.0%; Pred. No. 0.094;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
Db 26 GFTFSTYDMT 35
|||||:||||

RESULT 12
US-08-665-202-31
; Sequence 31, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-31

Query Match 86.8%; Score 46; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
Db 26 GFTFSSYEMN 35
|||||:||||

RESULT 13
US-08-545-809A-101
; Sequence 101, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku

```
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-101

Query Match      86.8%; Score 46; DB 3; Length 116;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTFSSYDM 9
Db      45 GFTFSNYDM 53

RESULT 14
US-08-983-607-36
; Sequence 36, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
```

```
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM14 scFv antibodies obtained from
; LIBRARY: fuses5 fusion phage construct
; CLONE: V474
; FEATURE:
; NAME/KEY: heavy chain
US-08-983-607-36

Query Match      86.8%; Score 46; DB 4; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GFTFSSYDMS 10
Db      26 GFTFSSYDMS 35

RESULT 15
US-08-276-852-80
; Sequence 80, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-80

Query Match 86.8%; Score 46; DB 1; Length 122;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 23 GFTFSSYEMN 32

Search completed: August 19, 2002, 06:34:38
Job time: 1199 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:03 ; Search time 78.53 seconds
(without alignments)
11.012 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QQSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	88.2	104	2 B43413	Ig kappa chain V r
2	45	88.2	138	2 A26471	Ig kappa chain pre
3	40	78.4	106	2 PL0267	Ig kappa chain V r
4	40	78.4	106	2 PC4282	Ig kappa chain (an
5	40	78.4	107	2 C45722	anti-glycoprotein
6	39	76.5	67	2 PH1081	Ig light chain V r
7	39	76.5	69	2 PH1080	Ig light chain V r
8	39	76.5	553	2 T15220	hypothetical prote
9	38	74.5	107	2 A45722	anti-glycoprotein
10	38	74.5	123	2 S35479	Ig kappa chain pre
11	38	74.5	506	2 AH2352	thymidylate kinase
12	37	72.5	102	2 S26346	Ig kappa chain V r
13	37	72.5	128	2 PN0445	Ig kappa chain pre
14	37	72.5	144	2 PN0406	Ig kappa chain pre
15	37	72.5	154	2 T17816	hypothetical prote
16	37	72.5	642	2 H69466	conserved hypothet
17	37	72.5	677	2 D97335	hypothetical prote
18	37	72.5	764	2 T48446	hypothetical prote
19	36	70.6	87	2 PH1082	Ig light chain V r
20	36	70.6	91	2 S37525	Ig kappa chain V r
21	36	70.6	108	2 C30502	Ig kappa chain V r
22	36	70.6	115	1 KVM5L7	Ig kappa chain pre
23	36	70.6	117	2 S40362	Ig kappa chain - h
24	36	70.6	169	2 D65126	probable general s
25	36	70.6	204	2 T32062	hypothetical prote
26	36	70.6	275	2 D70737	hypothetical prote
27	36	70.6	543	2 T06523	cytochrome P450 mo
28	36	70.6	1221	2 E83327	conserved hypothet
29	35	68.6	100	2 G81749	hypothetical prote

30 35 68.6 107 2 B45722 anti-glycoprotein
31 35 68.6 145 2 AD0929 conserved hypothet
32 35 68.6 181 2 A10861 syd protein [impor
33 35 68.6 235 1 S0MS parotid secretory
34 35 68.6 317 2 B82084 probable cobalamin
35 35 68.6 365 1 SAVLWE large surface anti
36 35 68.6 366 1 SAVLBD large surface anti
37 35 68.6 366 1 SAVLWD large surface anti
38 35 68.6 499 2 A27198 cellulase (EC 3.2.
39 35 68.6 508 2 A26874 cellulase (EC 3.2.
40 35 68.6 939 2 H71532 valine--trna ligas
41 35 68.6 939 2 H81686 valyl-trna synthet
42 35 68.6 940 2 F86502 alyl trna syntheta
43 35 68.6 940 2 B72120 valine--trna ligas
44 34 66.7 91 2 S37511 Ig kappa chain V r
45 34 66.7 96 2 JC5945 regulatory protein

ALIGNMENTS

RESULT 1

B43413
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B43413
R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct speci
A:Reference number: A43413; MUID:92388177
A:Accession: B43413
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <TOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 45; DB 2; Length 104;
Best Local Similarity 88.9%; Pred. No. 0.59; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0;

Qy 1 QQSGSWPLT 9

Db 86 QQSNWPLT 94

RESULT 2

A26471
Ig kappa chain precursor V region (MAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1998 #sequence_revision 05-Jun-1998 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K. Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
A:Reference number: A91572; MUID:87248058
A:Accession: A26471
A:Molecule type: mRNA
A:Residues: 1-138 <BUG>
A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 88.2%; Score 45; DB 2; Length 138;
Best Local Similarity 88.9%; Pred. No. 0.79; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0;

QY 1 QOSGSWPLT 9
 Db 109 QOSNSWPLT 117

RESULT 3
 PL0267
 Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C:Accession: PL0267
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0267
 A:Molecule type: mRNA
 A:Residues: 1-106 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-97/Region: complementarity-determining 3
 F:98-106/Region: framework 4

Query Match 78.4%; Score 40; DB 2; Length 106;
 Best Local Similarity 77.8%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSGSWPLT 9
 Db 89 QOSNSWPLT 97

RESULT 4

PC4282
 Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
 C:Accession: PC4282; PC4284
 R:Suzuki, H.; Takemura, H.; Sekine, Y.; Kashiwagi, H.
 Biochem. Biophys. Res. Commun. 232, 101-106, 1997
 A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltrating
 A:Reference number: PC4279; MUID:97236289
 A:Accession: PC4282
 A:Molecule type: protein
 A:Residues: 1-106 <SUZ>
 A:Note: E-42
 A:Accession: PC4284
 A:Molecule type: protein
 A:Residues: 1-106 <SU2>
 A:Note: E-56
 C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren's
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 40; DB 2; Length 106;
 Best Local Similarity 77.8%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSGSWPLT 9
 Db 87 QORASWPLT 95

RESULT 5

C45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: C45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdaloovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: C45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <STM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120591)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 40; DB 2; Length 107;
 Best Local Similarity 77.8%; Pred. No. 4.5;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSGSWPLT 9
 Db 89 QOSNSWPLT 97

RESULT 6

PH1081
 Ig light chain V region (clone 165.6) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
 C:Accession: PH1081
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1081
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-67 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 76.5%; Score 39; DB 2; Length 67;
 Best Local Similarity 77.8%; Pred. No. 4.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSGSWPLT 9
 Db 58 QOSNSWPLT 66

RESULT 7

PH1080
 Ig light chain V region (clone 165.60) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
 C:Accession: PH1080
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1080
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-69 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 76.5%; Score 39; DB 2; Length 69;
 Best Local Similarity 77.8%; Pred. No. 4.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||| ||| |
 Db 60 QQSNSWPQT 68

RESULT 8
 T15220
 hypothetical protein F57C9.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15220
 R:Geisler, C.; Kramer, J.; Gibson, A.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid F57C9.
 A:Reference number: Z18309
 A:Accession: T15220
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-553 <GET>
 A:Cross-references: EMBL:AF003142; NID:g2088743; PID:g2088751; PIDN:AAE54191.1; GSPDB:GN
 A:Experimental source: strain Bristol N2; clone F57C9
 C:Genetics:
 A:Gene: CESP:F57C9.8
 A:Map position: 1
 A:Introns: 184/1; 233/3; 286/3; 496/1

Query Match 76.5%; Score 39; DB 2; Length 553;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 |:|||||:
 Db 373 QRSGSWPFS 381

RESULT 9
 A45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fra
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdaloovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
 A:Reference number: A45722; MUID:93100833
 A:Accession: A45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 38; DB 2; Length 107;
 Best Local Similarity 77.8%; Pred. No. 9.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||| ||| |
 Db 89 QQSNSWPHT 97

RESULT 10
 S35479

Ig kappa chain precursor V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: S35479
 R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
 Nucleic Acids Res. 20, 4099, 1992
 A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from
 A:Reference number: S35479; MUID:92375706
 A:Accession: S35479
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-123 <TAK>
 A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
 C:Genetics:
 A:Map position: 6
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
 F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
 F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 38; DB 2; Length 123;
 Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||| ||| |
 Db 101 QQSNSWPHT 109

RESULT 11

AH3252
 thymidylate kinase (EC 2.7.4.9) [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C:Accession: AH3252
 R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Muijer, C.; Los, T.; Ivanov
 ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AH3252
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-506 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAL511187.1; PID:g17981871; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0005
 A:Map position: 1
 C:Keywords: phosphotransferase

Query Match 74.5%; Score 38; DB 2; Length 506;
 Best Local Similarity 75.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QSGSWPLT 9
 | | | | | |
 Db 135 QQGWPLT 142

RESULT 12

S26346
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26346
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protei
 A:Reference number: S26309; MUID:91341421

A:Accession: S26346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 102;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
|||:||||
Db 87 QOQNTWPT 95

RESULT 13

PN0445
Ig kappa chain precursor V-I region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PN0445
R:Kaluza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A:Title: A general method for chimeraization of monoclonal antibodies by inverse polymerase chain reaction
A:Reference number: PN0444; MUID:93138402

A:Accession: PN0445
A:Molecule type: mRNA
A:Residues: 1-128 <KAL>

A:Cross-references: GB:L02347
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-10/Domain: signal sequence #status predicted <SIG>
F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F:126-100/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 128;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
|||:||||
Db 99 QOQNTWPT 107

RESULT 14

PL0106
Ig kappa chain precursor V-J-C region (Ls1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma secretory cell line to the immunoglobulin gene locus
A:Reference number: PL0106; MUID:89235583

A:Accession: PL0106
A:Molecule type: mRNA
A:Residues: 1-144 <SIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-137/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match 72.5%; Score 37; DB 2; Length 144;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
|||:||||
Db 109 QOQNSWPLT 117

RESULT 15

TL7816
hypothetical protein a317L - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: TL7816
R:Graves, M.V.; Van Etten, J.L.
Submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806
A:Accession: TL7816
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-154 <GRA>
A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96685.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Note: a317L

Query Match 72.5%; Score 37; DB 2; Length 154;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPL 8
|||:||||
Db 33 QOQSGSWPV 40

Search completed: August 19, 2002, 06:36:04
Job time: 1285 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:05 ; Search time 51.81 Seconds
(without alignments)
6.726 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QSGSWPLT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	78.4	745	1 CUL2_HUMAN	Q13617 homo sapien
2	38	74.5	418	1 ORL3_DROME	Q9VX10 drosophila
3	38	74.5	471	1 P2X2_HUMAN	Q9UB19 homo sapien
4	36	70.6	115	1 KV51_MOUSE	P01642 mus musculus
5	36	70.6	169	1 GSPH_ECOLI	P41443 escherichia
6	36	70.6	544	1 C821_PEA	Q43068 pisum sativ
7	35	68.6	235	1 PSP_MOUSE	P07743 mus musculus
8	35	68.6	365	1 VMSA_HPBDC	P30029 duck hepati
9	35	68.6	366	1 VMSA_HPBDB	P17194 duck hepati
10	35	68.6	366	1 VMSA_HPBDB	P17195 duck hepati
11	35	68.6	499	1 GUN1_BACSU	P07983 bacillus su
12	35	68.6	939	1 SYV_CHLMU	Q9PK91 chlamydia m
13	35	68.6	939	1 SYV_CHLTPN	O84304 chlamydia t
14	35	68.6	940	1 SYV_CHLTPN	Q92987 chlamydia p
15	34	66.7	92	1 CAPC_RHOOP	P95609 rhodococcus
16	34	66.7	96	1 CTCL_ACILW	Q33947 acinetobact
17	34	66.7	146	1 YFCK_ECOLI	P77656 escherichia
18	34	66.7	470	1 IE63_HSVB	P28939 equine herp
19	34	66.7	470	1 IE63_HSVK	Q05906 equine herp
20	34	66.7	540	1 NUSA_MYCPN	P75591 mycoplasma
21	34	66.7	777	1 BISC_ECOLI	P20099 escherichia
22	34	66.7	1047	1 RIR1_CHLMU	Q9PL93 chlamydia m
23	34	66.7	1456	1 RRPO_PVX	P09395 potato viru
24	34	66.7	1456	1 RRPO_PVXCP	P22591 potato viru
25	34	66.7	1456	1 RRPO_PVXHB	Q07630 potato viru
26	34	66.7	1456	1 RRPO_PVXX3	P17779 potato viru
27	34	66.7	2329	1 YS89_CAEEL	Q09624 caenorhabdi
28	34	66.7	226	1 NUKM_NEUCR	Q47950 neurospora
29	33	64.7	251	1 BIQC_ECOLI	P12999 escherichia
30	33	64.7	300	1 GP40_HUMAN	Q14842 homo sapien
31	33	64.7	432	1 NFPI_RAT	Q9EP86 rattus norv
32	33	64.7	468	1 NIEB_KLEPN	P10390 klebsiella
33	33	64.7	516	1 Y4NN_RHISN	P55585 rhizobium s

34	33	64.7	517	1 LAD1_HUMAN	O00515 homo sapien
35	33	64.7	796	1 PTR_A_RAT	Q03348 rattus norv
36	33	64.7	802	1 PTR_A_HUMAN	P18433 homo sapien
37	33	64.7	829	1 PTR_A_MOUSE	P18052 mus musculu
38	33	64.7	3329	1 BRC2_MOUSE	P97929 mus musculu
39	33	64.7	3418	1 BRC2_HUMAN	P51587 homo sapien
40	32	62.7	302	1 CYSD_BUCAI	P57499 buchnera ap
41	32	62.7	302	1 CYSD_ECOLI	P21156 escherichia
42	32	62.7	336	1 CHI2_ORYSA	P25765 oryza sativ
43	32	62.7	401	1 FXH1_MOUSE	O88621 mus musculu
44	32	62.7	402	1 OPDE_PSEAE	Q01602 pseudomonas
45	32	62.7	471	1 STCH_HUMAN	P48723 homo sapien

ALIGNMENTS

RESULT 1
CUL2_HUMAN STANDARD; PRT: 745 AA.
AC Q13617; O00200; Q9UNF9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cullin homolog 2 (CUL-2).
GN CUL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT SER-109.
RC TISSUE=Kidney;
RX MEDLINE=97225922; PubMed=9122164;
RA Pause A., Lee S., Worrel R., Chen D.Y.T., Burgess W.H.,
RA Linehan W.M., Klausner R.D.;
RT "The von Hippel-Lindau tumor-suppressor gene product forms a stable
RT complex with human CUL-2, a member of the Cdc53 family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:2156-2161(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT SER-109.
RC TISSUE=Brain;
RX MEDLINE=99194561; PubMed=10092517;
RA Wada H., Yeh E.T.H., Kamitani T.;
RT "Identification of NEDD8-conjugation site in human cullin-2.";
RL Biochem. Biophys. Res. Commun. 257:100-105(1999).
RN [3]
RP SEQUENCE OF 95-745 FROM N.A.
RX MEDLINE=96279828; PubMed=8681378;
RA Kipreos E.T., Lander L.E., Wing J.P., He W.W., Hedgecock E.M.;
RT "cul-1 is required for cell cycle exit in C. elegans and identifies a
RT novel gene family.";
RL Cell 85:829-839(1996).
CC -!- FUNCTION: FORMS A STABLE COMPLEX WITH THE VHL TUMOR SUPPRESSOR.
CC -!- SIMILARITY: BELONGS TO THE CULLIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U83410; AAC51190.1; -;
DR EMBL; AF126404; AAD23581.1; -;
DR EMBL; U58088; AAC50545.1; -;
DR MIM; 603135; -;
DR InterPro; IPR001373; Cullin.
DR Pfam; PF00886; Cullin; 1.
DR SMART; SM00182; CULLIN; 1.
DR PROSITE; PS01256; CULLIN_1; 1.
DR PROSITE; PS50069; CULLIN_2; 1.

KW Polymorphism. 689 NEDD8
 FT BINDING 689 N -> S.
 FT VARIANT 109 /FTIG=VAR_011374.
 FT CONFLICT 95 SRGA -> IRHE (IN REF. 3).
 FT CONFLICT 681 Q -> H (IN REF. 3).
 SQ SEQUENCE 745 AA; 86983 MW; 30647248F671AB0E CRC64;

Query Match 78.4%; Score 40; DB 1; Length 745;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9
 I:|||||
 Db 513 QAGAWPLT 520

RESULT 2
 OR13_DROME

ID Q9VXL0; STANDARD; PRT; 418 AA.

AC Q9VXL0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Putative odorant receptor 13a.
 GN OR13A OR G12697.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

SEQUENCE FROM N.A.

RX STRAIN=BERKELEY;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foaier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy L., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).
 RN [2]
 RP CONCEPTUAL TRANSLATION.
 RA Robertson H.M.;
 RL Unpublished observations (MAY-2001).
 CC -1- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO DROSOPHILA ODORANT RECEPTOR FAMILY OF G-
 CC PROTEIN COUPLED RECEPTORS.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS AT SEVERAL POSITIONS FROM THAT
 CC SHOWN DUE TO DIFFERENCES IN THE PREDICTION OF SPICE SITES.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; AE003500; AAF48549.1; ALT_SEQ.
 DR FlyBase; FBgn0030715; Or13a.
 DR InterPro; IPR004117; 7tm_6.
 DR Pfam; PF02949; 7tm_6; 1.
 KW Hypothetical protein; Transmembrane; G-protein coupled receptor;
 KW GPCProtein; Olfaction; Multigene family.
 FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 39 59 1 (POTENTIAL).
 FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 71 91 2 (POTENTIAL).
 FT DOMAIN 92 140 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 141 161 3 (POTENTIAL).
 FT DOMAIN 162 195 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 196 216 4 (POTENTIAL).
 FT DOMAIN 217 273 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 274 294 5 (POTENTIAL).
 FT DOMAIN 295 299 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 300 320 6 (POTENTIAL).
 FT DOMAIN 321 385 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 386 406 7 (POTENTIAL).
 FT DOMAIN 407 418 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 22 22 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 118 118 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 418 AA; 48263 MW; 6E8EC466CF246F0E CRC64;

Query Match 74.5%; Score 38; DB 1; Length 418;
 Best Local Similarity 85.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPLT 9
 Db 22 NGSWPLT 28

RESULT 3
 P2X2_HUMAN

ID P2X2_HUMAN STANDARD; PRT; 471 AA.
 AC Q9UBU9; Q9Y637; Q9Y638; Q9UHD5; Q9UHD6; Q9UHD7; Q9NR37; Q9NR38;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE P2X purinoceptor 2 (ATP receptor) (P2X2) (Purinergic receptor).
 GN P2RX2 OR P2X2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
 RC TISSUE=pituitary;

DE transport protein hofH).
GN HOFH OR HOFH OR B3329.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RN SEQUENCE OF 1-30 FROM N.A.
RP STRAIN=K12;
RC MEDLINE=95204361; PubMed=7896718;
RX Stojiljkovic I., Schoenherr R., Kusters J.G.;
RT "Identification of the hopg gene, a component of Escherichia coli
RT K-12 type II export system, and its conservation among different
RT pathogenic Escherichia coli and Shigella isolates.";
RL J. Bacteriol. 177:1892-1895(1995)
CC -!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
CC EXPORT OF PROTEINS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PULH/OUTH/XPSH/XCPU FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U18997; AAA58126.1; -;
DR EMBL; AF000409; AAC76354.1; -;
DR EMBL; U20786; AAA69032.1; -;
DR EcoGene; EG12887; hofH.
DR InterPro; IPR002416; Bac_GSPH.
DR PRINTS; PR00885; BCTERIALGSPH.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Transport; Methylation; Complete proteome.
FT PROPEP 1 6 BY SIMILARITY
FT CHAIN 7 169 PUTATIVE GENERAL SECRETION PATHWAY
FT MOD_RES 7 METHYLATION (BY SIMILARITY).
SQ SEQUENCE 169 AA; 18565 MW; D42B1127FBB81A09 CRC64;
Query Match 70.6%; Score 36; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 SGSWPL 8
Db 154 SGSWPL 159
RESULT 6
ID C82L_PEA
AC C82L_PEA STANDARD; PRT; 544 AA.
AC Q43068;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome P450 82A1 (EC 1.14.-.-) (CYPLXXII) (Fragment).
GN CYP82A1 OR CYP82.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=96417083; PubMed=8819874;
RA Frank M.R., Deyneka J.M., Schuler M.A.;
RT "Cloning of wound-induced cytochrome P450 monooxygenases expressed in
RT pea.";
RL Plant Physiol. 110:1035-1046(1996).
RN [2]
RN REVISIONS TO 47-48; 127; 198-199; 304; 311; 333-335 AND 454.
RA Frank M.R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- INDUCTION: By wounding.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U29333; AAC49188.2; -;
DR InterPro; IPR001128; Cyt_P450.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00385; P450
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Membrane; Heme.
FT NON_TER 1 1
FT BINDING 480 480 HEME (BY SIMILARITY).
SQ SEQUENCE 544 AA; 62055 MW; DE006067C33DADE5 CRC64;
Query Match 70.6%; Score 36; DB 1; Length 544;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 SGSWPL 8
Db 39 SGSWPL 44
RESULT 7
ID PSP_MOUSE
AC PSP_MOUSE STANDARD; PRT; 235 AA.
AC P07743;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Parotid secretory protein precursor (PSP).
GN PSP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Parotid gland;
RX MEDLINE=85215456; PubMed=2582349;
RA Madsen H.O., Hjorth J.P.;
RT "Molecular cloning of mouse PSP mRNA.";
RL Nucleic Acids Res. 13:1-13(1985).
RN [2]
RN SEQUENCE OF 1-87 FROM N.A.
RC STRAIN=C3H; TISSUE=Spleen;
RX MEDLINE=87004556; PubMed=2428613;
RA Poulsen K., Jakobsen B.K., Mikkelson B.M., Harnmark K.,
RA Nielsen J.T., Hjorth J.P.;
RT "Coordination of murine parotid secretory protein and salivary

```

RT amylase expression."
RL EMBO J. 5:1891-1896(1986).
CC -I- FUNCTION: PSP IS THE MOST ABUNDANT PROTEIN IN THE PAROTID GLAND.
CC ITS FUNCTION IS NOT KNOWN; HOWEVER, ITS PRODUCTION IS COORDINATED
CC WITH THAT OF SALIVARY AMYLASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01697; CAA25846.1; -.
DR EMBL; M26807; AAA40009.1; -.
DR EMBL; M26806; AAA40009.1; JOINED.
DR PIR; A23031; SOMS.
DR MGD; MGI:97787; Psp.
KW Parotid gland; Signal.
FT SIGNAL 1 20
FT CHAIN 21 235
SQ SEQUENCE 235 AA; 24753 MW; 23311BAE1E5E2EF3 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 235;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPL 8
Db 54 QQATSWPL 61

RESULT 8
VMSA_HPBDC STANDARD; PRT; 365 AA.
AC P30029;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Duck hepatitis B virus (strain China) (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBL_TaxID=31510;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045091; PubMed=2235506;
RA Tong S., Mattes F., Teubner K., Blum H.E.;
RT "Complete nucleotide sequence of a Chinese duck hepatitis B virus.";
RL Nucleic Acids Res. 18:6139-6139(1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M21953; AAA45746.1; -.
DR PIR; S12842; SAVLWE.
DR InterPro; IPR000349; Hepadnavir_surfag.
DR Pfam; PF00695; VMSA; 2.
KW Antigen.
FT PROPEP 1 198
FT CHAIN 199 365
FT CARBOHYD 297 297
SQ SEQUENCE 365 AA; 40511 MW; 67F3A4174CB7D884 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 365;

```

```

Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7
Db 96 QQQGAWP 102

RESULT 9
VMSA_HPBDC STANDARD; PRT; 366 AA.
AC P17194;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Duck hepatitis B virus (brown Shanghai duck isolate S5) (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBL_TaxID=10439;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90085807; PubMed=2596031;
RA Uchida M., Esumi M., Shikata T.;
RT "Molecular cloning and sequence analysis of duck hepatitis B virus
RL genomes of a new variant isolated from Shanghai ducks.";
RN Virology 173:600-606(1989).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M32990; AAA45755.1; ALT_INIT.
DR PIR; C33746; SAVLBD.
DR InterPro; IPR000349; Hepadnavir_surfag.
DR Pfam; PF00695; VMSA; 2.
KW Antigen.
FT PROPEP 1 199
FT CHAIN 200 366
FT CARBOHYD 170 170
FT CARBOHYD 298 298
SQ SEQUENCE 366 AA; 40897 MW; 5B72879A182EFF38 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 366;
Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7
Db 96 QQQGAWP 102

RESULT 10
VMSA_HPBDC STANDARD; PRT; 366 AA.
AC P17195;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Duck hepatitis B virus (white Shanghai duck isolate S31) (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBL_TaxID=10440;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90085807; PubMed=2596031;
RA Uchida M., Esumi M., Shikata T.;

```

RT "Molecular cloning and sequence analysis of duck hepatitis B virus
 RL Genomes of a new variant isolated from Shanghai ducks.";
 CC Virology 173:600-606(1989).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M22991; AAA45752.1; ALT_INIT.
 DR PIR; D33746; SAVLWD.
 DR InterPro; IPR000349; Hepadnavir_surfac.
 DR Pfam; PF00695; VMSA; 2.
 KW Antigen.
 FT PROPEP 1 199
 FT CHAIN 200 366 MAJOR SURFACE ANTIGEN.
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 366 AA; 40858 MW; CF60E78B7B2FCD52 CRC64;
 CC -----
 Query Match 68.6%; Score 35; DB 1; Length 366;
 Best Local Similarity 71.4%; Pred. No. 40;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQSGSWP 7
 II I I I I
 Db 96 QQQGAWP 102
 CC -----
 RESULT 11
 GUN1_BACSU STANDARD; PRT; 499 AA.
 ID GUN1_BACSU
 AC P07983;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
 DE (Cellulase).
 GN BGLC OR GLB.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DLG;
 RX MEDLINE=87194581; PubMed=3106328;
 RA Robson L.M.; Chambliss G.H.;
 RT "Endo-beta-1,4-glucanase gene of Bacillus subtilis DLG.";
 RL J. Bacteriol. 169:2017-2025(1987).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M16185; AAA22496.1; ALT_INIT.
 DR PIR; A26874; A26874.
 DR HSP; O85465; 1A3H.
 DR InterPro; IPR001956; CBD_3.
 DR InterPro; IPR001547; Glyco_hydro_F5.
 DR Pfam; PF00942; CBD_3; 1.

DR Pfam; PF00150; cellulase; 1.
 DR PRODOM; PD001947; CBD_3; 1.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 499 ENDOGLUCANASE.
 FT ACT_SITE 169 169 PROTON DONOR (BY SIMILARITY).
 FT ACT_SITE 257 257 NUCLEOPHILE (BY SIMILARITY).
 FT DOMAIN 350 499 CELLULOSE-BINDING (BY SIMILARITY).
 SQ SEQUENCE 499 AA; 55187 MW; 339D04EE95A63EE1 CRC64;
 CC -----
 Query Match 68.6%; Score 35; DB 1; Length 499;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QSGSWPLT 9
 : : I I I I
 Db 309 KTGGMPLT 316
 CC -----
 RESULT 12
 SYV_CHLMU STANDARD; PRT; 939 AA.
 ID SYV_CHLMU
 AC Q9PK91;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Valyl--trna synthetase (EC 6.1.1.9) (Valine--trna ligase) (ValRS).
 GN VALS OR TC0576.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MOPN / NIGG;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 CC -!- CATALYTIC ACTIVITY: ATP + L-valine + trna(Val) = AMP + diphosphate
 CC + L-valyl--trna(Val).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AE002326; AAF39411.1; -.
 DR HSP; P96142; IGAX.
 DR TIGR; TC0576; -.
 DR InterPro; IPR002300; trna-synt_la.
 DR InterPro; IPR001412; trna-synt_i.
 DR InterPro; IPR002303; trna-synt_val.
 DR Pfam; PF00133; trna-synt_1; 1.
 DR PRINTS; PR00986; TRNASYNTHAL.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 KW Aminoacyl--trna synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 47 57 "HIGH" REGION.
 FT SITE 564 568 "KMSKS" REGION.
 FT BINDING 567 567 ATP (BY SIMILARITY).

SQ SEQUENCE 939 AA; 107121 MW; 1D141FA682187869 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 939;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCSWPLT 9
II IIII
DB 460 SGLWPLT 466

RESULT 13

```

SYV_CHLTR
ID SYV_CHLTR STANDARD; PRT; 939 AA.
AC OB4304;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).
GN VALS OR CT302.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/CX;
RA Kalman S., Mitchell W., Marathe R., Lammel C.J., Fan J., Marathe R., Aravind L., Stephens R.S., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
RA "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate + L-valyl-tRNA(Val).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
EMBL; AE001302; AAC67895.1; -
DR HSP; P96142; IGAX.
DR InterPro; IPR002300; tRNA-synt_la.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002303; tRNA-synt_val.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00986; TRNASYNTHVAL.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.
FT SITE 47 57 "HIGH" REGION.
FT SITE 563 566 "KMSKS" REGION.
FT BINDING 566 ATP (BY SIMILARITY).
SQ SEQUENCE 939 AA; 107036 MW; CEB8449DC7BB9066 CRC64;

```

Query Match 68.6%; Score 35; DB 1; Length 939;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCSWPLT 9
II IIII
DB 459 SGLWPLT 465

RESULT 14

```

SYV_CHLPN
ID SYV_CHLPN STANDARD; PRT; 940 AA.
AC Q92987; Q9JQA5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).
GN VALS OR CPN0094 OR CP0680.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
RT Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=JI38;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae JI38 from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate + L-valyl-tRNA(Val).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
EMBL; AE001595; AAD18247.1; -
DR EMBL; AE002226; AAF38490.1; -
DR EMBL; AP002545; BAA98304.1; -
DR HSP; P96142; IGAX.
DR TIGR; CP0680; -.
DR InterPro; IPR002300; tRNA-synt_la.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002303; tRNA-synt_val.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00986; TRNASYNTHVAL.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.
FT SITE 47 57 "HIGH" REGION.
FT SITE 564 568 "KMSKS" REGION.
FT BINDING 567 567 ATP (BY SIMILARITY).
SQ SEQUENCE 940 AA; 107111 MW; 28054683FB9D0404 CRC64;

```

Query Match 68.6%; Score 35; DB 1; Length 940;
 Best Local Similarity 85.7%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGSWPLT 9
 Db 460 SGLWPLT 466

RESULT 15
 CATC_RHOOP STANDARD; PRT; 92 AA.
 AC P95609;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Muconolactone delta-isomerase (EC 5.3.3.4) (Miae).
 GN CATC.
 OS Rhodococcus opacus (Nocardia opaca).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
 OX NCBI_TaxID=37919;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
 RC STRAIN=ICP;
 RX MEDLINE=97144521; PubMed=8990288;
 RA Eulberg D., Golovleva L.A., Schloemann M.;
 RT "Characterization of catechol catabolic genes from Rhodococcus
 erythropolis ICP".
 RL J. Bacteriol. 179:370-381(1997).
 CC -I- CATALYTIC ACTIVITY: 2,5-dihydro-5-oxofuran-2-acetate = 3,4-
 CC dihydro-5-oxofuran-2-acetate.
 CC -I- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
 CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
 CC -I- SUBUNIT: HOMODECAMER (BY SIMILARITY).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X99622; CAA67935.1; -
 DR InterPro; IPR003464; Miae.
 DR Pfam; PF02426; Miae; 1.
 KW Aromatic hydrocarbons catabolism; Isomerase.
 FT INIT_MET 0
 SQ SEQUENCE 92 AA; 10780 MW; 9CCE5A17DED4B153 CRC64;

Query Match 66.7%; Score 34; DB 1; Length 92;
 Best Local Similarity 71.4%; Pred. No. 16;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
 Db 35 QRSWKWP 41

Search completed: August 19, 2002, 06:59:07
 Job time: 1372 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:08 ; Search time 140.4 seconds
(without alignments)
11.089 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	80.4	153	Q9YH52	Q9YH52 gallus gall
2	40	78.4	706	Q9D4H8	Q9D4H8 mus musculus
3	40	78.4	1194	Q9VSI2	Q9VSI2 drosophila
4	39	76.5	553	Q01825	Q01825 caenorhabdi
5	39	76.5	793	Q01443	Q01443 caenorhabdi
6	37	72.5	154	Q84631	Q84631 paramecium
7	37	72.5	612	Q041S9	Q041S9 oryza sativ
8	37	72.5	642	Q28537	Q28537 archaeoglob
9	37	72.5	677	Q97DD2	Q97DD2 clostridium
10	37	72.5	737	Q9U9P1	Q9U9P1 drosophila
11	37	72.5	764	Q91Z75	Q91Z75 arabidopsis
12	37	72.5	781	Q9VRA2	Q9VRA2 drosophila
13	37	72.5	1346	Q98IR5	Q98IR5 rhizobium 1
14	36	70.6	204	Q95X90	Q95X90 caenorhabdi
15	36	70.6	275	Q50711	Q50711 mycobacteri
16	36	70.6	396	Q9RDF1	Q9RDF1 streptomyce

17	36	70.6	540	10	Q9FVK6	Q9FVK6 pisum sativ
18	36	70.6	613	5	Q9VHU1	Q9VHU1 drosophila
19	36	70.6	847	10	Q9SGW2	Q9SGW2 arabidopsis
20	36	70.6	1221	15	Q910U2	Q910U2 pseudomonas
21	36	70.6	1903	5	Q9U5D6	Q9U5D6 plautia sta
22	35	68.6	100	16	Q9PLT4	Q9PLT4 chlamydia m
23	35	68.6	123	4	Q9UKB9	Q9UKB9 homo sapien
24	35	68.6	235	11	Q9D734	Q9D734 mus musculu
25	35	68.6	317	15	Q9KPT7	Q9KPT7 vibrio chol
26	35	68.6	327	12	Q67852	Q67852 duck hepati
27	35	68.6	329	12	Q91HP5	Q91HP5 duck hepati
28	35	68.6	330	12	Q72885	Q72885 duck hepati
29	35	68.6	330	12	Q66405	Q66405 duck hepati
30	35	68.6	366	12	Q66404	Q66404 duck hepati
31	35	68.6	407	2	Q9R904	Q9R904 brachyspira
32	35	68.6	413	2	Q9R905	Q9R905 brachyspira
33	35	68.6	415	2	Q9R908	Q9R908 treponema h
34	35	68.6	415	2	Q9ZHI1	Q9ZHI1 brachyspira
35	35	68.6	415	2	Q9R902	Q9R902 brachyspira
36	35	68.6	416	2	Q9ZHI3	Q9ZHI3 brachyspira
37	35	68.6	418	2	Q9ZHI6	Q9ZHI6 brachyspira
38	35	68.6	420	2	Q9R907	Q9R907 treponema h
39	35	68.6	420	2	Q9ZHI7	Q9ZHI7 serpulina s
40	35	68.6	421	2	Q9R906	Q9R906 brachyspira
41	35	68.6	421	2	Q9ZHI8	Q9ZHI8 brachyspira
42	35	68.6	422	2	Q9R903	Q9R903 brachyspira
43	35	68.6	423	2	Q9ZHI2	Q9ZHI2 brachyspira
44	35	68.6	423	2	Q9ZHI0	Q9ZHI0 brachyspira
45	35	68.6	424	2	Q9ZHI9	Q9ZHI9 brachyspira

ALIGNMENTS

RESULT 1

Q9YH52 PRELIMINARY; PRT; 153 AA.

AC Q9YH52
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE HYPOTHEICAL 17.4 KDA PROTEIN.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-H.B19;

RX MEDLINE=90077532; PubMed=2592020;

RA Kaufman J., Salomonsen J., Skjoldt K.;

RT "B-G CDNA clones have multiple small repeats and hybridize to both

RL chicken MHC regions.";

RL Immunogenetics 30:440-451(1989).

DR EMBL; M27666; AAA69840.1; -

KW Hypothetical protein.

SQ SEQUENCE 153 AA; 17404 MW; 6D344F572FA7EE48 CRC64;

Query Match 80.4%; Score 41; DB 13; Length 153;
Best Local Similarity 87.5%; Pred. No. 6.8;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSGSWPLT 9

Db 65 QSGHWPLT 72

RESULT 2

Q9D4H8 PRELIMINARY; PRT; 706 AA.

ID Q9D4H8

AC Q9D4H8;

DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE 4932411N15RIK PROTEIN.
 GN 4932411N15RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK016520; BAB30283.1; -;
 DR MGD; MGI:1922970; 4932411N15RIK.
 DR InterPro; IPR001373; Cullin.
 DR Pfam; PF00888; Cullin; 2.
 DR SMART; SM00182; CULLIN; 1.
 DR PROSITE; PS01256; CULLIN; 1; 1.
 DR PROSITE; PS50069; CULLIN; 2; 1.
 SQ SEQUENCE 706 AA; 82298 MW; CBB796B20CA6E2B4 CRC64;

Query Match 78.4%; Score 40; DB 11; Length 706;
 Best Local Similarity 75.0%; Pred. No. 48;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 QSGSWPLT 9
 Db 513 QAGAWPLT 520
 ||:||||
 RESULT 3
 Q9VSI2 PRELIMINARY; PRT; 1194 AA.
 ID Q9VSI2;
 AC Q9VSI2;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CG7112 PROTEIN.
 GN CG7112.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003555; AAF50437.1; -;
 DR FlyBase; FBgn0035879; CG7112.
 DR InterPro; IPR000050; PID_domain.
 DR InterPro; IPR000195; RabGAP_TBC.
 DR Pfam; PF00566; TBC; 1.
 DR SMART; SM00462; PTB; 1.
 DR SMART; SM00164; TBC; 1.
 SQ SEQUENCE 1194 AA; 133393 MW; E0E3DB547B4924E0 CRC64;

Query Match 78.4%; Score 40; DB 5; Length 1194;
 Best Local Similarity 77.8%; Pred. No. 81;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 QSGSWPLT 9
 Db 461 QQSSSWPYT 469
 ||| ||| |
 RESULT 4
 O01825 PRELIMINARY; PRT; 553 AA.
 ID O01825
 AC O01825;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 60.8 KDA PROTEIN.
 GN F57C9.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for

RT Investigating biology. The C. elegans Sequencing Consortium. #;
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission. #";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003142; AAB54191.1; -;
 DR HSSP; P27986; IPBW.
 DR InterPro; IPR000198; RhoGAP.
 DR Pfam; PF00620; RhoGAP; 1.
 DR SMART; SM00324; RhoGAP; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 553 AA; 60849 MW; A50EDF9C2F560139 CRC64;

Query Match 76.5%; Score 39; DB 5; Length 553;
 Best Local Similarity 66.7%; Pred. No. 56;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGSWPLT 9
 I:|||||
 Db 373 QSGSWPFS 381

RESULT 5
 ID O01443 PRELIMINARY; PRT; 793 AA.
 AC O01443;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 87.6 KDA PROTEIN.
 GN C01F4.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE-99069613; PubMed-9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium. #";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Wamsley P., Geisel C.;
 RT "The sequence of C. elegans cosmid C01F4. #";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission. #";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U97192; AAB52435.2; -;
 DR InterPro; IPR000198; RhoGAP.
 DR Pfam; PF00620; RhoGAP; 1.
 DR SMART; SM00324; RhoGAP; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 793 AA; 87620 MW; 9BF89AEA54DAEA04 CRC64;

Query Match 76.5%; Score 39; DB 5; Length 793;
 Best Local Similarity 66.7%; Pred. No. 80;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGSWPLT 9
 I:|||||
 Db 613 QSGSWPFS 621

RESULT 6
 ID Q84631 PRELIMINARY; PRT; 154 AA.
 AC Q84631;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE A317L PROTEIN.
 GN A317L.
 OS Paramacium bursaria chlorella virus 1 (PBCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
 OC NCBI_taxid=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96187795; PubMed-8614977;
 RA Lu Z., Li Y., Que O., Kutish G.F., Rock D.L., Van Etten J.L.;
 RT "Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map
 positions 88 to 182. #";
 RL Virology 216:102-123(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20013326; PubMed-10544099;
 RA Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
 RA Lisec A.D., Nickerson K.W., Van Etten J.L.;
 RT "Chlorella virus PBCV-1 encodes a functional homosperridine
 RT synthase. #";
 RL Virology 263:254-262(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20478054; PubMed-11021991;
 RA Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
 RT "Characterization of a beta-1,3-glucanase encoded by chlorella virus
 PBCV-1. #";
 RL Virology 276:27-36(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Gurnon J.R., Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U42580; AAC9685.1; -;
 SQ SEQUENCE 154 AA; 18564 MW; 7B45EE2E7F518E15 CRC64;

Query Match 72.5%; Score 37; DB 12; Length 154;
 Best Local Similarity 75.0%; Pred. No. 35;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPL 8
| | | | |
DB 33 QTSQSWPV 40

RESULT 7
Q941S9 PRELIMINARY; PRT; 612 AA.
AC Q941S9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE HOMEODOMAIN PROTEIN.
GN P0005H10.19.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0005H10.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004127; BAB64282.1; -
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 612 AA; 65175 MW; A5B7AA5281CD28E4 CRC64;

Query Match 72.5%; Score 37; DB 10; Length 612;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWP 7
| | | | |
DB 93 QQHGSWP 99

RESULT 8
O28537 PRELIMINARY; PRT; 642 AA.
ID O28537
AC O28537;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-AUG-1998 (Tremblrel. 07, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN AFI737.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;

"The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).

DR EMBL; AE000983; AAB89512.1; -
DR TIGR; AFI737; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 642 AA; 74057 MW; 3E80BA624D747B5 CRC64;

Query Match 72.5%; Score 37; DB 17; Length 642;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSGSWPLT 9
| | | | |
DB 101 SSGWPLT 107

RESULT 9
Q97DD2 PRELIMINARY; PRT; 677 AA.
AC Q97DD2;
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE HIGHLY CONSERVED PROTEIN CONTAINING A DOMAIN RELATED TO CELLULOSE
DE CATALYTIC DOMAIN AND A THIOREDOXIN DOMAIN.
GN CAC3346.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Neelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabache F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007851; AAK81471.1; -
KW Complete proteome.
SQ SEQUENCE 677 AA; 78241 MW; F8ED0443466830F3 CRC64;

Query Match 72.5%; Score 37; DB 16; Length 677;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSGSWPLT 9
| | | | |
DB 108 SSGWPLT 114

RESULT 10
Q9U9P1 PRELIMINARY; PRT; 737 AA.
ID Q9U9P1
AC Q9U9P1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MAROON-LIKE PROTEIN.
GN MAL OR CG1692.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S;
RA Primus J., Arcangeli L., Finnerty V.;

"The maroon-like gene in Drosophila encodes a putative sulfatase.";
RT

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162681; AAD50777.1; -;
 DR FlyBase; FBgn0002641; mal
 SQ SEQUENCE 737 AA; 83139 MW; 76DFEE077E3F06D4 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 737;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GSWPLT 9

Db 533 GSWPLT 538

RESULT 11

ID Q9LZ75 PRELIMINARY; PRT; 764 AA.

AC Q9LZ75;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE HYPOTHEtical 86.3 KDA PROTEIN.

GN T32M21_100.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bevan M., Terry N., Ardiles W., Buysshaert C., Daseville R.,

RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,

RA Villarroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,

RA Rudd S., Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL162875; CAB85556.1; -;

KW Hypothetical protein.

SQ SEQUENCE 764 AA; 86299 MW; AFE0E482FF091CB8 CRC64;

Query Match 72.5%; Score 37; DB 10; Length 764;
 Best Local Similarity 62.5%; Pred. No. 1.7e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSGSWPLT 9

Db 112 ESGAWPVT 119

RESULT 12

ID Q9VRA2 PRELIMINARY; PRT; 781 AA.

AC Q9VRA2;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE MAL PROTEIN.

GN MAL OR CG1692.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng C., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

DR EMBL; AE003571; AAF50901.1; -;

DR FlyBase; FBgn0002641; mal.

SQ SEQUENCE 781 AA; 88103 MW; D2B2D5F52FDDF712 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GSWPLT 9

Db 533 GSWPLT 538

RESULT 13

ID Q98IR5

AC Q98IR5 PRELIMINARY; PRT; 1346 AA.

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)

DE MLL2286 PROTEIN.

GN MLL2286.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki I., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;

```

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RL Mesorhizobium loti.";
DR EMBL; AP002999; BAB49451.1; -.
DR InterPro; IPR003975; Shal_channel.
DR PRINTS; PR01497; SHALCHANNEL.
KW Complete proteome.
SQ SEQUENCE 1346 AA; 148727 MW; 7D1288A3FC26E879 CRC64;

Query Match 72.5%; Score 37; DB 16; Length 1346;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSGSWPLT 9
I:|||||
Db 204 QSGSWPKT 211

RESULT 14
Q95X90 PRELIMINARY; PRT; 204 AA.
AC Q95X90;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 22.8 KDA PROTEIN.
GN D2062.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Tin-Wollam A., Wohldmann P.;
RT "The sequence of C. elegans cosmid D2062.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston K.;
RT "Direct Submission.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016664; AAK72083.1; -.
KW Hypothetical protein.
SQ SEQUENCE 204 AA; 22758 MW; 27753F06500B35C8 CRC64;

Query Match 70.6%; Score 36; DB 5; Length 204;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSGSWPL 8
I|||I|
Db 107 QSGCWPL 113

RESULT 15
Q50711 PRELIMINARY; PRT; 275 AA.
AC Q50711;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

```

```

DE HYPOTHETICAL 28.7 KDA PROTEIN CY78.14.
GN RV3415C OR MTCY78.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
CC -!- SIMILARITY: STRONG, TO M.LEPRAE B229_CL_175 AND B1620_C3_232.
DR EMBL; 277165; CAB01008.1; -.
DR Tuberculiist; RV3415c; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 275 AA; 28659 MW; 47634BCA57C3CB3E CRC64;

```

```

Query Match 70.6%; Score 36; DB 16; Length 275;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSGSWPL 8
I|||||
Db 22 QPGSWPL 28

```

Search completed: August 19, 2002, 06:58:10
Job time: 1400 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:10 ; Search time 180.34 seconds

(without alignments)

5.543 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QQSGSWPLT 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

- 1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	51	100.0	9	19	AAW76035
2	51	100.0	9	22	AA861393
3	45	88.2	9	14	AAK37604
4	45	88.2	9	19	AAW76036
5	45	88.2	9	22	AA861394
6	45	88.2	107	14	AAK37612
7	45	88.2	107	14	AAK37610
8	44	86.3	9	19	AAW76013
9	44	86.3	9	22	AA861371
10	44	86.3	107	19	AAW76006
11	44	86.3	107	19	AAW76002

12	44	86.3	107	19	AAW76004
13	44	86.3	107	22	AA861388
14	44	86.3	107	22	AA861390
15	44	86.3	107	22	AA861360
16	44	86.3	107	22	AA861362
17	44	86.3	107	22	AA861364
18	42	82.4	9	21	AA810015
19	42	82.4	9	22	AA86063
20	42	82.4	9	22	AA86095
21	42	82.4	107	21	AA810023
22	42	82.4	107	22	AA86071
23	42	82.4	107	22	AA86109
24	42	82.4	127	21	AA832405
25	42	82.4	127	21	AA832407
26	41	80.4	105	20	AAW87456
27	41	80.4	105	20	AAW87458
28	41	80.4	107	20	AAW84098
29	41	80.4	108	20	AAW84094
30	41	80.4	112	20	AAW84100
31	40	78.4	107	14	AA83601
32	40	78.4	107	19	AAW58482
33	40	78.4	108	12	AA815438
34	40	78.4	109	15	AA852033
35	40	78.4	143	18	AAW19580
36	40	78.4	240	12	AA815443
37	40	78.4	1194	22	AB862985
38	39	76.5	9	19	AAW44180
39	39	76.5	9	20	AA826992
40	39	76.5	106	19	AAW71241
41	39	76.5	107	15	AA850190
42	39	76.5	107	18	AAW28531
43	39	76.5	107	19	AAW40820
44	39	76.5	107	20	AAW26979
45	39	76.5	107	20	AAW23243

ALIGNMENTS

RESULT 1
AAW76035
ID AAW76035 standard; Protein; 9 AA.
XX
AC AAW76035;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-L region CDR3 protein fragment #4.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

PD 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49872.

XX

LM609 antibody lig
A light chain vari
A light chain vari
Vitaxin light chai
Antibody LM609 lig
Light chain variab
H. pylori beta-ure
H. pylori beta-ure
H. pylori beta-ure
H. pylori beta-ure
Mouse anti-verotox
Mouse anti-verotox
Jk gene product.
Humanised anti-alp
Humanised anti-alp
Murine vitronectin
Vitronectin alpha-
HYH light chain.
Murine HYH antibod
Light chain variab
Light chain variab
Light chain variab
Mouse anti-idiotyp
Single chain Fv fr
Drosophila melanog
Monoclonal antibod
CDR3 domain reshap
Light chain variab
Light chain variab
Humanised cA2 ligh
Light chain variab
Light chain variab
Light chain variab

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 44; 129pp; English.
XX
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
|||||||
Db 1 qqsgswplt 9

RESULT 2

AAB61393
ID AAB61393 standard; peptide; 9 AA.

AC AAB61393;

XX 03-APR-2001 (first entry)

DE Mutant VL CDR3 peptide #3.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX

PS Claim 4; Page 41; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
|||||||
Db 1 qqsgswplt 9

RESULT 3

AAR37604
ID AAR37604 standard; peptide; 9 AA.

XX AAR37604;

XX 13-OCT-1993 (first entry)

XX hIL2R Ab L chain V region CDR3.

XX Complementarity-determining region; CDR; humanised; antibody; hIL2R;
KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
KW region; PCR; framework; plasmid.

XX Mus musculus.

XX WO9311238-A.

XX 10-JUN-1993.

XX 03-DEC-1992; 92WO-JP01583.

XX 06-DEC-1991; 91JP-0323319.

XX (BIOT) BIOTEST PHARMA GMBH.

PA (INNO-) INNOTHERAPIE LAB.

PA (SUMU) SUMITOMO PHARM CO LTD.

XX Gomi H, Nakatani T, Noguchi H, Wijdenes J;

XX WPI; 1993-197057/24.

XX Humanised antibody comprising - CDR region of mouse MAB B-B10
PT specific for IL-2 receptor useful for treating carcinoma
PT expressing IL-2 receptor

PS Claim 1; Page 43; 62pp; English.

XX The sequences given in AAR37599-604 represent the complementarity-
CC determining regions (CDRs) of a humanised antibody (Ab) which binds
CC specifically to human interleukin (IL)-2 receptor (hIL2R). These
CC CDRs were derived from the murine anti-human IL-2 receptor monoclonal
CC Ab (WAB) B-B10 (see also AAQ43242-43). This MAB is antagonistic to the
CC binding of IL-2 to the IL-2 receptor on human T-cells. It also
CC inhibits the human mixed lymphocyte reaction. The cDNA encoding the
CC variable (V) region of the B-B10 Ab was cloned by PCR and sequenced
CC (see also AAQ43226-32 and AAQ43233-36). A human Ab with high levels of
CC amino acid sequence homology to the murine sequence was selected and
CC the framework of this Ab was bound with the B-B10 V region CDR and a
CC part of the framework to design several kinds of the humanised B-B10 V
CC region (see also AAQ43244-45). The DNA sequence coding this humanised
CC B-B10 was synthesised and a plasmid expressing humanised B-B10 was
CC constructed.

```

XX SQ Sequence 9 AA;
Query Match 88.2%; Score 45; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 1 qsgswpqt 9

RESULT 5
AAB61394
ID AAB61394 standard; peptide; 9 AA.
XX AC AAB61394;
XX DT 03-APR-2001 (first entry)
XX DE Mutant VL CDR3 peptide #4.
XX KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX DR WPI; 2001-050110/06.
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta3 integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis -
XX PS Disclosure; Page 41; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphaVbeta3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX SQ Sequence 9 AA;

Query Match 88.2%; Score 45; DB 22; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 1 qsgswpqt 9

RESULT 6
AAR37612
ID AAR37612 standard; Protein; 107 AA.
XX AC AAR37612;
XX DT 13-OCT-1993 (first entry)

```

XX DE HIL2R Ab L chain V region.
 XX KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;
 XX KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
 KW KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
 KW KW region; PCR; framework; plasmid; heavy; H; light; L.
 XX OS Mus musculus/Homo sapiens.
 XX XX WO9311238-A.
 XX PN 10-JUN-1993.
 XX PD
 XX PF 03-DEC-1992; 92WO-JP01583.
 XX XX 06-DEC-1991; 91JP-0323319.
 XX XX (BIOT) BIOTEST PHARMA GMBH.
 PA (INNO-) INNOTHERAPIE LAB.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 XX PI Gomi H, Nakatani T, Noguchi H, Wijdenes J;
 XX WPI: 1993-197057/24.
 DR N-PSDB; AAQ43245.
 XX Humanised antibody comprising - CDR region of mouse MAB B-B10
 PT specific for IL-2 receptor useful for treating carcinoma
 PT expressing IL-2 receptor
 XX Claim 2: Fig 5: 62pp; English.
 XX The sequences given in AAR37611-12 represent the heavy (H) and light (L)
 CC chain variable (V) regions of a humanised antibody (Ab) which binds
 CC specifically to human interleukin (IL)-2 receptor (hIL2R). The
 CC complementarity-determining regions (CDRs) of these V regions were
 CC derived from the murine anti-human IL-2 receptor monoclonal Ab (MAB)
 CC B-B10 (see also AAR37599-04). This MAB is antagonistic to the binding
 CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
 CC the human mixed lymphocyte reaction. The cDNA encoding the variable
 CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
 CC AAQ43226-32 and AAQ43233-36). A human Ab with high levels of amino acid
 CC sequence homology to the murine sequence was selected and the
 CC framework of this Ab was bound with the B-B10 V region CDR and a
 CC part of the framework to design several kinds of the humanised B-B10
 CC V region. The DNA sequence coding this humanised B-B10 was
 CC synthesised and a plasmid expressing humanised B-B10 was constructed.
 XX Sequence 107 AA;
 SQ
 Query Match 88.2%; Score 45; DB 14; Length 107;
 Best Local Similarity 88.9%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQSGSWPLT 9
 Db 89 qqsswpl 97
 RESULT 7
 AAR37610
 ID AAR37610 standard; Protein; 107 AA.
 XX
 AC AAR37610;
 XX 13-OCT-1993 (first entry)
 DT B-B10 MAB L chain V region.
 XX
 DE Complementarity-determining region; CDR; humanised; antibody; hIL2R;
 KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;

KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
 KW region; PCR; framework; plasmid; heavy; H; light; L.
 XX Mus musculus.
 OS WO9311238-A.
 PN 10-JUN-1993.
 XX PD
 XX PF 03-DEC-1992; 92WO-JP01583.
 XX XX 06-DEC-1991; 91JP-0323319.
 XX XX (BIOT) BIOTEST PHARMA GMBH.
 PA (INNO-) INNOTHERAPIE LAB.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 XX PI Gomi H, Nakatani T, Noguchi H, Wijdenes J;
 XX WPI: 1993-197057/24.
 DR N-PSDB; AAQ43243.
 XX Humanised antibody comprising - CDR region of mouse MAB B-B10
 PT specific for IL-2 receptor useful for treating carcinoma
 PT expressing IL-2 receptor
 XX Disclosure: Fig 2: 62pp; English.
 XX The sequences given in AAR37609-10 represent the heavy (H) and light (L)
 CC chain variable (V) regions of the murine anti-human IL-2 receptor
 CC monoclonal antibody (MAB) B-B10, respectively. This MAB was used in
 CC the construction of a humanised antibody (Ab) which binds specifically
 CC to human interleukin (IL)-2 receptor (hIL2R). The complementarity-
 CC determining regions (CDRs) for the hIL2R MAB were derived from B-B10
 CC (see also AAR37599-04). The hIL2R MAB is antagonistic to the binding
 CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
 CC the human mixed lymphocyte reaction. The cDNA encoding the variable
 CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
 CC AAQ43226-32 and AAQ43233-36). A human Ab with high levels of amino acid
 CC sequence homology to the murine sequence was selected and the
 CC framework of this Ab was bound with the B-B10 V region CDR and a
 CC part of the framework to design several kinds of the humanised B-B10
 CC V region. The DNA sequence coding this humanised B-B10 was
 CC synthesised and a plasmid expressing humanised B-B10 was constructed.
 XX Sequence 107 AA;
 SQ
 Query Match 88.2%; Score 45; DB 14; Length 107;
 Best Local Similarity 88.9%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQSGSWPLT 9
 Db 89 qqsswpl 97
 RESULT 8
 AAR76013
 ID AAR76013 standard; Protein; 9 AA.
 XX
 AC AAR76013;
 XX 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-L region CDR3 protein fragment #1.
 XX
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

XX OS Mus sp.
 XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 DR N-PSDB; AAV49850.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure: Page 40; 129pp; English.
 XX
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integration-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 9 AA;
 Query Match 86.3%; Score 44; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QQSGSWPLT 9
 Db 1 qqsgswpht 9
 RESULT 9
 AAB61371
 ID AAB61371 standard; peptide; 9 AA.
 AC AAB61371;
 XX
 XX 03-APR-2001 (first entry)
 DT
 DE LM609 VL CDR3 peptide.
 DE
 XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 KW
 XX Unidentified.
 OS
 XX WO200078815-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 23-JUN-2000; 2000WO-US17454.
 PF
 XX 24-JUN-1999; 99US-0339922.
 PR
 XX

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX Huse WD, Wu H;
 XX WPI: 2001-050110/06.
 XX
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 XX Disclosure: Page 39; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 9 AA;
 Query Match 86.3%; Score 44; DB 22; Length 9;
 Best Local Similarity 88.9%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QQSGSWPLT 9
 Db 1 qqsgswpht 9
 RESULT 10
 AAW76006
 ID AAW76006 standard; Protein; 107 AA.
 XX
 AC AAW76006;
 XX
 XX 02-NOV-1998 (first entry)
 DT
 DE LM609 grafted antibody light chain variable region protein fragment.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 KW
 XX Mus sp.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 49
 FT /label= Arg, Met
 FT
 XX WO9833919-A2.
 XX
 XX 06-AUG-1998.
 PD
 XX
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX (IXSY-) IXSYS INC.
 PA
 XX Glaser SM, Huse WD;
 PI
 XX WPI: 1998-437472/37.
 XX
 DR N-PSDB; AAV49843.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 19; Fig 7; 129pp; English.
 XX
 CC This sequence represents a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 1.6;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 ||||| |
 DB 89 qsgswpht 97

RESULT 11

AAW76002
 ID AAW76002 standard; Protein; 107 AA.

XX
 AC AAW76002;

XX 02-NOV-1998 (first entry)

DE Vitaxin antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49821.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 1; Fig 1b; 129pp; English.

XX This sequence represents the vitaxin antibody variable light chain

CC region. Vitaxin and the antibody LM609 bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
 CC ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 1.6;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 ||||| |
 DB 89 qsgswpht 97

RESULT 12

AAW76004
 ID AAW76004 standard; Protein; 107 AA.

XX
 AC AAW76004;

XX 02-NOV-1998 (first entry)

DE LM609 antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAW76004.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 46; Fig 2b; 129pp; English.

XX This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more

CC than 90 times greater than that of parent the parent antibody.

XX
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
| | | | | | | |
Db 89 qsgswpht 97

RESULT 13
AAG63588
ID AAG63588 standard; Protein: 107 AA.
XX AC AAG63588;
XX
DT 15-OCT-2001 (first entry)
XX
DE A light chain variable region of LM609 grafted antibody.
XX
KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW cancer.
XX
OS Synthetic.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 49
FT /note= "unspecified residue encoded by MKK"
XX
PN US2001011125-A1.
XX
PD 02-AUG-2001.
XX
PF 30-JAN-1997; 97US-0790540.
XX
PR 30-JAN-1997; 97US-0790540.
XX
PA (HUSE/) HUSE W D.
XX
PI Huse WD;
XX
DR WPI; 2001-496171/54.
DR N-PSDB; AAH74624.
XX
XX New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer -
XX
PS Claim 1; Fig 1B; 25pp; English.
XX
XX The present sequence represents the light chain variable region of the
CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC specifically recognises the integrin alphavbeta3, and inhibits is
CC functional activity. The LM609 grafted antibody has the
CC complementary determining regions (CDRs) substituted into a non-murine
CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC polypeptides and fragments are useful in diagnostic and therapeutic
CC purposes, such as in the production of LM609 grafted antibodies and
CC fragments having binding specificity and inhibitory activity against
CC the integrin alphavbeta3. The antibody can be used for the diagnosis
CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC disorders, chronic articular rheumatism, psoriasis, disorders
CC associated with inappropriate or inopportune invasion of vessels such
CC as diabetic retinopathy, neovascular glaucoma and capillary
CC proliferation in atherosclerotic plaques, or cancers), and to inhibit

CC binding activity of alphavbeta3 that are necessary for progression of
CC an alphavbeta3-mediated disease.

XX
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 22; Length 107;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
| | | | | | | |
Db 89 qsgswpht 97

RESULT 14
AAG63590
ID AAG63590 standard; Protein: 107 AA.
XX AC AAG63590;
XX

DT 15-OCT-2001 (first entry)
XX
DE A light chain variable region of LM609 antibody.
XX

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW cancer.
XX
OS Mus sp.
XX

PN US2001011125-A1.
XX
PD 02-AUG-2001.
XX
PF 30-JAN-1997; 97US-0790540.
XX
PR 30-JAN-1997; 97US-0790540.
XX

PA (HUSE/) HUSE W D.
XX
PI Huse WD;
XX
DR WPI; 2001-496171/54.
DR N-PSDB; AAH74626.
XX

XX New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer -
XX
PS Disclosure; Fig 2B; 25pp; English.
XX

XX The present sequence represents the light chain variable region of the
CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
CC recognises the integrin alphavbeta3, and inhibits is functional activity.
CC The specification describes a LM609 grafted antibody which has the
CC complementarity determining regions (CDRs) substituted into a non-murine
CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC polypeptides and fragments are useful in diagnostic and therapeutic
CC purposes, such as in the production of LM609 grafted antibodies and
CC fragments having binding specificity and inhibitory activity against
CC the integrin alphavbeta3. The antibody can be used for the diagnosis
CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC disorders, chronic articular rheumatism, psoriasis, disorders
CC associated with inappropriate or inopportune invasion of vessels such
CC as diabetic retinopathy, neovascular glaucoma and capillary
CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC binding activity of alphavbeta3 that are necessary for progression of
CC an alphavbeta3-mediated disease.

XX Sequence 107 AA;

Job time: 1472 sec

Query Match 86.3%; Score 44; DB 22; Length 107;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
| | | | | | | |
Db 89 qqsgswpht 97

RESULT 15
AAB61360
ID AAB61360 standard; protein; 107 AA.
XX
AC AAB61360;
XX
DT 03-APR-2001 (first entry)
XX
DE Vitaxin light chain variable region protein.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Fig 1; 132pp; English.
XX

CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 22; Length 107;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
| | | | | | | |
Db 89 qqsgswpht 97

Search completed: August 19, 2002, 06:39:11

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:38 ; Search time 61.75 Seconds
(without alignments)
3.560 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QOSGSWPLT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	88.2	9	2	US-08-232-081B-6
2	45	88.2	103	1	US-08-436-463-21
3	45	88.2	107	2	US-08-232-081B-9
4	45	88.2	107	2	US-08-232-081B-40
5	45	88.2	127	1	US-08-436-463-18
6	40	78.4	33	4	US-08-525-539A-12
7	40	78.4	107	1	US-08-436-463-20
8	40	78.4	107	1	US-08-107-669D-1
9	40	78.4	107	1	US-08-472-788A-1
10	40	78.4	107	2	US-08-477-531B-1
11	40	78.4	107	2	US-08-082-842A-1
12	40	78.4	109	1	US-07-942-245-4
13	40	78.4	143	2	US-08-653-402B-8
14	39	76.5	9	2	US-08-476-176B-55
15	39	76.5	9	3	US-08-127-721A-55
16	39	76.5	9	3	US-08-485-246A-55
17	39	76.5	13	1	US-08-221-580-7
18	39	76.5	13	5	PCT-US95-04018-69
19	39	76.5	106	2	US-08-800-198-4
20	39	76.5	106	3	US-09-296-595-4
21	39	76.5	107	1	US-08-192-102-3
22	39	76.5	107	1	US-08-324-799-3
23	39	76.5	107	2	US-08-192-861A-3
24	39	76.5	107	2	US-08-476-176B-4
25	39	76.5	107	3	US-08-127-721A-4
26	39	76.5	107	3	US-08-485-246A-4
27	39	76.5	107	4	US-09-133-119-3

28	39	76.5	107	4	US-08-192-093A-3	Sequence 3, Appli
29	39	76.5	127	2	US-08-476-176B-6	Sequence 6, Appli
30	39	76.5	127	2	US-08-476-176B-8	Sequence 8, Appli
31	39	76.5	127	2	US-08-476-176B-10	Sequence 10, Appli
32	39	76.5	127	3	US-08-127-721A-6	Sequence 6, Appli
33	39	76.5	127	3	US-08-127-721A-8	Sequence 8, Appli
34	39	76.5	127	3	US-08-127-721A-10	Sequence 10, Appli
35	39	76.5	127	3	US-08-485-246A-6	Sequence 6, Appli
36	39	76.5	127	3	US-08-485-246A-8	Sequence 8, Appli
37	39	76.5	127	3	US-08-485-246A-10	Sequence 10, Appli
38	39	76.5	240	2	US-08-800-198-8	Sequence 8, Appli
39	39	76.5	240	3	US-09-296-595-8	Sequence 8, Appli
40	38	74.5	100	1	US-08-436-463-19	Sequence 19, Appli
41	38	74.5	107	1	US-07-634-278-62	Sequence 62, Appli
42	38	74.5	107	1	US-07-634-278-63	Sequence 63, Appli
43	38	74.5	107	1	US-07-634-278-87	Sequence 87, Appli
44	38	74.5	107	1	US-08-477-728-62	Sequence 62, Appli
45	38	74.5	107	1	US-08-477-728-63	Sequence 63, Appli

ALIGNMENTS

RESULT 1
US-08-232-081B-6
; Sequence 6, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJDENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-232-081B-6

Query Match 88.2%; Score 45; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSGSWPLT 9
||| |||||

Db 1 QOSSSWPLT 9

RESULT 2

US-08-436-463-21
; Sequence 21, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-21

Query Match 88.2%; Score 45; DB 1; Length 103;
Best Local Similarity 88.9%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSGSWPLT 9

Db 86 QOSSSWPLT 94

RESULT 3

US-08-232-081B-9
; Sequence 9, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH

; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-232-081B-9

Query Match 88.2%; Score 45; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSGSWPLT 9

Db 89 QOSSSWPLT 97

RESULT 4

US-08-232-081B-40
; Sequence 40, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000

```

; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-232-081B-40

Query Match      88.2%; Score 45; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSSSWPLT 97

RESULT 5
US-08-436-463-18
; Sequence 18, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-18

Query Match      88.2%; Score 45; DB 1; Length 127;
Best Local Similarity 88.9%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSSSWPLT 97

US-08-525-539A-12
; Sequence 12, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: M63 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-12

Query Match      78.4%; Score 40; DB 4; Length 33;
Best Local Similarity 77.8%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 21 QQSSSWPYT 29

US-08-436-463-20
; Sequence 20, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
```

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-463-20

Query Match 78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQNSNWPYT 97

RESULT 8
US-08-107-669D-1
; Sequence 1, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala

; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-107-669D-1

Query Match 78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQNSNWPYT 97

RESULT 9
US-08-472-788A-1
; Sequence 1, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-472-788A-1

```

Query Match      78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
   ||| ||| |
Db 89 QQSNWPTYT 97

RESULT 10
US-08-477-531B-1
; Sequence 1, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-531B-1

Query Match      78.4%; Score 40; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
   ||| ||| |
Db 89 QQSNWPTYT 97

RESULT 11
US-08-082-842A-1
; Sequence 1, Application US/08082842A
; Patent No. 5865619
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.

```

```

; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,842A
; FILING DATE: 23-JUN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-082-842A-1

Query Match      78.4%; Score 40; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
   ||| ||| |
Db 89 QQSNWPTYT 97

RESULT 12
US-07-942-245-4
; Sequence 4, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation

```

OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-4

Query Match 78.4%; Score 40; DB 1; Length 109;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
| | | | |
DB 89 QOQNSWPYT 97

RESULT 13
US-08-653-402B-8
; Sequence 8, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; TITLE OF INVENTION: Immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-653-402B-8

Query Match 78.4%; Score 40; DB 2; Length 143;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
| | | | |
DB 109 QOQNSWPYT 117

RESULT 14
US-08-476-176B-55
; Sequence 55, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-176B-55

Query Match 76.5%; Score 39; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
| | | | |
DB 1 QOQSDSWPTT 9

RESULT 15
US-08-127-721A-55
; Sequence 55, Application US/08127721A
; Patent No. 6066718

GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6066718artis Patent and Trademark Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-127-721A-55

Query Match 76.5%; Score 39; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 QQSGSWPLT 9
Db 1 QQSDSWPTT 9

Search completed: August 19, 2002, 06:34:39
Job time: 1200 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:04 ; Search time 78.53 Seconds
(without alignments)
20.801 Million cell updates/sec

Title: US-09-339-922A-102

Perfect score: 88

Sequence: 1 KVSSGGSTYYLDTVQG 17

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	80.7	113	2 S26468	Ig heavy chain V r
2	71	80.7	117	1 HVMS34	Ig heavy chain pre
3	68	77.3	117	1 HVMS84	Ig heavy chain pre
4	67	76.1	108	2 PLO248	Ig heavy chain V r
5	67	76.1	111	2 PH1007	Ig heavy chain V r
6	67	76.1	118	2 S00700	Ig heavy chain V r
7	64	72.7	118	2 PH1006	Ig heavy chain V r
8	64	72.7	118	2 S20841	Ig heavy chain V r
9	64	72.7	138	2 S09258	Ig heavy chain V r
10	62	70.5	113	2 S02717	Ig heavy chain V r
11	62	70.5	115	2 PH1538	Ig H chain V regio
12	62	70.5	117	1 HVMSRF	Ig heavy chain pre
13	62	70.5	119	2 PH1548	Ig H chain V regio
14	62	70.5	119	2 PH1549	Ig H chain V regio
15	60	68.2	83	2 S21593	Ig heavy chain V r
16	60	68.2	111	2 S51211	Ig heavy chain V r
17	60	68.2	145	2 I47203	Ig heavy chain var
18	59	67.0	90	2 S24248	Ig heavy chain V r
19	59	67.0	98	2 S26889	Ig heavy chain V r
20	59	67.0	99	2 S24259	Ig heavy chain V r
21	59	67.0	100	2 S24258	Ig heavy chain V r
22	59	67.0	101	2 S24257	Ig heavy chain V r
23	59	67.0	102	2 S24260	Ig heavy chain V r
24	59	67.0	104	2 S24255	Ig heavy chain V r
25	59	67.0	105	2 S24249	Ig heavy chain V r
26	59	67.0	106	2 S24256	Ig heavy chain V r
27	59	67.0	108	2 PH1648	Ig heavy chain V r
28	59	67.0	109	2 PH1649	Ig heavy chain V r
29	59	67.0	109	2 S24254	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J. submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <NAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 71; DB 2; Length 113;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17

DB 47 ISSGGSTYYPTVKG 62

RESULT 2

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: J0502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J0501; MUID:89279149

A:Accession: J0502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A>Note: This sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 80.7%; Score 71; DB 1; Length 117;
 Best Local Similarity 81.2%; Pred. No. 0.00056;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 70 ISSGGGTTYPDVKG 85

RESULT 3

HWMS84

Ig heavy chain precursor V region (5-84) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0505

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0505

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Dissulfide bonds: #status predicted

Query Match

Best Local Similarity 77.3%; Score 68; DB 1; Length 117;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 70 ISNGGGTTYPDVKG 85

RESULT 4

PL0248

Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0248

R:Shlomchik, M.; Mascellli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618

A:Accession: PL0248

A:Molecule type: mRNA

A:Residues: 1-108 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-24/Region: framework 1

F:9-92/Domain: immunoglobulin homology <IMM>

F:25-29/Region: complementarity-determining 1

F:30-43/Region: framework 2

F:44-60/Region: complementarity-determining 2

F:61-92/Region: framework 3

F:93-99/Region: complementarity-determining 3

F:100-108/Region: framework 4

Query Match

Best Local Similarity 76.1%; Score 67; DB 2; Length 108;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 74

Db 45 ISSGGGTTYPDSVKG 60

RESULT 5

PH1007

Ig heavy chain V region (clone 163-cl) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1007

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1007

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <TIL>

A:Experimental source: B cell, strain [N2B x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.1%; Score 67; DB 2; Length 111;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 51 ISSGGGTTYPDSVKG 66

RESULT 6

S00700

Ig heavy chain V region - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999

C:Accession: S00700

R:Yamawaki-Kataoka, Y.; Honjo, T.

Nucleic Acids Res. 15, 5888, 1987

A:Title: Nucleotide sequences of variable region segments of the immunoglobulin heavy

A:Reference number: S00700; MUID:87289054

A:Accession: S00700

A:Molecule type: DNA

A:Residues: 1-118 <YAM>

A:Cross-references: EMBL:Y00380; NID:G64810; PIDN:CAA68452.1; PID:G64811

A:Note: the sequence was determined from the germline gene

C:Genetics:

A:Introns: 15/3

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.1%; Score 67; DB 2; Length 118;

Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KVSSGGGTTYLDTVQG 17

Db 69 RISDGGGTTYADSVKG 85

RESULT 7

PH1006

Ig heavy chain V region (clone 202.33) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1006

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1006

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-108 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 64; DB 2; Length 108;

Best Local Similarity 68.8%; Pred. No. 0.0065;

Matches 11; Conservative 3; Mismatches 2; Indels 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 46 ISGGGNTYPTVKG 61

RESULT 8

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20641

R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react

A:Reference number: S20639

A:Accession: S20641

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-118 <LOS>

A:Cross-references: EMBL:X65003; NID:g52602; PIDN:CAA46136.1; PID:g52603

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 64; DB 2; Length 118;

Best Local Similarity 68.8%; Pred. No. 0.0071;

Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 51 ISGGGNTYPTVKG 66

RESULT 9

Ig heavy chain V region precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999

C:Accession: S09258

R:Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A:Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK

A:Reference number: S09258; MUID:90245594

A:Accession: S09258

A:Molecule type: DNA

A:Residues: 1-138 <HAM>

A:Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 64; DB 2; Length 138;

Best Local Similarity 68.8%; Pred. No. 0.0084;

Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 70 ISGGGNTYPTVKG 85

RESULT 10

S02717

Ig heavy chain V region (clone pH62) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C:Accession: S02717

R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Glotz, D.; Capra, J.D.; Zanetti, M.

submitted to the EMBL Data Library, February 1989

A:Reference number: S02717

A:Accession: S02717

A:Molecule type: DNA

A:Residues: 1-113 <SOL>

A:Cross-references: EMBL:Y00744; NID:g52472; PIDN:CAA68713.1; PID:g1334095

A:Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 62; DB 2; Length 113;

Best Local Similarity 68.8%; Pred. No. 0.014;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 51 INSGGTTYPTVKG 66

RESULT 11

PH1538

Ig H chain V region (clone 13G12) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

C:Accession: PH1538

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma

A:Reference number: PH1528; MUID:93210465

A:Accession: PH1538

A:Molecule type: mRNA

A:Residues: 1-115 <MUK>

A:Note: the stop codons X appear in residues 82, 85 and 106

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 62; DB 2; Length 115;

Best Local Similarity 68.8%; Pred. No. 0.014;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 50 INSGGTTYPTVKG 65

RESULT 12

HMSRF

Ig heavy chain precursor V region (RF) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0503

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0503

A:Status: translation not shown

A:Molecule type: mRNA
A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; hybridoma; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 70.5%; Score 62; DB 1; Length 117;
Best Local Similarity 68.8%; Pred. No. 0.014;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
::: ||||| |||:|
Db 70 INSGGGTTYYPDTVKG 85

RESULT 13

PH1548

Ig H chain V region (clone 12F4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1548

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A>Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465

A:Accession: PH1548

A:Molecule type: mRNA

A:Residues: 1-119 <MUK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 62; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.015;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
::: ||||| |||:|
Db 51 INSGGGTTYYPDTVKG 66

RESULT 14

PH1549

Ig H chain V region (clone 13F1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1549

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A>Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465

A:Accession: PH1549

A:Molecule type: mRNA

A:Residues: 1-119 <MUK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 62; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.015;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
::: ||||| |||:|
Db 51 INSGGGTTYYPDTVKG 66

RESULT 15

S21593

Ig heavy chain V region (10C5) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S21593

R:Kaartinen, M.

submitted to the EMBL Data Library, May 1992

A:Reference number: S21591

A:Accession: S21593

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-83 <KAA>

A:Cross-references: EMBL:X66457; NID:g51598; PIDN:CAA47072.1; PID:g51599

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 68.2%; Score 60; DB 2; Length 83;
Best Local Similarity 68.8%; Pred. No. 0.021;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
::: ||||| |||:|
Db 21 ITSGGVSTYISDTVKG 36

Search completed: August 19, 2002, 06:36:04
Job time: 1285 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:07 ; Search time 51.81 Seconds
(without alignments)
12.705 Million cell updates/sec

Title: US-09-339-922a-102

Perfect score: 88

Sequence: 1 KVSSGGSTYYLDTVQG 17

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	80.7	117	1 HV55_MOUSE	P18526 mus musculus
2	68	77.3	117	1 HV54_MOUSE	P18525 mus musculus
3	62	70.5	117	1 HV53_MOUSE	P18524 mus musculus
4	56	63.6	117	1 HV3C_HUMAN	P01764 homo sapien
5	54	61.4	97	1 HV56_MOUSE	P18527 mus musculus
6	53	60.2	119	1 HV3L_HUMAN	P01773 homo sapien
7	52	59.1	116	1 HV05_CARAU	P19181 carassius a
8	51	58.0	98	1 HV57_MOUSE	P18528 mus musculus
9	51	58.0	117	1 HV58_MOUSE	P18529 mus musculus
10	49	55.7	115	1 HV3F_HUMAN	P01767 homo sapien
11	47	53.4	136	1 HV16_MOUSE	P01783 mus musculus
12	45	51.1	117	1 HV02_CANFA	P01785 canis fami
13	45	51.1	814	1 DMSA_ECOLI	P18775 escherichia
14	44	50.0	503	1 CP7A_RAT	P18125 rattus norv
15	43	48.9	340	1 THPS_SULAC	P17118 sulfobolus
16	43	48.9	516	1 T2D5_YEAST	P53040 saccharomyc
17	43	48.9	2300	1 CYAA_NEUCR	Q01631 neurospora
18	42	47.7	117	1 HV59_MOUSE	P18530 mus musculus
19	42	47.7	480	1 6PGD_CHLTR	O84066 chlamydia t
20	42	47.7	807	1 YNFE_ECOLI	P77783 escherichia
21	41.5	47.2	114	1 HV3B_HUMAN	P01763 homo sapien
22	41.5	47.2	122	1 HV3A_HUMAN	P01762 homo sapien
23	41	46.6	442	1 CELF_BACSU	P46320 bacillus su
24	41	46.6	449	1 TBA2_SCHPO	P04689 schizosacch
25	41	46.6	468	1 6PG2_BACSU	P80859 bacillus su
26	41	46.6	652	1 ABG5_MOUSE	Q99pe8 mus musculus
27	41	46.6	652	1 ABG5_MOUSE	Q99pe8 mus musculus
28	40	45.5	72	1 NIPT_AZOVI	P09427 azotobacter
29	40	45.5	120	1 HV3U_HUMAN	P01782 homo sapien
30	40	45.5	383	1 MANA_STRLI	P51529 streptomyce
31	40	45.5	412	1 Y157_YEAST	Q12358 saccharomyc
32	40	45.5	462	1 DRTS_PARTE	Q27828 paramemom
33	40	45.5	652	1 T3MO_SALTY	P40814 salmonella

ALIGNMENTS

RESULT 1

HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Mallipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J0502; HVMS34.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 80.7%; Score 71; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 0.00012;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
Db 70 ISSGGGTTYTPDVKVKG 85

RESULT 2

HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: J0505; HVMS84.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 77.3%; Score 68; DB 1; Length 117;
 Best Local Similarity 75.0%; Pred. No. 0.00036;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYVLDTVQG 17
 :|:||||||| |::|
 Db 70 ISGGGTYVDPVKG 85

RESULT 3
 HV53_MOUSE ID HV53_MOUSE STANDARD; PRT; 117 AA.
 AC P18524;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region RF precursor.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: J0503; HVMSRF.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Hybridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 70.5%; Score 62; DB 1; Length 117;
 Best Local Similarity 68.8%; Pred. No. 0.0033;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTYVLDTVQG 17
 :|:||||||| |::|
 Db 70 ISGGGTYVDPVKG 85

RESULT 4
 HV3C_HUMAN ID HV3C_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region VH26 precursor.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81101090; PubMed=6450418;
 RA Matthyssens G., Rabbitts T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 heavy chain variable region.";
 RT Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; J00236; AAA53516.1; -;
 DR EMBL; M35415; AAA58735.1; -;
 DR PIR: A02047; H3HU26.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 63.6%; Score 56; DB 1; Length 117;
 Best Local Similarity 62.5%; Pred. No. 0.03;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYVLDTVQG 17
 :|:||||||| |::|
 Db 70 ISGGGTYVDPVKG 85

RESULT 5
 HV56_MOUSE ID HV56_MOUSE STANDARD; PRT; 97 AA.
 AC P18527;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 914.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: J0504; HWS94.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT NON_TER 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 61.4%; Score 54; DB 1; Length 97;
 Best Local Similarity 71.4%; Pred. No. 0.052; 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2;

QY 4 SGGSTYYLDTVQG 17
 I I I I I I I I I I
 DB 52 SSGSTYYPDVSKG 65

RESULT 6
 HV3L_HUMAN STANDARD; PRT; 119 AA.
 AC P01773;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region BUR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN BUR).
 RX MEDLINE=79151016; PubMed=107164;
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
 RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
 RT amino acid sequence of the alpha 1 heavy chain.";
 RL J. Biol. Chem. 254:2865-2874(1979).
 DR PIR: A02056; ALHUBR.
 DR HSSP: P01772; ZIG2.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT MOD_RES 1
 FT DISULFID 22 96 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 60.2%; Score 53; DB 1; Length 119;
 Best Local Similarity 56.2%; Pred. No. 0.094;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17
 I I I I I I I I I I

DB 51 ISYGGSBTYADSVRG 66
 I I I I I I I I I I

RESULT 7
 HV05_CARAU STANDARD; PRT; 116 AA.
 ID HV05_CARAU
 AC P19181;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5A precursor.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88144476; PubMed=3125551;
 RA Wilson M.R., Middleton D., Warr G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure
 RT and family relationships of two genes and a pseudogene in a teleost
 fish.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 DR PIR: B28966; B28966.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DISULFID 41 114 BY SIMILARITY.
 FT NON_TER 116
 SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 59.1%; Score 52; DB 1; Length 116;
 Best Local Similarity 75.0%; Pred. No. 0.13;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGSTYYLDTVQG 17
 I I I I I I I I I I
 DB 73 GGSTYYADSVKG 84

RESULT 8
 HV57_MOUSE STANDARD; PRT; 98 AA.
 ID HV57_MOUSE
 AC P18528;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 6.96.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR PIR; JT0501; HVMS96.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 58.0%; Score 51; DB 1; Length 98;
Best Local Similarity 56.2%; Pred. No. 0.16;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVOG 17
: ||| ||| :
Db 51 ISDGGSTYYTPDSVKG 66

RESULT 9

ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0506; HVMS57.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 58.0%; Score 51; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 0.19;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVOG 17
: |||| ||| :
Db 70 ISSGGLTYTPDSVKG 85

RESULT 10

ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=78137069; PubMed=416441;
RA TORANO A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -I- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.

DR PIR; A02050; A2HUBU.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 55.7%; Score 49; DB 1; Length 115;
Best Local Similarity 66.7%; Pred. No. 0.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGSYYLDTVOG 17
||| ||| :
Db 54 GGTYYADSVKG 65

RESULT 11

ID HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch>)
or send an email to license@isb-sib.ch.
CC -----
CC EMBL; J00522; AAD15290.1; -.
DR PIR; A02066; GIMS21.
DR HSSP; P01772; 2PB4.

```

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG; 1.
DR Immunoglobulin V region: Signal.
FT FT NON_TER 1 1
FT FT SIGNAL <1 16
FT CHAIN 17 136
FT DOMAIN 115 119
FT DOMAIN 120 136
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90
FT CONFLICT 115 113
FT CONFLICT 120 120
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 53.4%; Score 47; DB 1; Length 136;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17
Db 67 ISSGSSTLHYADTVKG 82

RESULT 12
HV02_CANFA STANDARD; PRT; 117 AA.
AC P01785;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOO.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE OF 1-112.
RX MEDLINE-77242268; PubMed=407924;
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
immunoglobulin heavy chains."
RL Biochemistry 16:3160-3168(1977).
RN [2]
RP SEQUENCE OF 113-117.
RX MEDLINE-80077682; PubMed=117299;
RA McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain."
RL Mol. Immunol. 16:565-570(1979).
CC 1- MISCELLANEOUS; THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A02068; MDCMO.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG; 1.
DR Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;

Query Match 51.1%; Score 45; DB 1; Length 117;
Best Local Similarity 57.1%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 SGGSTYYLDTVQG 17
Db 52 SSSGQTYADAVKG 65

RESULT 13
DMSA_ECOLI STANDARD; PRT; 814 AA.
AC P18775;
DT 01-NOV-1990 (Rel. 16, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Anaerobic dimethyl sulfoxide reductase chain A precursor (EC 1.8.99.-)
DE (DMSO reductase).
GN DMSA OR B0894.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 46-51.
RC STRAIN=K12 / C60;
RX MEDLINE-89096500; PubMed=3062312;
RA Bilous P.T., Cole S.T., Anderson W.F., Weiner J.H.;
RT "Nucleotide sequence of the dmsABC operon encoding the anaerobic
dimethylsulphoxide reductase of Escherichia coli."
RL Mol. Microbiol. 2:785-795(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE-97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE-97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemura K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map."
RL DNA Res. 3:137-155(1996).
RN [4]
RP MUTAGENESIS.
RX MEDLINE-94171715; PubMed=8125918;
RA Trieber C.A., Rothery R.A., Weiner J.H.;
RT "Multiple pathways of electron transfer in dimethyl sulfoxide
reductase of Escherichia coli."
RL J. Biol. Chem. 269:7103-7109(1994).
CC 1- FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON
VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS. ALLOWS E.COLI TO GROW
ANAEROBICALLY ON ME(2)SO AS RESPIRATORY OXIDANT.
CC 1- CATALYTIC ACTIVITY: REDUCES VARIOUS N-OXIDE AND SULFOXIDE
COMPOUNDS INCLUDING TRIMETHYLAMINE N-OXIDE.
CC 1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN); MAY BIND A 4FE-4S CLUSTER.
CC 1- SUBUNIT: HOMODIMER. THE COMPLEX CONSIST OF THREE SUBUNITS: DMSA,
THE REDUCTASE; DMSB, AN ELECTRON TRANSFER PROTEIN, AND DMSC,
A MEMBRANE ANCHOR PROTEIN.
CC 1- SUBCELLULAR LOCATION: CYTOSOL; CYTOSOLIC FACE OF THE MEMBRANE.
CC 1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
OXIDOREDUCTASE FAMILY.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----

```



```

DR EMBL: J03412: AAA83843.1; ALT_INIT.
DR EMBL: AR000191: AAC73980.1; ALT_INIT.
DR EMBL: D90727: BAA35626.1; ALT_INIT.
DR PIR: S03785; S03785.
DR HSP: Q57366; IEU1.
DR EcoGene: EG10232; dmsA.
DR InterPro: IPR001467; Molybdopterin.
DR Pfam: PF00384; molybdopterin; 1.
DR Pfam: PF01588; Molybd-binding; 1.
DR PROSITE: PS00551; MOLYBDOPTERIN_PROK_1; 1.
DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; 1.
DR Oxidoreductase: Signal; Molybdenum; 4Fe-4S; Iron-sulfur;
KW Complete proteome.
FT SIGNAL 1 45
FT CHAIN 46 814 ANAEROBIC DIMETHYL SULFOXIDE REDUCTASE
FT CHAIN A.
FT METAL 63 63 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 67 67 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 71 71 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 104 104 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 814 AA; 90398 MW; B97C830ABAC7C32C CRC64;

Query Match 51.1%; Score 45; DB 1; Length 814;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SGGSGTYILD 13
Db 248 SGGGVTVYLE 257

RESULT 14
CP7A_RAT STANDARD; PRT; 503 AA.
AC P18125; P51543;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome P450 7A1 (Cholesterol 7-alpha-monooxygenase) (CYPVII)
DE (BC 1.14.13.17) (Cholesterol 7-alpha-hydroxylase).
GN CYP7A1 OR CYP7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=90307735; PubMed=1694852;
RA Li Y.C., Wang D.P., Chiang J.Y.L.;
RT "Regulation of cholesterol 7 alpha-hydroxylase in the liver. Cloning,
RT sequencing, and regulation of cholesterol 7 alpha-hydroxylase mRNA.";
RL J. Biol. Chem. 265:12012-12019(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=90243699; PubMed=2335522;
RA Jelinek D.F., Andersson S., Slaughter C.A., Russell D.W.;
RT "Cloning and regulation of cholesterol 7 alpha-hydroxylase, the rate-
RT limiting enzyme in bile acid biosynthesis.";
RL J. Biol. Chem. 265:8190-8197(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90033362; PubMed=2806567;
RA Nishimoto M., Nishimoto M., Morohashi K., Okuda K.;
RT "Molecular cloning of cDNA for cholesterol 7 alpha-hydroxylase from
RT rat liver microsomes. Nucleotide sequence and expression.";
RL FEBS Lett. 257:97-100(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;

```

```

RX MEDLINE=90277612; PubMed=1693613;
RA Nishiro M., Nishimoto M., Okuda K.;
RT "Rat liver cholesterol 7 alpha-hydroxylase. Pretranslational
RT regulation for circadian rhythm.";
RL J. Biol. Chem. 265:10036-10041(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=91177904; PubMed=2007596;
RA Nishimoto M., Gotoh O., Okuda K., Nishiro M.;
RT "Structural analysis of the gene encoding rat cholesterol alpha-
RT hydroxylase, the key enzyme for bile acid biosynthesis.";
RL J. Biol. Chem. 266:6467-6471(1991).
RN [6]
RP SEQUENCE OF 1-325 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=94292507; PubMed=8021257;
RA Chiang J.Y., Stroup D.;
RT "Identification and characterization of a putative bile acid-
RT responsive element in cholesterol 7 alpha-hydroxylase gene promoter.";
RL J. Biol. Chem. 269:17502-17507(1994).
RN [7]
RP SEQUENCE OF 1-27 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=91084435; PubMed=2261433;
RA Jelinek D.F., Russell D.W.;
RT "Structure of the rat gene encoding cholesterol 7 alpha-hydroxylase.";
RL Biochemistry 29:7781-7785(1990).
RN [8]
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=93041942; PubMed=1420318;
RA Chiang J.Y., Yang T.P., Wang D.P.;
RT "Cloning and 5'-flanking sequence of a rat cholesterol 7 alpha-
RT hydroxylase gene.";
RL Biochim. Biophys. Acta 1132:337-339(1992).
CC -!- CATALYTIC ACTIVITY: Cholesterol + NADPH + O(2) = 7-alpha-
CC hydroxycholesterol + NADP(+) + H(2)O.
CC -!- ENZYME REGULATION: INHIBITION OF ACTIVITY BY BILE ACID FEEDBACK.
CC -!- PATHWAY: FIRST AND RATE-LIMITING STEP IN THE CONVERSION OF
CC CHOLESTEROL TO BILE ACIDS.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- TISSUE SPECIFICITY: LIVER.
CC -!- INDUCTION: BY CHOLESTYRAMINE AND CHOLESTEROL.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J05509; AAA40839.1; -
DR EMBL: J02926; AAA40923.1; -
DR EMBL: J05430; AAA41041.1; -
DR EMBL: J05460; AAA03649.1; -
DR EMBL: M59189; AAA41042.1; -
DR EMBL: M59184; AAA41042.1; JOINED.
DR EMBL: M59185; AAA41042.1; JOINED.
DR EMBL: M59186; AAA41042.1; JOINED.
DR EMBL: M59187; AAA41042.1; JOINED.
DR EMBL: M59188; AAA41042.1; JOINED.
DR EMBL: U01962; AAA21144.2; -
DR EMBL: X17595; CAB57878.1; -
DR EMBL: Z14108; CAA78481.1; -
DR PIR: A35376; A35376.
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum; Cholesterol metabolism; NADP.
FT BINDING 444 444 HEME (BY SIMILARITY).

```

FT CONFLICT 371 371 T -> S (IN REF. 5).
SQ SEQUENCE 503 AA; 56882 MW; EA825AA6E74BF5F6 CRC64;

Query Match 50.0%; Score 44; DB 1; Length 503;
Best Local Similarity 69.2%; Pred. No. 13;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 SGGGTTYLDTVQ 16
| ||| ||| ||
Db 327 SGGSAIYLDQVQ 339

RESULT 15

THPS_SULAC
ID THPS_SULAC STANDARD; PRT; 340 AA.
AC P17118;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thermopsin precursor (EC 3.4.23.42).
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 42-76.
RX MEDLINE=90110209; PubMed=2104843;
RA Lin X.-L.; Tang J.;
RT "Purification, characterization, and gene cloning of thermopsin, a
thermostable acid protease from Sulfolobus acidocaldarius.";
RL J. Biol. Chem. 265:1490-1495(1990).
CC -I- FUNCTION: MAY REPRESENT A NEW CLASS OF ACID PROTEASES. IT DIGEST
PROTEINS AND PEPTIDES IN ACIDIC SOLUTION, AND IS THERMOSTABLE. IT
HAS MAXIMAL PROTEOLYTIC ACTIVITY AT PH 2 AND 90 DEGREES CELSIUS.
CC -I- CATALYTIC ACTIVITY: Specificity similar to pepsin A, prefers bulky
hydrophobic side-chains on either side of the scissile bond.
CC -I- SUBCELLULAR LOCATION: MAY BE LINKED TO CELLS BY COVALENT LINKAGES
THROUGH SOME SIDE CHAINS.
CC -I- MISCELLANEOUS: THERMOPROTEIN HAS PERHAPS A DIFFERENT TYPE OF ACTIVE
SITE THAN OTHER ASPARTIC PROTEASES.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A5.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J05184; AAA72221.1; -.
DR PIR; A35009; A35009.
DR MEROPS; A05.001; -.
KW Hydrolase; Aspartyl
FT SIGNAL 1 28
FT PROPEP 29 41
FT CHAIN 42 340
FT CARBOHYD 31 31 N-LINKED (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (PROBABLE).
FT CARBOHYD 69 69 N-LINKED (PROBABLE).
FT CARBOHYD 85 85 N-LINKED (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (POTENTIAL).
SQ SEQUENCE 340 AA; 37262 MW; E2758C0BC287FCE1 CRC64;

Query Match 48.9%; Score 43; DB 1; Length 340;
Best Local Similarity 63.6%; Pred. No. 12;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 SGGGTTYLD 13
|:|||||:|
Db 169 SAGGGQTFYVD 179

Search completed: August 19, 2002, 06:59:08
Job time: 1373 sec

DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Medline=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -;
 DR HSSP; P01772; 2FB4
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 121
 SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 65.9%; Score 58; DB 4; Length 121;
 Best Local Similarity 62.5%; Pred. No. 0.086;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 VSSGGGTYLDTVOG 17
 : | ||||| | : | : |
 Db 51 ISGGGGTYADSVKVG 66

RESULT 3
 Q91WP5 PRELIMINARY; PRT; 479 AA.
 ID Q91WP5;
 AC Q91WP5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 51.6 KDA PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straussberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013656; AAH13656.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 64.8%; Score 57; DB 11; Length 479;
 Best Local Similarity 56.2%; Pred. No. 0.56;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 VSSGGGTYLDTVOG 17
 : | ||||| | : | : |
 Db 70 INSGNGTYSDTMKG 85

RESULT 4
 Q920E7 PRELIMINARY; PRT; 119 AA.
 ID Q920E7;
 AC Q920E7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PTERIN-MIMICKING ANTI-IDIOPOPE HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
 RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
 RT in Mammalian Cells.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF307937; AAL09421.1; -;
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;
 Query Match 62.5%; Score 55; DB 11; Length 119;
 Best Local Similarity 62.5%; Pred. No. 0.26;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 VSSGGGTYLDTVOG 17
 : |||| | | : | : |
 Db 51 ISSGGSYTPDSVKG 66

RESULT 5
 Q9UL72 PRELIMINARY; PRT; 118 AA.
 ID Q9UL72;
 AC Q9UL72;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035042; AAD56278.1; -;
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 58.0%; Score 51; DB 4; Length 118;
 Best Local Similarity 56.2%; Pred. No. 1.1;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 VSSGGGTYLDTVOG 17
 : | |||| | : | : |
 Db 50 VTYSGGSSYYADSVKVG 65

RESULT 6
 Q9D8R6 PRELIMINARY; PRT; 211 AA.
 ID Q9D8R6;
 AC Q9D8R6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE 181004A24RIK PROTEIN.
GN 181004A24RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasedawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007766; BAB25242.1; -;
DR MGD: MGI:1923760; 181004A24RIK.
SQ SEQUENCE 211 AA; 23482 MW; 018A9D083CACBBDB8 CRC64;

Query Match 58.0%; Score 51; DB 11; Length 211;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVQ 16
: | | | | | | | | | |
DB 144 ISFVGSSTFYLDVQ 158

RESULT 7
Q99KA4 PRELIMINARY; PRT; 487 AA.
ID Q99KA4;
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 52.6 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004786; AAH04786.1; -;
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 3.
DR SMART: SM00407; IGC1; 3.
DR SMART: SM00406; IGv; 1.
DR SMART: SM00410; IG-like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
Query Match 56.8%; Score 50; DB 11; Length 487;
Best Local Similarity 56.2%; Pred. No. 7.6;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 2 VSSGGGTYLDTVQ 17
: | | | | | | | | | |
DB 70 ISDGGSTYYPDNVKG 85
RESULT 8
Q9BQA2 PRELIMINARY; PRT; 211 AA.
ID Q9BQA2;
AC Q9BQA2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:4769) (SIMILAR TO RIKEN CDNA 181004A24
DE GENE).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG CARCINOMA;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG CARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006206; AAH06206.1; -;
DR EMBL: BC003650; AAH03650.1; -;
SQ SEQUENCE 211 AA; 23486 MW; 3CB581BC07F42018 CRC64;

Query Match 53.4%; Score 47; DB 4; Length 211;
Best Local Similarity 66.7%; Pred. No. 9.3;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVQ 16
: | | | | | | | | | |
DB 144 VSFVGSSTFYLDVQ 158

RESULT 9
Q91Z05 PRELIMINARY; PRT; 473 AA.
ID Q91Z05;
AC Q91Z05;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010327; AAH10327.1; -;
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 53.4%; Score 47; DB 11; Length 473;
Best Local Similarity 50.0%; Pred. No. 23;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 VSSGGSTYYLDTVOG 17
: : : : :
Db 70 INSGSTYYADTVKG 85

RESULT 10

Q91207 ID Q91207 PRELIMINARY; PRT; 486 AA.
AC Q91207;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 52.7 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH0324.1; -.
KW Hypothetical protein.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 53.4%; Score 47; DB 11; Length 486;

Best Local Similarity 57.1%; Pred. No. 23;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 SGGGSTYYLDTVOG 17
: : : : :
Db 71 TSGGNTYYPDNVKG 84

RESULT 11

Q96SL2 ID Q96SL2 PRELIMINARY; PRT; 545 AA.
AC Q96SL2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDNA FLJ14783 FIS, CLONE NT2RP4000541.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027689; BAB55299.1; -.
SQ SEQUENCE 545 AA; 59981 MW; 939276D65D3B94BD CRC64;

Query Match 53.4%; Score 47; DB 4; Length 545;

Best Local Similarity 66.7%; Pred. No. 26;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 VSSGGSTYYLDTVOG 16
: : : : :
Db 478 VSFVGSSTFYLDVAVG 492

RESULT 12

Q9RKFO ID Q9RKFO PRELIMINARY; PRT; 798 AA.

AC Q9RKFO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE SECRETED HYDROLASE.
GN SCE65.23.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy L., Harris D.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL133236; CAB61811.1; -.
KW Hydrolase.
SQ SEQUENCE 798 AA; 88595 MW; 47244CEF60FC555C CRC64;

Query Match 53.4%; Score 47; DB 2; Length 798;

Best Local Similarity 66.7%; Pred. No. 40;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 VSSGGSTYYLD 13
: : : : :
Db 151 VPAGGGTYFD 162

RESULT 13

Q96Q05 ID Q96Q05 PRELIMINARY; PRT; 1176 AA.
AC Q96Q05;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KIAA1882 PROTEIN (FRAGMENT).
GN KIAA1882.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXI.
The complete sequences of 60 new cDNA clones from brain which code for
large proteins."
RL DNA Res. 8:179-187(2001).
DR EMBL; AB067469; BAB67775.1; -.
FT NON_TER
SQ SEQUENCE 1176 AA; 131327 MW; A2159158981D2098 CRC64;

Query Match

Best Local Similarity 53.4%; Score 47; DB 4; Length 1176;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYVLDTVQ 16
 ||| ||| ||| |||
 Db 1109 VSVGSGSTYVLDVAQ 1123

RESULT 14

Q9D8L4 PRELIMINARY; PRT: 473 AA.
 AC Q9D8L4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 1810060009RIK PROTEIN.
 GN IGH-1 OR 1810060009RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; Pubmed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK007918; BAB25349.1; -.
 DR HSSP; P01842; 7FAB.
 DR MGD; MGI:96443; Igh-1.
 DR InterPro; IPR003599; Igh.
 DR InterPro; IPR003597; Igh-cl.
 DR InterPro; IPR003600; Igh-lik.
 DR InterPro; IPR003006; Igh_MHC.
 DR InterPro; IPR003596; Igh_v.
 DR Pfam; PF00047; Igh; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG_lik; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 52.3%; Score 46; DB 11; Length 473;
 Best Local Similarity 47.1%; Pred. No. 33;
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 KVSSGGSTYVLDTVQ 17
 |:| ||||| :|
 Db 69 KIGPGSGSTYINERFKG 85

RESULT 15

Q60111 PRELIMINARY; PRT: 129 AA.
 ID Q60111
 AC Q60111;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 6-PHOSPHOGLUCONATE DEHYDROGENASE (EC 1.1.1.44) (FRAGMENT).
 GN GND.
 OS Yersinia pseudotuberculosis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 OX NCBI_TaxID=633;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GROUP V;
 RA Thanpapillai G., Lan R., Reeves P.R.;
 RT "Molecular evolution in the gnd locus of Salmonella enterica.";
 RL Mol. Biol. Evol. 0:0-0(1994).
 DR EMBL; U14633; AAA58595.1; -.
 DR HSSP; P00349; 2PGD.
 DR InterPro; IPR001744; 6PGD.
 DR Pfam; PF00393; 6PGD; 1.
 KW Oxidoreductase.
 FT NON_TER 1 129
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 13859 MW; 8856FC8ECF4F570 CRC64;
 Query Match 51.1%; Score 45; DB 2; Length 129;
 Best Local Similarity 63.6%; Pred. No. 11;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 6 GGSTYYLDTVQ 16
 ||:|||||:
 Db 95 GGNTYYKDTIR 105
 Search completed: August 19, 2002, 06:58:12
 Job time: 1402 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:11 ; Search time 180.34 Seconds
(without alignments)
10.471 Million cell updates/sec

Title: US-09-339-922A-102

Perfect score: 88

Sequence: 1 KVSSGGSTYYLDIVQG 17

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	17	22 AAB61399	Enhanced 6H6LH hea
2	88	100.0	117	19 AAW76001	Vitaxin antibody h
3	88	100.0	117	19 AAW76003	LM609 antibody hea
4	88	100.0	117	20 AAY06381	Murine monoclonal
5	88	100.0	117	22 AAG63587	A heavy chain vari
6	88	100.0	117	22 AAG63589	A heavy chain vari
7	88	100.0	117	22 AAB61359	Vitaxin heavy chai
8	88	100.0	117	22 AAB61361	Antibody LM609 hea
9	88	100.0	130	20 AAY06379	Murine monoclonal
10	81	92.0	17	22 AAB61400	Enhanced LM609 VH
11	68	77.3	87	22 AAE06990	Mouse germline hea

12	68	77.3	98	22	AAE06978	Mouse germline hea
13	68	77.3	120	17	AAW00240	EGF receptor chime
14	68	77.3	123	19	AAW66099	anti-CD22 monoclon
15	67	76.1	119	16	AAW11919	Humanised MAB SK48
16	67	76.1	125	22	AAW48937	Anti-TrkA murine m
17	67	76.1	247	16	AAW11917	Murine MAB SK48-E2
18	67	76.1	295	22	AAW48934	Anti-TrkA single c
19	66	75.0	159	22	AAU14226	Human novel protel
20	65	73.9	125	20	AAW39817	Llama antibody VHH
21	64	72.7	98	22	AAE06981	Mouse germline hea
22	64	72.7	119	19	AAW69322	15D3 antibody hea
23	64	72.7	119	20	AAW32832	15D3 VH chain prot
24	64	72.7	119	20	AAW73503	Antibody 15D3 hea
25	64	72.7	138	13	AAW20064	MRK16-H chain. Ch
26	64	72.7	139	18	AAW21652	Humanised reshaped
27	64	72.7	139	18	AAW21656	Chimeric MAB 15 PC
28	64	72.7	140	18	AAW21654	Mouse MAB 15 heavy
29	63	71.6	98	21	AAW40094	Anti-hil12 antibod
30	63	71.6	98	21	AAW40095	Anti-hil12 antibod
31	63	71.6	98	21	AAW40107	Anti-hil12 antibod
32	63	71.6	98	21	AAW40108	Anti-hil12 antibod
33	63	71.6	118	18	AAW19877	CEA-specific antib
34	63	71.6	120	17	AAW88510	VHmu for antibody
35	63	71.6	132	22	AAU00576	VH ligand-binding
36	63	71.6	132	22	AAU00580	Modified VH ligand
37	63	71.6	132	22	AAU00581	Modified VH ligand
38	63	71.6	132	22	AAU00582	Modified VH ligand
39	63	71.6	132	22	AAU00583	Modified VH ligand
40	63	71.6	132	22	AAU00584	Modified VH ligand
41	62	70.5	110	18	AAW06207	Rat antibody heavy
42	62	70.5	117	19	AAW48865	Murine monoclonal
43	62	70.5	117	19	AAW48866	Chimeric humanized
44	62	70.5	117	20	AAW86135	Protein sequence o
45	62	70.5	117	20	AAW86137	Protein sequence o

ALIGNMENTS

RESULT 1

AAW61399
ID AAB61399 standard; peptide; 17 AA.

AC AAB61399;

XX 03-APR-2001 (first entry)

DT DT

XX Enhanced 6H6LH heavy chain CDR2.

DE LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;

XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;

KW Inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

OS Unidentified.

XX WO200078815-A1.

PN WO200078815-A1.

XX 28-DEC-2000.

PD 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

PF 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

PR 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

PS Claim 4; Page 46; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta₃ integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta₃-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX Sequence 17 AA;

SQ

Query Match 100.0%; Score 88; DB 22; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.6e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSSGGSTYYLDTVQG 17

Db 1 kvssgggstyyldtvqg 17

RESULT 2

AAW76001

ID AAW76001 standard; Protein; 117 AA.

XX

AC AAW76001;

XX

DT 02-NOV-1998 (first entry)

XX

DE Vitaxin antibody heavy chain variable region protein fragment.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI: 1998-437472/37.

DR N-PSDB; AAV49820.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta₃

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 1; Fig 1a; 129pp; English.

XX

CC This sequence represents a fragment of the vitaxin antibody variable

CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to

CC integrin alphavbeta₃ and can be used to inhibit binding of alphavbeta₃

CC to a ligand and thus block integrin-mediated signal transduction. This is

CC useful in the treatment, prevention and diagnosis of alphavbeta₃-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.

CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,

CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,

CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity

CC more than 90 times greater than that of parent the parent antibody.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 88; DB 19; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.1e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSSGGSTYYLDTVQG 17

Db 50 kvssgggstyyldtvqg 66

RESULT 3

AAW76003

ID AAW76003 standard; Protein; 117 AA.

XX

AC AAW76003;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 antibody heavy chain variable region protein fragment.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI: 1998-437472/37.

DR N-PSDB; AAV49822.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta₃

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 43; Fig 2a; 129pp; English.

XX

CC This sequence represents the LM609 antibody variable heavy chain region.

CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta₃

CC and can be used to inhibit binding of alphavbeta₃ to a ligand and thus

CC block integrin-mediated signal transduction. This is useful in the

CC treatment, prevention and diagnosis of alphavbeta₃-mediated disease,

CC specifically angiogenesis and restenosis (but also e.g. (non-)immune

CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,

CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis

CC etc.). The antibodies contain non-murine framework regions so are

CC suitable for use in humans. Enhanced types of LM609 have affinity more

CC than 90 times greater than that of parent the parent antibody.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 88; DB 19; Length 117;

```

Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSSGGGTYLDTVQG 17
Db 50 kvssgggstyyldtvqg 66

RESULT 4
ID AAY06381 standard; Protein; 117 AA.
AC AAY06381;
XX
DT 06-SEP-1999 (first entry)
DE Murine monoclonal antibody LM609 VH region.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Mus musculus.
XX
PN WO9929888-A1.
XX
PD 17-JUN-1999.
XX
PF 04-DEC-1998; 98WO-US25828.
XX
PR 05-DEC-1997; 97US-0986016.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C;
XX
DR WPI; 1999-394979/33.
XX
PT Production of humanized mouse monoclonal antibodies
XX
PS Disclosure; Page 52-53; 55pp; English.
XX
CC This sequence represents the heavy chain variable region of murine
CC monoclonal antibody LM609. LM609 is directed to integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 88; DB 20; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSSGGGTYLDTVQG 17
Db 50 kvssgggstyyldtvqg 66

RESULT 5
ID AAG63587 standard; Protein; 117 AA.
XX

```

```

AC AAG63587;
XX
DT 15-OCT-2001 (first entry)
DE A heavy chain variable region of LM609 grafted antibody.
XX
KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW cancer.
XX
OS Synthetic.
OS Mus sp.
XX
PN US2001011125-A1.
XX
PD 02-AUG-2001.
XX
PF 30-JAN-1997; 97US-0790540.
XX
PR 30-JAN-1997; 97US-0790540.
XX
PA (HUSE/) HUSE W D.
XX
PI Huse WD;
XX
DR WPI; 2001-496171/54.
DR N-PSDB; AAH74623.
XX
PT New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer
XX
PS Claim 1; Fig 1A; 25pp; English.
XX
CC The present sequence represents the heavy chain variable region of the
CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC specifically recognises the integrin alphavbeta3, and inhibits its
CC functional activity. The LM609 grafted antibody has the
CC complementarity determining regions (CDRs) substituted into a non-murine
CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC polypeptides and fragments are useful in diagnostic and therapeutic
CC purposes, such as in the production of LM609 grafted antibodies and
CC fragments having binding specificity and inhibitory activity against
CC the integrin alphavbeta3. The antibody can be used for the diagnosis
CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC disorders, chronic articular rheumatism, psoriasis, disorders
CC associated with inappropriate or inopportune invasion of vessels such
CC as diabetic retinopathy, neovascular glaucoma and capillary
CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC binding activity of alphavbeta3 that are necessary for progression of
CC an alphavbeta3-mediated disease.
XX
SQ Sequence 117 AA;

```

```

Query Match 100.0%; Score 88; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KVSSGGGTYLDTVQG 17
Db 50 kvssgggstyyldtvqg 66

```

```

RESULT 6
AAG63589
ID AAG63589 standard; Protein; 117 AA.
XX
AC AAG63589;
XX
DT 15-OCT-2001 (first entry)

```



```

XX Huse WD, Wu H;
XX WPI; 2001-050110/06.
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX osteoporosis -
XX Disclosure; Fig 2; 132pp; English.
XX The present invention relates to enhanced LM609 grafted antibodies
XX exhibiting selective binding affinity to alphavbeta_3 integrin or
XX their functional fragments. The antibodies or their functional
XX fragments can be used in the diagnosis and treatment of
XX alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX diseases (such as psoriasis and chronic articular rheumatism),
XX disorders associated with inappropriate or inopportune invasion of
XX vessels (such as diabetic retinopathy, neovascular glaucoma and
XX cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX Sequence 117 AA;

Query Match 100.0%; Score 88; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSSGGSTYYLDTVQG 17
Db 50 kvssgggstyyldtvqg 66

RESULT 9
AAY06379
ID AAY06379 standard; Protein; 130 AA.
XX
AC AAY06379;
XX
DT 06-SEP-1999 (first entry)
XX
DE Murine monoclonal antibody LM609 V kappa.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..2
XX /note= "vector-encoded residues"
XX Region 28..32
XX /note= "CDR1"
XX Region 47..63
XX /note= "CDR2"
XX Region 96..103
XX /note= "CDR3"
XX
XX WO9929888-A1.
XX
XX 17-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX
XX (SCRI ) SCRIPPS RES INST.
XX

```

```

PI Barbas CF, Rader C;
XX
DR WPI; 1999-394979/33.
XX
PT Production of humanized mouse monoclonal antibodies
XX
PS Disclosure; Page 49-50; 55pp; English.
XX
XX This sequence represents the light chain V kappa region of murine
XX monoclonal antibody LM609. LM609 is directed to integrin
XX alpha-v beta-3. It selectively promotes apoptosis of vascular
XX cells that have been stimulated to undergo angiogenesis, making it
XX a tool for cancer diagnosis and therapy. The invention provides
XX humanised antibodies, especially humanised LM609. In such humanized
XX antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX grafted onto a human light chain, and a heavy chain CDR from a mouse
XX antibody is grafted onto a human antibody heavy chain to produce
XX libraries from which a humanised murine antibody having the desired
XX specificity is selected. By preserving the original CDR sequences
XX such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
XX humanisation strategy ensures epitope conservation.
XX Sequence 130 AA;

Query Match 100.0%; Score 88; DB 20; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSSGGSTYYLDTVQG 17
Db 47 kvssgggstyyldtvqg 63

RESULT 10
AAB61400
ID AAB61400 standard; peptide; 17 AA.
XX
AC AAB61400;
XX
DT 03-APR-2001 (first entry)
XX
DE Enhanced LM609 VH CDR2 peptide.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX osteoporosis -
XX Claim 1; Page 45; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
XX exhibiting selective binding affinity to alphavbeta_3 integrin or
XX their functional fragments. The antibodies or their functional

```

CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 17 AA;

Query Match 92.0%; Score 81; DB 22; Length 17;
 Best Local Similarity 94.1%; Pred. No. 4.5e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGSTYYLDTVQG 17
 DB 1 kvssgggstyydpdvvg 17

RESULT 11
 AAE06990
 ID AAE06990 standard; Protein; 87 AA.
 XX
 AC AAE06990;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Mouse germline heavy chain variable (VH) region, VH7183.13.
 XX
 KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VH; heavy chain variable region.
 XX
 OS Mus sp.
 XX
 PN WO200157226-A1.
 XX
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-US03537.
 XX
 PR 03-FEB-2000; 2000US-0497625.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX
 DR WPI; 2001-488888/53.
 XX
 XX Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT -
 XX
 PS Disclosure; Page 159; 183pp; English.
 XX
 XX The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid

CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline heavy chain variable (VH)
 CC region, VH7183.13.
 XX
 SQ Sequence 87 AA;

Query Match 77.3%; Score 68; DB 22; Length 87;
 Best Local Similarity 75.0%; Pred. No. 0.0029;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17
 DB 40 isngggstyydpdvkg 55
 :||:||||| |||:|
 :||:||||| |||:|

RESULT 12
 AAE06978
 ID AAE06978 standard; Protein; 98 AA.
 XX
 AC AAE06978;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Mouse germline heavy chain variable (VH) region, V(H) 50.1.
 XX
 KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VH; heavy chain variable region.
 XX
 OS Mus sp.
 XX
 PN WO200157226-A1.
 XX
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-US03537.
 XX
 PR 03-FEB-2000; 2000US-0497625.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX
 DR WPI; 2001-488888/53.
 XX
 XX Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT -
 XX
 PS Disclosure; Page 154-155; 183pp; English.
 XX
 XX The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin

CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline heavy chain variable (VH)
 CC region, V(H)50.1.
 XX
 SQ Sequence 98 AA;

Query Match 77.3%; Score 68; DB 22; Length 98;
 Best Local Similarity 75.0%; Pred. No. 0.0033;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVQG 17
 Db 51 isngggstyyptvkg 66
 :||||||| |||:

RESULT 13
 AAW00240
 ID AAW00240 standard; Protein; 120 AA.
 XX
 AC AAW00240;
 XX
 DT 22-NOV-1996 (first entry)
 XX
 DE EGF receptor chimeric MAb chMint5 VH chain.
 XX
 KW Mouse-human chimeric antibody; monoclonal antibody; chMint5;
 KW Epidermal growth factor receptor; EGF-R; diagnosis; therapy;
 KW Immunotoxin; Immunocytokine; tumour; cancer.
 XX
 OS Mus musculus.

Key Location/Qualifiers
 Region 31..35
 /label= CDR1
 Region 51..66
 /label= CDR2
 Region 99..109
 /label= CDR3

WO9627010-A1.
 06-SEP-1996.
 01-MAR-1996; 96WO-EP00805.
 01-MAR-1995; 95IT-OFI0036.
 (ITU-Y-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
 Anastasi AM, Colnaghi MT, De Santis R, Di Massimo AM;
 Ferrer Marsal C, Mele A;
 WPI; 1996-412776/41.
 N-PSDB; AAT33445.

PT Murine/human chimeric monoclonal antibody, chMint5 specific for
 PT EGF-R - shows a lower immunogenicity when administered to humans
 XX
 PS Claim 7; Page 15; 28pp; English.
 XX
 CC The amino acid sequence (AAW00240) of the heavy chain variable region
 CC (VH) of the epidermal growth factor receptor (EGF-R)-specific mouse-
 CC human chimeric antibody chMint5 was deduced from a cDNA clone
 CC (AAT33445) obtd. by PCR amplification of murine Mint5 hybridoma DSM
 CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused
 CC to human C-gamma and CK regions. Constructs were expressed in
 CC CHO cell transfectants. chMint5 shows lower immunogenicity than
 CC Mint5 when administered to humans. It can be used in diagnostic
 CC assays or used to produce immunotoxins or immunocytokines useful
 CC for tumour therapy.
 XX
 SQ Sequence 120 AA;

Query Match 77.3%; Score 68; DB 17; Length 120;
 Best Local Similarity 75.0%; Pred. No. 0.0041;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVQG 17
 Db 51 isngggstyyptvkg 66
 :||||||| |||:

RESULT 14
 AAW66099
 ID AAW66099 standard; Protein; 123 AA.
 XX
 AC AAW66099;
 XX
 DT 10-DEC-1998 (first entry)
 XX
 DE anti-CD22 monoclonal antibody heavy chain variable region.
 XX
 KW anti-CD22 monoclonal antibody heavy chain variable region; VL;
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;
 KW malignant B-cell; immunodiagnosis; RFB4 IgG.
 XX
 OS Mammalia.

Key Location/Qualifiers
 FT Misc-difference 121
 FT /note= "Encoded by gtc"

WO9841641-A1.
 24-SEP-1998.
 19-MAR-1998; 98WO-US05453.
 20-MAR-1997; 97US-0041437.
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Fitzgerald D, Kreitman R, Mansfield E, Pastan I;
 WPI; 1998-521227/44.
 N-ESDB; AAV07642.

Recombinant anti-CD22 antibodies and immuno-conjugates - of
 antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin
 or a label; for inhibiting malignant B-cells
 Claim 6; Fig 1; 71pp; English.

The invention claims for a recombinant immunoconjugate comprising
 of a therapeutic agent (e.g. Pseudomonas exotoxin) or a detectable
 label peptide bonded to a recombinant anti-CD22 antibody (RFB4 IgG)
 having the present variable heavy (VH) chain with a cysteine residue

CC at amino acid 44 and a variable light (VL; AAW66098) chain with a
 CC cysteine residue at amino acid 100. The immunconjugate is claimed
 CC to inhibit the growth of malignant B-cells in vivo, such as rodent,
 CC canine or primate B-cells. The anti-CD22 antibody is claimed useful
 CC for detecting CD22 protein in a sample or in vivo in a mammal, and
 CC can be used in diagnostic kits.
 XX
 SQ Sequence 123 AA;

Query Match 77.3%; Score 68; DB 19; Length 123;
 Best Local Similarity 75.0%; Pred. No. 0.0043;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
 :||||| ||| |||:
 Db 51 issgggttyypdtvkg 66

RESULT 15
 AAW11919
 ID AAW11919 standard; Protein; 119 AA.
 XX AC AAW11919;
 XX
 DT 24-JUN-1997 (first entry)
 DE Humanised MAb SK48-E26 heavy chain.
 XX
 KW Interleukin-1 beta; IL-1 beta; recombinant antibody;
 KW humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAb; SK48-E26; inflammation; therapy.
 XX
 OS Chimeric Homo sapiens;.
 OS Chimeric Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 1..30
 FT /label= FR1
 FT /note= "framework region 1"
 FT Region 31..35
 FT /label= CDR1
 FT /note= "complementarity determining region 1
 FT (Claim 10, page 48)"
 FT Region 36..49
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 50..66
 FT /label= CDR2
 FT /note= "complementarity determining region 2
 FT (Claim 10, page 48)"
 FT Region 67..98
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 99..108
 FT /label= CDR3
 FT /note= "complementarity determining region 3
 FT (Claim 10, page 48)"
 FT Region 109..119
 FT /label= FR4
 FT /note= "framework region 4"
 XX
 PN WO9501997-A1.
 XX
 PD 19-JAN-1995.
 XX
 PF 07-JUL-1994; 94WO-US07659.
 XX
 PR 09-JUL-1993; 93US-0090534.
 PR 04-MAR-1994; 94US-0206190.
 XX
 PA (SHIK) SMITHKLINE BEECHAM CORP.

PI Gross MS, Hurle MR, Jackson JR, Jonak ZL, Theisen TW;
 PI Young PR;
 XX
 DR WPI; 1995-066868/09.
 DR N-PSDB; AAT51438.
 XX
 PT Recombinant and humanised chimeric antibodies against human
 PT interleukin-1-beta - for preventing and treating
 PT interleukin-mediated inflammatory disorders
 XX
 PS Claim 39; Page 40-41; 62pp; English.
 XX
 CC The heavy chain variable region (AAW11919) and light chain variable
 CC region (AAW11920) of humanised anti-human interleukin-1 beta (IL-1
 CC beta) murine monoclonal antibody (MAb) SK48-E26 comprise the
 CC complementarity determining regions from MAb SK48-E26 (see also
 CC AAW11917-18) grafted into human frameworks. The humanised antibody
 CC can be produced in e.g. COS cells transfected with vectors carrying
 CC humanised heavy and light chain nucleic acids (AAT51437-39) for use
 CC in the treatment and prevention of IL-1 mediated inflammatory
 CC disorders.
 XX
 SQ Sequence 119 AA;

Query Match 76.1%; Score 67; DB 16; Length 119;
 Best Local Similarity 75.0%; Pred. No. 0.0059;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
 :||||| ||| |||:
 Db 51 issgggttyypdtvkg 66

Search completed: August 19, 2002, 06:39:12
 Job time: 1473 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:39 ; Search time 61.75 Seconds
(without alignments)
6.724 Million cell updates/sec

Title: US-09-339-922A-102

Perfect score: 88

Sequence: 1 KVSQGGSTYYLDTVQG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	77.3	125	1	US-08-331-398A-65
2	68	77.3	125	2	US-08-331-397B-65
3	68	77.3	125	2	US-08-759-804A-64
4	67	76.1	119	5	PCT-US94-07659-6
5	67	76.1	247	5	PCT-US94-07659-2
6	64	72.7	119	2	US-08-475-000-16
7	64	72.7	119	2	US-08-483-199-16
8	64	72.7	119	2	US-08-484-508-16
9	63	71.6	17	1	US-08-264-093-22
10	63	71.6	118	2	US-08-552-816A-11
11	63	71.6	120	1	US-08-264-093-14
12	62	70.5	117	4	US-08-752-693A-3
13	62	70.5	117	4	US-08-752-693A-4
14	62	70.5	118	1	US-08-326-362-2
15	62	70.5	136	1	US-08-253-877C-57
16	62	70.5	136	2	US-08-452-164A-57
17	62	70.5	136	4	US-08-976-183A-31
18	62	70.5	136	4	US-08-976-183A-32
19	62	70.5	136	4	US-08-976-183A-33
20	62	70.5	136	4	US-08-976-183A-34
21	62	70.5	150	4	US-08-576-183A-55
22	62	70.5	158	2	US-08-653-402B-6
23	62	70.5	158	2	US-08-653-402B-10
24	62	70.5	237	2	US-08-224-591-16
25	62	70.5	237	2	US-08-926-789-16
26	62	70.5	241	2	US-08-224-591-18
27	62	70.5	241	2	US-08-926-789-18

28 62 70.5 265 4 US-09-420-592A-5 Sequence 5, Appl
29 60 68.2 120 2 US-08-428-197-20 Sequence 20, Appl
30 60 68.2 120 2 US-08-428-197-22 Sequence 22, Appl
31 60 68.2 120 2 US-08-428-197-24 Sequence 24, Appl
32 60 68.2 120 2 US-08-428-197-26 Sequence 26, Appl
33 60 68.2 120 2 US-08-428-197-28 Sequence 28, Appl
34 60 68.2 120 2 US-08-428-197-30 Sequence 30, Appl
35 60 68.2 120 2 US-08-428-197-32 Sequence 32, Appl
36 60 68.2 120 2 US-08-428-197-34 Sequence 34, Appl
37 60 68.2 120 2 US-08-428-197-40 Sequence 40, Appl
38 60 68.2 120 5 PCT-US93-10555-20 Sequence 20, Appl
39 60 68.2 120 5 PCT-US93-10555-22 Sequence 22, Appl
40 60 68.2 120 5 PCT-US93-10555-24 Sequence 24, Appl
41 60 68.2 120 5 PCT-US93-10555-26 Sequence 26, Appl
42 60 68.2 120 5 PCT-US93-10555-28 Sequence 28, Appl
43 60 68.2 120 5 PCT-US93-10555-30 Sequence 30, Appl
44 60 68.2 120 5 PCT-US93-10555-32 Sequence 32, Appl
45 60 68.2 120 5 PCT-US93-10555-34 Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-331-398A-65
; Sequence 65, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-1361100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
HEAVY chain region"
US-08-331-398A-65

Query Match 77.3%; Score 68; DB 1; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.0018;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGTTYLDTVQG 17
Db 51 ISNGGGSTYYPDVKG 66

RESULT 2
US-08-331-397B-65
Sequence 65, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-Specific Antibody Fragments, Fusion Proteins, and Uses Thereof
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
HEAVY chain region"
US-08-331-397B-65

Query Match 77.3%; Score 68; DB 2; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.0018;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 2 VSSGGGTTYLDTVQG 17
Db 51 ISNGGGSTYYPDVKG 66

RESULT 3
US-08-759-804A-64
Sequence 64, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments, Fusion Proteins, and Uses Thereof
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
HEAVY chain region"
US-08-759-804A-64

Query Match 77.3%; Score 68; DB 2; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.0018;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGTTYLDTVQG 17
Db 51 ISNGGGSTYYPDVKG 66

Db 51 ISNGGGSTYYPDTVKG 66

RESULT 4

PCT-US94-07659-6
; Sequence 6, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurler, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 76.1%; Score 67; DB 5; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.0024; 2; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VSSGGGTYLDTVQ 17

Db 51 ISNGGGTYYPDTVKG 66

RESULT 5

PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurler, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta

; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 76.1%; Score 67; DB 5; Length 247;
Best Local Similarity 75.0%; Pred. No. 0.0052;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VSSGGGTYLDTVQ 17

Db 70 ISSGGGTYPDYK 85

RESULT 6

US-08-475-000-16
; Sequence 16, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424

```

; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-000-16

```

```

Query Match 72.7%; Score 64; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.0068;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2 VSSGGGSTYYLDTVOG 17
:|||||:|||||:|:|
Db 51 ISSGGGNTYYPDSVKG 66

```

```

RESULT 7
US-08-483-199-16
; Sequence 16, Application US/08483199
; Patent No. 5849877
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94562-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,199
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-199-16

```

```

Query Match 72.7%; Score 64; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.0068;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2 VSSGGGSTYYLDTVOG 17
:|||||:|||||:|:|
Db 51 ISSGGGNTYYPDSVKG 66

```

```

RESULT 8
US-08-484-508-16
; Sequence 16, Application US/08484508
; Patent No. 5948647
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94562-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,508
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-508-16

```

```

Query Match 72.7%; Score 64; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.0068;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2 VSSGGGSTYYLDTVOG 17
:|||||:|||||:|:|
Db 51 ISSGGGNTYYPDSVKG 66

```

```

RESULT 9
US-08-264-093-22
; Sequence 22, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible

```


SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ORGANISM: Mice A33

ORIGINAL SOURCE:
OBCANTSM, Human A35

US-08-752-693A-4

Query Match 70.5%; Score 62; DB 4; Length 117;
Best Local Similarity 68.8%; Pred. No. 0.014;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Caps 0;

QY 2 VSSGGSTYYLDTVQG 17
:||||| :||||| :|:
Db 51 ISSGGSTYYLDSVKG 66

```

RESULT 14
US-08-326-62-2
; Sequence 2, Application US/08326362
; Patent No. 5730981
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; APPLICANT: Dippold, Wolfgang
; TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
; TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315

```

```
Query Match          70.5%; Score 62; DB 1; Length 118;
Best Local Similarity 68.8%; Pred. No. 0.014;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 VSSGGSTYYLDTVQG 17
:||||| ||||| |:|:|
Db 51 ISSGGASTYYRDSVKG 66

RESULT 15
US-08-253-877C-57

```

; Sequence 57, Application US/08253877C
; Patent No. 5773001
;
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinmann, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
;
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; Agents and Intermediates for Their Synthesis
;
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-253-877C-57

```

Query Match 70.5%; Score 62; DB 1; Length 136;
Best Local Similarity 68.8%; Pred. No. 0.016;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17
 :||| | ||| |:|
Db 70 ISSGGSYTYLDSVKG 85

Search completed: August 19, 2002, 06:34:40
Job time: 1201 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:04 ; Search time 78.53 Seconds
(Without alignments)
20.801 Million cell updates/sec

Title: US-09-339-922A-104
Perfect score: 91
Sequence: 1 KVSSGGSTYYPDVTQV 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	89.0	113	2 S26468	Ig heavy chain V r
2	81	89.0	117	1 HVMS34	Ig heavy chain pre
3	78	85.7	117	1 HVMS84	Ig heavy chain pre
4	77	84.6	108	2 PL0248	Ig heavy chain V r
5	77	84.6	111	2 PH1007	Ig heavy chain V r
6	74	81.3	108	2 PH1006	Ig heavy chain V r
7	74	81.3	118	2 S20641	Ig heavy chain V r
8	74	81.3	138	2 S09258	Ig heavy chain V r
9	72	79.1	113	2 S02717	Ig heavy chain V r
10	72	79.1	115	2 PH1538	Ig H chain V regio
11	72	79.1	117	1 HVMSRF	Ig heavy chain pre
12	72	79.1	119	2 PH1548	Ig H chain V regio
13	72	79.1	119	2 PH1549	Ig H chain V regio
14	70	76.9	111	2 S51211	Ig heavy chain V r
15	69	75.8	117	2 PH1552	Ig H chain V regio
16	68	74.7	117	2 PH1553	Ig H chain V regio
17	68	74.7	121	2 H27888	Ig heavy chain V r
18	68	74.7	254	2 B31790	Ig heavy chain V r
19	67	73.6	118	2 S00700	Ig heavy chain V r
20	67	73.6	119	2 PH0098	Ig heavy chain V r
21	67	73.6	124	2 I27888	Ig heavy chain V r
22	66	72.5	106	2 PH1008	Ig heavy chain V r
23	66	72.5	108	2 PH1011	Ig heavy chain V r
24	66	72.5	123	2 G27888	Ig heavy chain V r
25	65	71.4	83	2 S25913	Ig heavy chain V r
26	65	71.4	94	2 S14580	Ig heavy chain V r
27	65	71.4	102	2 S14581	Ig heavy chain V r
28	65	71.4	108	2 PH1010	Ig heavy chain V r
29	65	71.4	111	2 S40090	Ig heavy chain - m

30 65 71.4 119 2 F27888 Ig heavy chain V r
31 65 71.4 119 2 B34353 anti-peptide Fab'
32 65 71.4 120 2 S55336 Ig heavy chain V r
33 65 71.4 120 2 S55337 Ig heavy chain V r
34 65 71.4 122 2 E27888 Ig heavy chain V r
35 64 70.3 70 2 PL0250 Ig heavy chain V r
36 64 70.3 97 1 HVMS91 Ig heavy chain V r
37 64 70.3 112 2 S26327 Ig heavy chain V r
38 64 70.3 112 2 A27889 Ig heavy chain V r
39 64 70.3 117 2 PL0249 Ig heavy chain V r
40 64 70.3 117 2 PL0252 Ig heavy chain V r
41 63 69.2 121 2 I27887 Ig heavy chain V r
42 63 69.2 123 2 S63597 Ig heavy chain V r
43 63 69.2 124 2 C27888 Ig heavy chain V r
44 63 69.2 548 2 S38864 Ig epsilon chain C
45 62 68.1 114 2 PH1009 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991

A:Reference number: S26459
A:Accession: S26468
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 81; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.3e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPDVTQV 17
:|||||||:|
Db 47 ISSGGSTYYPDVTQV 62

RESULT 2

HVMS34
Ig heavy chain precursor V region (345) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: J00502
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: J00501; MUID:89279149
A:Accession: J00502
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A>Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

```
Query Match      89.0%; Score 81; DB 1; Length 117;
Best Local Similarity 87.5%; Pred. No. 2.4e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17
:|||||
Db 70 ISSGGGTTYPTVKG 85

RESULT 3
HVM584
Ig heavy chain precursor V region (5-84) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: J0505
R:Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: J0501; MUID:89279149
A:Accession: J0505
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <NAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match      85.7%; Score 78; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 6.9e-05;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17
:|||||
Db 70 ISNGGGTTYPTVKG 85

RESULT 4
PL0248
Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0248
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 263-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0248
A:Molecule type: mRNA
A:Residues: 1-108 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-24/Region: framework 1
F:9-92/Domain: immunoglobulin homology <IMM>
F:25-29/Region: complementarity-determining 1
F:30-43/Region: framework 2
F:44-60/Region: complementarity-determining 2
F:61-92/Region: framework 3
F:93-99/Region: complementarity-determining 3
F:100-108/Region: framework 4

Query Match      84.6%; Score 77; DB 2; Length 108;
Best Local Similarity 81.2%; Pred. No. 9e-05;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17
:|||||
```

```
Db 45 ISSGGGTTYPDSVKG 60

RESULT 5
PHI007
Ig heavy chain V region (clone 163-cl) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PHI007
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PHI007
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-111 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      84.6%; Score 77; DB 2; Length 111;
Best Local Similarity 81.2%; Pred. No. 9.3e-05;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17
:|||||
Db 51 ISSGGGTTYPDSVKG 66

RESULT 6
PHI006
Ig heavy chain V region (clone 202.33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PHI006
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PHI006
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match      81.3%; Score 74; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 0.00026;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17
:|||||
Db 46 ISGGGNTYPTVKG 61

RESULT 7
S20641
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20641
R:Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice re
A:Reference number: S20639
A:Accession: S20641
A:Status: preliminary
```


A:Molecule type: DNA
 A:Residues: 1-118 <LOS>
 A:Cross-references: EMBL:X65003; NID:952602; PID:CAA46136.1; PID:g52603
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 74; DB 2; Length 118;
 Best Local Similarity 75.0%; Pred. No. 0.00029;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VSSGGGTTYPDVTQVQ 17
 Db 51 ISSGGGTTYPDVSKG 66

RESULT 8
 S09258
 Ig heavy chain V region precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999
 C:Accession: S09258
 R:Hamada, H.; Maetzawa, K.; Tsuruo, T.
 Nucleic Acids Res. 18, 1900, 1990
 A:Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK
 A:Reference number: S09258; MUID:90245594
 A:Accession: S09258
 A:Molecule type: DNA
 A:Residues: 1-138 <HAM>
 A:Cross-references: EMBL:X51719; NID:953207; PID:CAA36012.1; PID:g297545
 C:Genetics:
 A:Introns: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 74; DB 2; Length 130;
 Best Local Similarity 75.0%; Pred. No. 0.00034;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VSSGGGTTYPDVTQVQ 17
 Db 70 ISSGGGTTYPDVSKG 85

RESULT 9
 S02717
 Ig heavy chain V region (clone pH62) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:Accession: S02717
 R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Glotz, D.; Capra, J.D.; Zanetti, M.
 submitted to the EMBL Data Library, February 1989
 A:Reference number: S02717
 A:Accession: S02717
 A:Molecule type: DNA
 A:Residues: 1-113 <SOL>
 A:Cross-references: EMBL:Y00744; NID:952472; PID:CAA68713.1; PID:g1334095
 A:Note: this sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 72; DB 2; Length 113;
 Best Local Similarity 75.0%; Pred. No. 0.00056;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 VSSGGGTTYPDVTQVQ 17
 Db 51 INSGGGTTYPDVTQVQ 66

RESULT 10
 PH1538
 Ig H chain V region (clone 13G12) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
 C:Accession: PH1538
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma
 A:Reference number: PH1528; MUID:93210465
 A:Accession: PH1538
 A:Molecule type: mRNA
 A:Residues: 1-115 <MUR>
 A:Note: the stop codons X appear in residues 82, 85 and 106
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 72; DB 2; Length 115;
 Best Local Similarity 75.0%; Pred. No. 0.00057;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 VSSGGGTTYPDVTQVQ 17
 Db 50 INSGGGTTYPDVTQVQ 65

RESULT 11
 HVMSRF
 Ig heavy chain precursor V region (RF) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: JT0503
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar
 A:Reference number: JT0501; MUID:89279149
 A:Accession: JT0503
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: this sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; hybridoma; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 79.1%; Score 72; DB 1; Length 117;
 Best Local Similarity 75.0%; Pred. No. 0.00058;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 VSSGGGTTYPDVTQVQ 17
 Db 70 INSGGGTTYPDVTQVQ 85

RESULT 12
 PH1548
 Ig H chain V region (clone 12F4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1548
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma
 A:Reference number: PH1528; MUID:93210465

A:Accession: PH1548
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 72; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.00059;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17
: : | | | | | | | | :
DB 51 INSHGGTTYPTVKG 66

RESULT 13

PH1549
Ig H chain V region (clone 13F1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1549
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1549
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 72; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.00059;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17
: : | | | | | | | | :
DB 51 INSHGGTTYPTVKG 66

RESULT 14

S51211
Ig heavy chain V region (AC7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
C:Accession: S51211; S58929
R:Jarrin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G.
FEBS Lett. 354, 169-172, 1994
A:Title: A synthetic peptide with anti-platelet activity derived from a CDR of an anti-G
A:Reference number: S51210; MUID:95046326
A:Accession: S51211
A:Molecule type: mRNA
A:Residues: 9-111 <JAR>
A:Accession: S58929
A:Molecule type: protein
A:Residues: 1-20 <JAR2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 70; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 0.0011;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17
: : | | | | | | | | :
DB 51 INSHGGTTYPTVKG 66

RESULT 15

PH1552
Ig H chain V region (clone 16E4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: PH1552
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1552
A:Molecule type: mRNA
A:Residues: 1-117 <MUK>

A:Note: the stop codon X appears in residue 87
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 69; DB 2; Length 117;
Best Local Similarity 68.8%; Pred. No. 0.0017;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17
: : | | | | | | | | :
DB 51 INTNGGTTYPTVKG 66

Search completed: August 19, 2002, 06:36:05
Job time: 1286 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:08 ; Search time 51.81 Seconds
(without alignments)
12.705 Million cell updates/sec

Title: US-09-339-922A-104
Perfect score: 91
Sequence: 1 KVSSGGSTYPDTVQG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	81	89.0	117	1 HV55_MOUSE	P18526 mus musculus
2	78	85.7	117	1 HV54_MOUSE	P18525 mus musculus
3	72	79.1	117	1 HV53_MOUSE	P18524 mus musculus
4	64	70.3	97	1 HV56_MOUSE	P18527 mus musculus
5	61	67.0	98	1 HV57_MOUSE	P18528 mus musculus
6	61	67.0	117	1 HV58_MOUSE	P18529 mus musculus
7	58	63.7	117	1 HV3C_HUMAN	P01764 homo sapien
8	53	58.2	119	1 HV3L_HUMAN	P01773 homo sapien
9	52	57.1	116	1 HV05_CARAU	P19181 carassius a
10	52	57.1	117	1 HV59_MOUSE	P18530 mus musculus
11	51	56.0	442	1 CELF_BACSU	P46320 bacillus su
12	49	53.8	115	1 HV3F_HUMAN	P01767 homo sapien
13	48	52.7	449	1 CELF_ECOLI	P17411 escherichia
14	47	51.6	136	1 HV16_MOUSE	P01783 mus musculus
15	45	49.5	117	1 HV02_CANPA	P01785 canis famil
16	45	49.5	964	1 CAPT_TOBAC	P27154 nicotiana t
17	44	48.4	749	1 CAT_AASPFU	P78574 aspergillus
18	43	47.3	426	1 GUNZ_ERWCH	P07103 erwinia chr
19	43	47.3	472	1 6PGD_LACIL	Q9chu6 lactococcus
20	43	47.3	472	1 6PGD_LACIL	P96789 lactococcus
21	43	47.3	862	1 POLG_ECI6H	Q68790 echovirus 1
22	43	47.3	879	1 MANB_BOVIN	Q29444 bos taurus
23	43	47.3	2196	1 POLG_ECO5N	Q9ylj1 e genome po
24	42.5	46.7	147	1 AIF1_HUMAN	P55008 homo sapien
25	42	46.2	96	1 YC4_TYLCV	P27271 tomato yell
26	42	46.2	449	1 TBA2_SCHPO	P04689 schizosacch
27	42	46.2	468	1 6PG2_BACSU	P80859 bacillus su
28	42	46.2	492	1 6PG2_SCHPO	P78812 schizosacch
29	41.5	45.6	114	1 HV3B_HUMAN	P01763 homo sapien
30	41.5	45.6	122	1 HV3A_HUMAN	P01762 homo sapien
31	41	45.1	289	1 BSNL_BACSU	Q03091 bacillus su
32	41	45.1	340	1 THPS_SULAC	P17118 sulfotobus
33	41	45.1	1070	1 RPOB_TOBAC	P06271 nicotiana t

ALIGNMENTS

RESULT 1

HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.

AC P18526;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region 345 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/CJ;

RX MEDLINE=89279149; PubMed=2499654;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during

the primary immune response.";

RL J. Exp. Med. 169:2007-2019(1989).

CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR PIR; JT0502; HVMS34.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.

FT DOMAIN 20 49 FRAMEWORK-1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 55 68 FRAMEWORK-2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 86 117 FRAMEWORK-3.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 89.0%; Score 81; DB 1; Length 117;

Best Local Similarity 87.5%; Pred. No. 8.5e-06;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGSTYPDTVQG 17

DB 70 ISSGGSTYPDTVKG 85

RESULT 2

HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.

AC P18525;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region 5-84 precursor.

```

OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0505; HVMS84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 117 FRAMEWORK-1.
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 54 FRAMEWORK-2.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 85.7%; Score 78; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 2.5e-05;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
DB 70 ISNGGGTYYPDTVKG 85

RESULT 3
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0503; HVMSRF.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1
FT CHAIN 19 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 117 FRAMEWORK-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.

```

```

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 79.1%; Score 72; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00021;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
DB 70 ISNGGGTYYPDTVKG 85

RESULT 4
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 70.3%; Score 64; DB 1; Length 97;
Best Local Similarity 78.6%; Pred. No. 0.0029;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SGGGTYYPDTVQG 17
DB 52 SSGGTYYPDSVKG 65

RESULT 5
HV57_MOUSE
ID HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

```

RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JT0501; HVMS596.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT NON_TER 98
 SQ SEQUENCE 98 AA: 11007 MW: 864447F92FBF59B CRC64;

Query Match 67.0%; Score 61; DB 1; Length 98;
 Best Local Similarity 62.5%; Pred. No. 0.0085;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
 :||| |||||:|
 Db 51 ISDGGTYYPDSVKG 66

RESULT 6

HV58_MOUSE
 ID HV58_MOUSE STANDARD; PRT; 117 AA.
 AC P18529;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5-76 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JT0506; HVMS57.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA: 12991 MW: 93A04782B7858FA0 CRC64;

Query Match 67.0%; Score 61; DB 1; Length 117;
 Best Local Similarity 68.8%; Pred. No. 0.01;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
 :||| |||||:|
 Db 70 ISSGLXYYPDSVKG 85

RESULT 7

HV3C_HUMAN
 ID HV3C_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region VH26 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (MVELOMA PROTEIN BUR).
 RX MEDLINE=79151016; PubMed=107164;
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
 IgA1 protease, digestion, Fab and Fc fragments, and the complete
 RT amino acid sequence of the alpha 1 heavy chain.";
 RL J. Biol. Chem. 254:2865-2874(1979).
 DR PIR: A02056; ALHBR.
 DR HSSP: P01772; 2IG2.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.

ID HV3C_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region VH26 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81101090; PubMed=6450418;
 RA Matthysens G., Rabbitts T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 RT heavy chain variable region."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J00236; AAA53516.1; -;
 DR EMBL: M35415; AAA58735.1; -;
 DR PIR: A02047; H3HU26.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
 FT NON_TER 117 117
 FT SEQUENCE 117 AA: 12582 MW: E826733F1A3CB0F1 CRC64;

Query Match 63.7%; Score 58; DB 1; Length 117;
 Best Local Similarity 62.5%; Pred. No. 0.03;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
 :| ||||| |:
 Db 70 ISGSGGTYYGDSVKG 85

RESULT 8

HV3L_HUMAN
 ID HV3L_HUMAN STANDARD; PRT; 119 AA.
 AC P01773;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region BUR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (MVELOMA PROTEIN BUR).
 RX MEDLINE=79151016; PubMed=107164;
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
 RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
 RT amino acid sequence of the alpha 1 heavy chain.";
 RL J. Biol. Chem. 254:2865-2874(1979).
 DR PIR: A02056; ALHBR.
 DR HSSP: P01772; 2IG2.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin v region; Glycoprotein.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 58.2%; Score 53; DB 1; Length 119;
 Best Local Similarity 56.2%; Pred. No. 0.18;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYPPTVQV 17
 :||| ||| :|||
 Db 51 ISYGSBTYYADSVRG 66

RESULT 9
 ID HV05_CARAU STANDARD; PRT; 116 AA.
 AC P19181;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain v region 5A precursor.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=88144476; PubMed=3125551;
 RA Wilson M.R., Middleton D., Warr G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure
 and family relationships of two genes and a pseudogene in a teleost
 fish.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 DR PIR: B28966; B28966.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin v region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DISULFID 41 114 BY SIMILARITY.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 57.1%; Score 52; DB 1; Length 116;
 Best Local Similarity 75.0%; Pred. No. 0.25;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGSTYPPTVQV 17
 :||| ||| :|||
 Db 73 GGSTYYADSVKG 84

RESULT 10
 ID HV59_MOUSE STANDARD; PRT; 117 AA.
 AC P18530;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain v region 7-39 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JTO507; HVMS39.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin v region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 57.1%; Score 52; DB 1; Length 117;
 Best Local Similarity 56.2%; Pred. No. 0.25;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYPPTVQV 17
 :||| ||| :|||
 Db 70 ISGGVSTYTPDSVKG 85

RESULT 11
 ID CELF_BACSU STANDARD; PRT; 442 AA.
 AC P46320;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Probable 6-phospho-beta-glucosidase (EC 3.2.1.86).
 GN CELF OR CELF OR LICH.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RX MEDLINE=97144536; PubMed=8950303;
 RA Tobisch S., Glaser P., Krueger S., Hecker M.;
 RT "Identification and characterization of a new beta-glucoside
 utilization system in Bacillus subtilis.";
 RL J. Bacteriol. 179:496-506(1997).
 RN [2]
 RN SEQUENCE OF 1-305 FROM N.A.
 RP STRAIN=168 / BGSC1A1;
 RX MEDLINE=97124196; PubMed=8969509;
 RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
 RA Miwa Y., Fujita Y.;
 RT "Sequencing of a 65 kb region of the Bacillus subtilis genome
 containing the lic and cel loci, and creation of a 177 kb contig
 covering the gnt-sacXI region.";
 RL Microbiology 142:3113-3123(1996).

CC -1- FUNCTION: HYDOLYZES A WIDE VARIETY OF P-BETA-GLUCOSIDES INCLUDING
 CC CELLULOSE-6P, SALICIN-6P, ARUTIN-6P, GENTIOBIOS-6P, METHYL-
 CC BETA-GLUCOSIDE-6P AND P-NITROPHENYL-BETA-D-GLUCOPYRANOSIDE-6P (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 6-phospho-beta-D-glucoside-(1,4)-D-glucose +
 CC H(2)O = D-glucose 6-phosphate + glucose.
 CC -1- COFACTOR: NAD AND A DIVALENT METAL ION. MANGANESE, COBALT AND
 CC NICKEL IONS ENHANCE ACTIVITY WHEREAS MAGNESIUM, CALCIUM,
 CC STRONTIUM AND ZINC IONS DO NOT (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTETRAMER OF FOUR NONCOVALENTLY LINKED SUBUNITS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 4 OF GLYCOSYL HYDROLASES.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z49992; CAA90288.1; -;
 CC EMBL; D83026; BAA11746.1; -;
 CC EMBL; Z99123; CAB15882.1; -;
 CC Subtilist; BG11350; celf.
 CC InterPro; IPR001088; Glyco_hydro.4.
 CC Pfam; PF02056; Glyco_hydro.4; 1.
 CC PRINTS; PR00732; GLHYDRLASE4.
 CC PRODOM; PD006892; Glyco_hydro.4; 1.
 CC PROSITE; PS01324; GLYCOSYL_HYDROL_F4; 1.
 CC Hydrolase; Glycosidase; NAD; Cobalt; Manganese; Nickel;
 CC Complete proteome.
 CC NP_BIND 7 40 NAD (POTENTIAL).
 CC ACT_SITE 112 112 PROTON DONOR (BY SIMILARITY).
 CC ACT_SITE 354 354 NUCLEOPHILE (BY SIMILARITY).
 CC SEQUENCE 442 AA; 48711 MW; 91CB42C8BB93F567 CRC64;
 CC
 CC Query Match 56.0%; Score 51; DB 1; Length 442;
 CC Best Local Similarity 56.2%; Pred. NO. 1.4;
 CC Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC Qy 2 VSSGGGTYYPPTVOG 17
 CC I: | | | | | | | | | |
 CC Db 8 VTIGGGSSYTPPEVG 23
 CC
 CC RESULT 12
 CC HV3F_HUMAN
 CC ID HV3F_HUMAN STANDARD; PRT; 115 AA.
 CC AC P01767;
 CC DT 21-JUL-1986 (Rel. 01, Created)
 CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
 CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
 CC DE Ig heavy chain V-II region BUT.
 CC OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE.
 CC RX MEDLINE=78137069; PubMed=416441;
 CC RA Torano A., Putnam F.W.;
 CC RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
 CC RT IgA2 immunoglobulin of the A2m (2) allotype";
 CC Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPES, C
 CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
 CC PIR; A02050; A2HUBU.
 CC DR HSSP; P01789; 1MCP.
 CC DR InterPro; IPR003006; Ig_MHC.
 CC DR InterPro; IPR003596; Ig_V.
 CC DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;
 CC
 CC Query Match 53.8%; Score 49; DB 1; Length 115;
 CC Best Local Similarity 66.7%; Pred. NO. 0.71;
 CC Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Qy 6 GGSTYYPTVOG 17
 CC I: | | | | | | | | | |
 CC Db 54 GGTYYADSVKG 65
 CC
 CC RESULT 13
 CC CELF_ECOLI
 CC ID CELF_ECOLI STANDARD; PRT; 449 AA.
 CC AC P17411; P78290; P37795;
 CC DT 01-AUG-1990 (Rel. 15, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE 6-phospho-beta-glucosidase (EC 3.2.1.86) (Cellulose-6-phosphate
 CC DE hydrolase).
 CC GN CELF OR B1734.
 CC OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 CC OX NCBI_TaxID=562;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=K12;
 CC RX MEDLINE=90185127; PubMed=2179047;
 CC RA Parker L.L., Hall B.G.;
 CC RT "Characterization and nucleotide sequence of the cryptic cell operon
 CC RT of Escherichia coli K12";
 CC RL Genetics 124:455-471(1990).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=K12 / MG1655;
 CC RX MEDLINE=97426617; PubMed=9278503;
 CC RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 CC RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 CC RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 CC RA Mau B., Shao Y.;
 CC RT "The complete genome sequence of Escherichia coli K-12";
 CC RL Science 277:1453-1474(1997).
 CC RN [3]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=K12;
 CC RX MEDLINE=97251357; PubMed=9097039;
 CC RA Aliba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 CC RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 CC RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 CC RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima J.,
 CC RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
 CC RA Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
 CC RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 CC RT corresponding to the 28.0-40.1 min region on the linkage map";
 CC RL DNA Res. 3:363-377(1996).
 CC RN [4]
 CC RP SEQUENCE OF 361-449 FROM N.A.
 CC RC STRAIN=K12;
 CC RX MEDLINE=94166755; PubMed=8121401;
 CC RA Guzzo A., Dubow M.S.;
 CC RT "A luxAB transcriptional fusion to the cryptic celf gene of
 CC RT Escherichia coli displays increased luminescence in the presence of
 CC RT nickel";
 CC RL Mol. Gen. Genet. 242:455-460(1994).
 CC RN [5]
 CC RP SEQUENCE OF 1-30, AND CHARACTERIZATION.
 CC RX MEDLINE=20042356; PubMed=10572139;
 CC RA Thompson J., Ruvinov S.B., Freedberg D.I., Hall B.G.;

RT "Cellobiose-6-phosphate hydrolase (CelF) of Escherichia coli:
 RT characterization and assignment to the unusual family 4 of
 RL glycosylhydrolases.";

CC J. Bacteriol. 181:7339-7345(1999).

CC -1- FUNCTION: HYDOLYZES A WIDE VARIETY OF P-BETA-GLUCOSIDES INCLUDING
 CC CELLULOSE-6P, SALICIN-6P, ARUTIN-6P, GENTIOBIOS-6P, METHYL-
 CC BETA-GLUCOSIDE-6P AND P-NITROPHENYL-BETA-D-GLUCOPYRANOSIDE-6P.

CC -1- CATALYTIC ACTIVITY: 6-phospho-beta-D-glucoside-(1,4)-D-glucose +
 CC H(2)O = D-glucose 6-phosphate + glucose.

CC -1- COFACTOR: NAD AND A DIVALENT METAL ION. MANGANESE, COBALT AND
 CC NICKEL IONS ENHANCE ACTIVITY WHEREAS MAGNESIUM, CALCIUM,
 CC STRONTIUM AND ZINC IONS DO NOT.

CC -1- PATHWAY: FERMENTATION OF THE BETA-GLUCOSIDES CELLOBIOS-
 CC ARBUTIN, AND SALICIN.

CC -1- SIMILARITY: BELONGS TO FAMILY 4 OF GLYCOSYL HYDROLASES.

CC -1- CAUTION: REF.1 AND REF.4 SEQUENCES DIFFER FROM THAT SHOWN IN
 CC POSITIONS 371 ONWARD DUE TO NUMBER OF FRAMESHIFTS AS WELL AS OTHER
 CC SEQUENCE ERRORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; X52890; CAA37073.1; ALT_FRAME.

DR EMBL; M64438; AAA23550.1; -.

DR EMBL; AE000268; AAC74804.1; -.

DR EMBL; D90816; BAA15515.1; -.

DR EMBL; D90817; BAA15523.1; -.

DR EMBL; X66725; CAA47257.1; ALT_FRAME.

DR EMBL; X66725; CAA47259.1; ALT_FRAME.

DR PIR; S10874; S10874.

DR EcoGene; EG10144; celF.

DR InterPro; IPR001088; Glyco_hydro.4.

DR Pfam; PF02056; Glyco_hydro.4; 1.

DR PRINTS; PR00732; GLYDRLASE4.

DR PRODOM; PD006892; Glyco_hydro.4; 1.

DR PROSITE; PS01324; GLYCOSYL_HYDROL_F4; 1.

DR Hydrolase; Glycosidase; NAD; Cobalt; Manganese; Nickel;

KW Complete proteome.

FT INIT_MET 0 0

FT NP_BIND 6 39 NAD (POTENTIAL).

FT ACT_SITE 111 111 PROTON DONOR (BY SIMILARITY).

FT ACT_SITE 355 355 NUCLEOPHILE (BY SIMILARITY).

SQ SEQUENCE 449 AA; 50381 MW; 1B36FFDE05E0AE56 CRC64;

Query Match 52.7%; Score 48; DB 1; Length 449;

Best Local Similarity 50.0%; Pred. No. 4.2;

Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17

I: |||||:|:|:

Db 7 VTIGGGSSYTPPELLGG 22

RESULT 14

HV16_MOUSE

ID HV16_MOUSE STANDARD; PRT; 136 AA.

AC P01783;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region MOPC 21 precursor (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M.; Paskind M.; Reth M.; Imanishi-Kari T.; Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 RN [2]
 RP SEQUENCE OF 17-136.
 RA MEDLINE=77100368; PubMed=401950;
 RA Adetugbo K.; Milstein C.; Secher D.S.;
 RT "Molecular analysis of spontaneous somatic mutants.";
 RL Nature 265:299-304(1977).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; J00522; AAD15290.1; -.

DR PIR; A02066; GIMS21.

DR HSRP; P01772; 2F84.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Signal.

FT NON_TER 1 1

FT SIGNAL <1 16

FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.

FT DOMAIN 115 119 D SEGMENT.

FT DOMAIN 120 136 JH4 SEGMENT.

FT DISULFID 38 112

FT CONFLICT 75 78 HVAD -> DYAH (IN REF. 2).

FT CONFLICT 89 90 DN -> ND (IN REF. 2).

FT CONFLICT 115 115 W -> H (IN REF. 2).

FT CONFLICT 120 120 Y -> W (IN REF. 2).

FT NON_TER 136 136

SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 51.6%; Score 47; DB 1; Length 136;

Best Local Similarity 50.0%; Pred. No. 1.7;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17

I: ||||:|:|:|:

Db 67 ISSGSSTLHYADTVKG 82

RESULT 15

HV02_CANFA

ID HV02_CANFA STANDARD; PRT; 117 AA.

AC P01785;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region MOO.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE OF 1-112.

RA MEDLINE=77242268; PubMed=407924;

RA Wasserman R.L.; Capra J.D.;

RT "Primary structure of the variable regions of two canine

RT immunoglobulin heavy chains.";

RL Biochemistry 16:3160-3168(1977).

RN [2]

RP SEQUENCE OF 113-117.

RX MEDLINE=80077682; PubMed=117299;
RA McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain.";
RL Mol. Immunol. 16:565-570(1979).
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A02068; MHDGMO.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;

Query Match 49.5%; Score 45; DB 1; Length 117;
Best Local Similarity 57.1%; Pred. No. 3;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 4 SGGGSTYYPTVQG 17
Db 52 SSSGQYYADAVKG 65

Search completed: August 19, 2002, 06:59:09
Job time: 1374 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:12 ; Search time 140.4 Seconds
(without alignments)
20.947 Million cell updates/sec

Title: US-09-339-922a-104
Perfect score: 91
Sequence: 1 KVSSGGSTYYPDTVQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	71.4	119	11 Q920E7	Q920E7 mus musculus
2	60	65.9	487	11 Q99KA4	Q99KA4 mus musculus
3	59	64.8	597	4 Q96BB9	Q96BB9 homo sapien
4	58	63.7	121	4 Q9UL71	Q9UL71 homo sapien
5	58	63.7	479	11 Q91LWP5	Q91LWP5 mus musculus
6	57	62.6	486	11 Q91Z07	Q91Z07 mus musculus
7	51	56.0	118	4 Q9UL72	Q9UL72 homo sapien
8	51	56.0	345	10 Q94HD3	Q94HD3 oryza sativ
9	51	56.0	440	16 Q92EC0	Q92EC0 listeria in
10	49	53.8	124	5 Q95TE1	Q95TE1 drosophila
11	49	53.8	421	2 Q9L260	Q9L260 streptomyc
12	48	52.7	440	16 Q9KSH2	Q9KSH2 vibrio chol
13	48	52.7	442	16 Q9KGC1	Q9KGC1 bacillus ha
14	48	52.7	480	11 Q91XEL	Q91XEL mus musculus
15	47	51.6	415	16 Q9X108	Q9X108 thermotoga
16	47	51.6	438	16 Q92ED4	Q92ED4 listeria in

17	47	51.6	441	16 Q9KEE0	Q9KEE0 bacillus ha
18	47	51.6	473	11 Q9D8L4	Q9D8L4 mus musculus
19	47	51.6	473	11 Q91Z05	Q91Z05 mus musculus
20	46	50.5	129	2 Q60111	Q60111 yersinia ps
21	46	50.5	258	5 Q9Y0E9	Q9Y0E9 drosophila
22	46	50.5	331	5 Q9VR49	Q9VR49 drosophila
23	46	50.5	426	2 Q9REW0	Q9REW0 erwinia chr
24	46	50.5	435	16 Q928S8	Q928S8 listeria in
25	46	50.5	724	16 Q926C6	Q926C6 rhizobium m
26	45	49.5	162	10 Q9FJ12	Q9FJ12 arabidopsis
27	45	49.5	446	2 Q93351	Q93351 escherichia
28	45	49.5	594	8 Q9T3A0	Q9T3A0 nephroselm
29	45	49.5	965	10 Q9FV66	Q9FV66 flavaria tr
30	45	49.5	1439	5 Q9VC41	Q9VC41 drosophila
31	44	48.4	211	11 Q9D8R6	Q9D8R6 mus musculus
32	44	48.4	348	16 Q92UR6	Q92UR6 rhizobium m
33	44	48.4	437	11 Q9R1A4	Q9R1A4 mus musculus
34	44	48.4	517	11 Q63206	Q63206 rattus norv
35	44	48.4	738	3 Q13658	Q13658 schizosacch
36	43	47.3	112	4 Q9HCC1	Q9HCC1 homo sapien
37	43	47.3	532	16 Q97IF3	Q97IF3 clostridium
38	43	47.3	798	2 Q9RKF0	Q9RKF0 streptomyc
39	43	47.3	857	5 Q9VR54	Q9VR54 drosophila
40	43	47.3	912	10 Q9SUE7	Q9SUE7 arabidopsis
41	43	47.3	962	12 Q89443	Q89443 african swi
42	43	47.3	1301	17 Q96Y03	Q96Y03 sulfolobus
43	43	47.3	2316	2 Q9FDJ9	Q9FDJ9 bacteroides
44	42.5	46.7	93	4 Q9UIV4	Q9UIV4 homo sapien
45	42.5	46.7	95	6 Q9GMH2	Q9GMH2 macaca mula

ALIGNMENTS

RESULT 1

Q920E7 ID Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PTERIN-MIMICKING ANTI-IDIOTOPE HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -
FT NON_TER
FT NON_TER
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 71.4%; Score 65; DB 11; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.01;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPDTVQG 17
:|||||:|||||:
Db 51 ISSGGSTYYPDSVKG 66

RESULT 2

Q99KA4 ID Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 52.6 KDA PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004786; AAH04786.1; -.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; Ig; 3.
 DR SMART; SM00407; Igc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; Ig_like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 65.9%; Score 60; DB 11; Length 487;
 Best Local Similarity 62.5%; Pred. No. 0.29; Indels 4; Gaps 0;
 Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
 :||| ||||| :|||
 Db 70 ISDGGSTYYPDNVKG 85

RESULT 3
 Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.
 AC Q96BB9
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 65.0 KDA PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015760; AAH15760.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 64.8%; Score 59; DB 4; Length 597;
 Best Local Similarity 62.5%; Pred. No. 0.52; Indels 3; Gaps 0;
 Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
 :||| ||||| :|||
 Db 70 ISDGGSTYYPDNVKG 85

RESULT 4
 Q9UL71 ID Q9UL71 PRELIMINARY; PRT; 121 AA.
 AC Q9UL71
 DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -.
 DR HSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 121
 FT SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 63.7%; Score 58; DB 4; Length 121;
 Best Local Similarity 62.5%; Pred. No. 0.13; Indels 3; Gaps 0;
 Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
 :||| ||||| :|||
 Db 51 ISDGGSTYYADSVKG 66

RESULT 5
 Q91WP5 ID Q91WP5 PRELIMINARY; PRT; 479 AA.
 AC Q91WP5
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 51.6 KDA PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013656; AAH13656.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;

Query Match 63.7%; Score 58; DB 11; Length 479;
 Best Local Similarity 56.2%; Pred. No. 0.58; Indels 2; Gaps 0;
 Matches 9; Conservative 5; Mismatches 2; Indels 2; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
 :||| ||||| :|||
 Db 70 INSGNGTYSDTMKG 85

RESULT 6
 Q91Z07 ID Q91Z07 PRELIMINARY; PRT; 486 AA.
 AC Q91Z07
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 OS Eukaryota
 DE HYPOTHETICAL 52.7 KDA PROTEIN.
 OS Mus musculus (Mouse)
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DE EMBL: BC010324; AAH10324.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 486 AA; 52682 MW; 4FEF935125DA870B CRC64;
 Query Match 62.6%; Score 57; DB 11; Length 486;
 Best Local Similarity 64.3%; Pred. No. 0.85;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 4 SGGGTTYPDVQV 17
 Db : ||| ||||| |:
 71 TSGGNTYYPNVKG 84
 RESULT 7
 Q9UL72 PRELIMINARY; PRT; 118 AA.
 ID Q9UL72
 AC Q9UL72;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98277139; PubMed=9614934;
 RX Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035042; AAD56278.1; -;
 DR HSSP: P01772; 2FB4.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 118 118
 FT SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;
 Query Match 56.0%; Score 51; DB 4; Length 118;
 Best Local Similarity 56.2%; Pred. No. 1.6;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 2 VSSGGGTTYPDVQV 17
 Db : ||| ||||| |:
 50 VTYSGGSSYVADSVKG 65
 RESULT 8
 Q94HD3 PRELIMINARY; PRT; 345 AA.
 ID Q94HD3
 AC Q94HD3;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE PROTEIN WITH SIMILARITY TO GLUCAN

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 OS Hypothetical 52.7 KDA PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 KW Hypothetical protein.
 SQ SEQUENCE 486 AA; 52682 MW; 4FEF935125DA870B CRC64;

 Query Match 62.6%; Score 57; DB 11; Length 486;
 Best Local Similarity 64.3%; Pred. No. 0.85;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 QY 4 SGGGTTYPDVQV 17
 Db : ||||| |:
 71 TSGGTTYPDNVKG 84

 RESULT 7
 ID Q9UL72 PRELIMINARY; PRT; 118 AA.
 AC Q9UL72;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98277139; PubMed=9614934;
 RX Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035042; AAD56278.1; -.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 118 118
 FT SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

 Query Match 56.0%; Score 51; DB 4; Length 118;
 Best Local Similarity 56.2%; Pred. No. 1.6;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

 QY 2 VSSGGGTTYPDVQV 17
 Db : ||||| |:
 50 VTYSGGSYYADSVKG 65

 RESULT 8
 ID Q94HD3 PRELIMINARY; PRT; 345 AA.
 AC Q94HD3;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE PROTEIN WITH SIMILARITY TO GLUCAN

```

RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL596165; CAC95772.1; -.
DR ListiList; LIN00540; -.
KW Complete proteome.
SQ SEQUENCE 440 AA; 49273 MW; 5DAE3008B4241E83 CRC64;

Query Match 56.0%; Score 51; DB 16; Length 440;
Best Local Similarity 56.2%; Pred. No. 6.7;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 VSSGGSTYYPDTVOG 17
I: ||||| : : |
Db 8 VTIGGSSYTPELVEG 23

RESULT 10
Q95TE1 PRELIMINARY; PRT; 124 AA.
AC Q95TE1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE LD25304P.
GN CG12581.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059451; AAL13357.1; -.
SQ SEQUENCE 124 AA; 13415 MW; C3280F3689AA469E CRC64;

Query Match 53.8%; Score 49; DB 5; Length 124;
Best Local Similarity 61.5%; Pred. No. 3.5;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGSTYYPDTVOG 17
||||| : : |
Db 106 GGGASYGPDVSKG 118

RESULT 11
Q9L260 PRELIMINARY; PRT; 421 AA.
AC Q9L260
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE SUGAR HYDROLASE.
GN SC6D10.04.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;

```

```

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RL the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL138538; CAB711199.1; -.
DR InterPro; IPR001088; Glyco_hydro_4.
DR Pfam; PF02056; Glyco_hydro_4; 1.
DR PRINTS; PR00732; GLHYDRLASE4.
DR ProDom; PD006892; Glyco_hydro_4; 1.
KW Hydrolase.
SQ SEQUENCE 421 AA; 45017 MW; 3FCC9D4135567035 CRC64;

Query Match 53.8%; Score 49; DB 2; Length 421;
Best Local Similarity 61.5%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGGSTYYPDTVOG 17
||||| : : |
Db 7 GGGSTYTPELIDG 19

RESULT 12
Q9KSH2 PRELIMINARY; PRT; 440 AA.
AC Q9KSH2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 6-PHOSPHO-BETA-GLUCOSIDASE.
GN VC1284.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004207; AAF94443.1; -.
DR TIGR; VC1284; -.
DR InterPro; IPR001088; Glyco_hydro_4.
DR Pfam; PF02056; Glyco_hydro_4; 1.
DR PRINTS; PR00732; GLHYDRLASE4.
DR ProDom; PD006892; Glyco_hydro_4; 1.
KW Complete proteome.
SQ SEQUENCE 440 AA; 48512 MW; 65A3C3A1742C7486 CRC64;

Query Match 52.7%; Score 48; DB 16; Length 440;
Best Local Similarity 61.5%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

Qy 5 GGGSTYPTVVOG 17
 |||||:|:|:|
 Db 12 GGGSSYTPELVEG 24

RESULT 13

Q9KGC1 PRELIMINARY; PRT; 442 AA.
 AC Q9KGC1:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86).
 GN LICH OR BH0183.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001507; BAB03902.1; -.
 DR InterPro: IPR001088; Glyco_hydro_4.
 DR Pfam: PF02056; Glyco_hydro_4; 1.
 DR PRINTS: PR00732; GLHYDRLASE4.
 DR ProDom: PD006892; Glyco_hydro_4; 1.
 DR PROSITE; PS01324; GLYCOSYL_HYDROL_F4; 1.
 DR Hydrolase; Glycosidase; Complete proteome.
 SQ SEQUENCE 442 AA; 49204 MW; B039DFDCD2EB4C08 CRC64;

Query Match 52.7%; Score 48; DB 16; Length 442;

Best Local Similarity 61.5%; Pred. No. 20;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGGSTYPTVVOG 17
 |||||:|:|:|
 Db 11 GGGSSYTPELVEG 23

RESULT 14

Q91XE1 PRELIMINARY; PRT; 480 AA.
 AC Q91XE1:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE UNKNOWN (PROTEIN FOR IMAGE:4224494) (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010798; AAH10798.1; -.
 FT NON_TER 1
 SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match 52.7%; Score 48; DB 11; Length 480;

Best Local Similarity 43.8%; Pred. No. 22;

Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VSSGGSTYPTVVOG 17
 :|:|:|:|:|:|
 Db 69 ISNSGYATHYPDSMKG 84

RESULT 15

Q9X108 PRELIMINARY; PRT; 415 AA.
 AC Q9X108:
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 6-PHOSPHO-BETA-GLUCOSIDASE.
 GN TM1281.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima.";
 RL Nature 399:323-329(1999).
 DR EMBL; AE001783; AAD36356.1; -.
 DR TIGR; TM1281; -.
 DR InterPro: IPR001088; Glyco_hydro_4.
 DR Pfam: PF02056; Glyco_hydro_4; 1.
 DR PRINTS: PR00732; GLHYDRLASE4.
 DR ProDom: PD006892; Glyco_hydro_4; 1.
 KW Complete proteome.
 SQ SEQUENCE 415 AA; 47626 MW; FB4E3B358245BFEE CRC64;

Query Match 51.6%; Score 47; DB 16; Length 415;

Best Local Similarity 61.5%; Pred. No. 27;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGGSTYPTVVOG 17
 |||||:|:|:|
 Db 7 GGGSSYTPELVKG 19

Search completed: August 19, 2002, 06:58:13
 Job time: 1403 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:12 ; Search time 180.34 Seconds
(without alignments)
10.471 Million cell updates/sec

Title: US-09-339-922a-104
Perfect score: 91
Sequence: 1 KVSSGGSTYYPTVVG 17

Scoring table: BLOSSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802.*
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	91	100.0	17	22	AA61400 Enhanced LM609 VH
2	81	89.0	17	22	AA61399 Enhanced 6H6LH hea
3	81	89.0	117	19	AAW76001 Vitaxin antibody h
4	81	89.0	117	19	AAW76003 LM609 antibody hea
5	81	89.0	117	20	AAV06381 Murine monoclonal
6	81	89.0	117	22	AAG63587 A heavy chain vari
7	81	89.0	117	22	AAG63589 A heavy chain vari
8	81	89.0	117	22	AA61359 Vitaxin heavy chai
9	81	89.0	117	22	AA61361 Antibody LM609 hea
10	81	89.0	130	20	AAV06379 Murine monoclonal
11	78	85.7	87	22	AAE06990 Mouse germline hea

12	78	85.7	98	22	AAE06978	Mouse germline hea
13	78	85.7	120	17	AAW00240	EGF receptor chine
14	78	85.7	123	19	AAW66099	anti-CD22 monoclon
15	77	84.6	119	16	AAW11919	Humanised MAB SK48
16	77	84.6	125	22	AA48937	Anti-TrKA murine m
17	77	84.6	247	16	AAW11917	Murine MAB SK48-E2
18	77	84.6	295	22	AA48934	Anti-TrKA single c
19	74	81.3	98	22	AAE06981	Mouse germline hea
20	74	81.3	119	20	AAW69322	15D3 antibody heav
21	74	81.3	119	20	AAW32832	15D3 VH chain prot
22	74	81.3	119	20	AAW73503	Anti-body 15D3 heav
23	74	81.3	138	13	AAW20064	MRK16-H chain. Ch
24	74	81.3	139	18	AAW21652	Humanised reshaped
25	74	81.3	139	18	AAW21856	Chimeric MAB 15 PC
26	74	81.3	140	18	AAW21654	Mouse MAB 15 heav
27	72	79.1	158	18	AAW19577	Mouse anti-idiotyp
28	72	79.1	158	18	AAW19579	Mouse anti-idiotyp
29	71	78.0	136	11	AAW06251	Variable region of
30	71	78.0	249	22	AAW20435	Anti-FIX/fixa anti
31	71	78.0	249	22	AAW20436	Anti-FIX/fixa anti
32	71	78.0	294	22	AAW20442	Anti-FIX/fixa anti
33	71	78.0	325	22	AAW20438	Anti-FIX/fixa anti
34	71	78.0	732	22	AAW20437	Anti-FIX/fixa anti
35	70	76.9	17	18	AAW27342	CDR2 from murine a
36	70	76.9	117	16	AAW79155	Human IgE receptor
37	70	76.9	117	18	AAW27357	Heavy chain variab
38	70	76.9	117	18	AAW27526	Heavy chain variab
39	70	76.9	117	18	AAW27354	Heavy chain variab
40	70	76.9	131	22	AAW84293	Amino acid sequenc
41	70	76.9	239	20	AAW73874	Human antiFc epsil
42	70	76.9	242	20	AAW73876	Human antiFc epsil
43	68	74.7	89	22	AAE06985	Mouse germline hea
44	68	74.7	117	16	AAW79157	Human IgE receptor
45	68	74.7	247	9	AAW80156	Biosynthetic antib

ALIGNMENTS

RESULT 1
AAB61400
ID AAB61400 standard; peptide; 17 AA.
XX AAB61400;
AC AAB61400;
DT 03-APR-2001 (first entry)
XX
DE Enhanced LM609 VH CDR2 peptide.
XX
KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
(MOLE-) APPLIED MOLECULAR EVOLUTION.

PA Huse WD, Wu H;
PI
XX
DR WPI; 2001-050110/06.

Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -

PS Claim 1; Page 45; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

SQ Sequence 17 AA;

Query Match 100.0%; Score 91; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.le-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSSGGGTYYPDTVQG 17
 Db 1 kvssgggstyyptvqg 17
 |||||

RESULT 2
 AAB61399
 ID AAB61399 standard; peptide; 17 AA.
 AC AAB61399;
 XX AAB61399;
 DT 03-APR-2001 (first entry)
 DE Enhanced 6H6LH heavy chain CDR2.
 KW LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX Unidentified.
 OS
 XX WO200078815-A1.
 PN 28-DEC-2000.
 PD 23-JUN-2000; 2000WO-US17454.
 PF 24-JUN-1999; 99US-0339922.
 PR (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA Huse WD, Wu H;
 XX WPI; 2001-050110/06.
 DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 XX to alpha(V)beta₃ integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Claim 4; Page 46; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX SQ Sequence 17 AA;

Query Match 89.0%; Score 81; DB 22; Length 17;
 Best Local Similarity 94.1%; Pred. No. 4e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGGTYYPDTVQG 17
 Db 1 kvssgggstyyldtvqg 17
 |||||

RESULT 3
 AAW76001
 ID AAW76001 standard; Protein; 117 AA.
 XX AAW76001;
 AC AAW76001;
 XX 02-NOV-1998 (first entry)
 DT Vitaxin antibody heavy chain variable region protein fragment.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX Mus sp.
 OS
 XX WO9833919-A2.
 PN 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 PF 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 DR N-ESDB; AAV49820.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta₃
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 1; Fig 1a; 129pp; English.

CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphaVbeta₃ and can be used to inhibit binding of alphaVbeta₃
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphaVbeta₃-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 117 AA;

Query Match 89.0%; Score 81; DB 19; Length 117;
 Best Local Similarity 94.1%; Pred. No. 3.5e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGGTYYPDTVQG 17

Db 50 kvssgggstyyldtvqg 66
 |||||

RESULT 4

AAW76003
 ID AAW76003 standard; Protein: 117 AA.
 AC AAW76003;

DT 02-NOV-1998 (first entry)
 XX

XX LM609 antibody heavy chain variable region protein fragment.
 XX

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX

OS Mus sp.
 XX

PN WO9833919-A2.
 XX

PD 06-AUG-1998 . .
 XX

PF 30-JAN-1998; 98WO-US01826.
 XX

PR 30-JAN-1997; 97US-0791391.
 XX

PA (IXSY-) IXSYS INC.
 XX

PI Glaser SM, Huse WD;
 XX

XX WPI; 1998-437472/37.
 DR

DR N-PSDB; AAV49822.
 XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX

PS Claim 43; Fig 2a; 129pp; English.
 XX

XX This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX

SQ Sequence 117 AA;

Query Match 89.0%; Score 81; DB 19; Length 117;
 Best Local Similarity 94.1%; Pred. No. 3.5e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGGSTYYPDVQV 17
 |||||
 Db 50 kvssgggstyyldtvqg 66

RESULT 5

AAV06381
 ID AAV06381 standard; Protein: 117 AA.
 XX

AC AAV06381;

XX
 DT

06-SEP-1999 (first entry)

XX

Murine monoclonal antibody LM609 VH region.

XX

Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX

OS Mus musculus.
 XX

PN WO9929888-A1.
 XX

PD 17-JUN-1999.
 XX

PF 04-DEC-1998; 98WO-US25828.
 XX

PR 05-DEC-1997; 97US-0986016.
 XX

PA (SCRI) SCRIPPS RES INST.
 XX

PI Barbas CF, Rader C;
 XX

DR WPI; 1999-394979/33.
 XX

PT Production of humanized mouse monoclonal antibodies
 XX

PS Disclosure; Page 52-53; 55pp; English.
 XX

XX This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX

SQ Sequence 117 AA;

Query Match 89.0%; Score 81; DB 20; Length 117;
 Best Local Similarity 94.1%; Pred. No. 3.5e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGGSTYYPDVQV 17
 |||||
 Db 50 kvssgggstyyldtvqg 66

RESULT 6

AAAG63587
 ID AAAG63587 standard; Protein: 117 AA.
 XX

AC AAAG63587;

XX 15-OCT-2001. (first entry)
 XX

DT A heavy chain variable region of LM609 grafted antibody.
 XX

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX

OS Synthetic.
 XX

OS Mus sp.

```

XX  US2001011125-A1.
PN
XX
XX  02-AUG-2001.
PD
XX
XX  30-JAN-1997; 97US-0790540.
PF
XX
XX  30-JAN-1997; 97US-0790540.
PR
XX
XX  (HUSE/) HUSE W D.
PA
XX
XX  Huse WD;
PI
XX
XX  WPI; 2001-496171/54.
DR
XX  N-PSDB; AAH74625.
DR
XX
XX  New LM609 grafted antibody exhibiting selective binding affinity to
PT  alphavbeta3, comprising at least one LM609 grafted heavy and light
PT  chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT  disorders or cancer.
XX
XX  Claim 1; Fig 1A; 25pp; English.
PS
XX
XX  The present sequence represents the heavy chain variable region of the
CC  grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC  specifically recognises the integrin alphavbeta3, and inhibits its
CC  functional activity. The LM609 grafted antibody has the
CC  complementarity determining regions (CDRs) substituted into a non-murine
CC  framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC  polypeptides and fragments are useful in diagnostic and therapeutic
CC  purposes, such as in the production of LM609 grafted antibodies and
CC  fragments having binding specificity and inhibitory activity against
CC  the integrin alphavbeta3. The antibody can be used for the diagnosis
CC  of disorders, chronic articular rheumatism, psoriasis, disorders
CC  associated with inappropriate or inopportune invasion of vessels such
CC  as diabetic retinopathy, neovascular glaucoma and capillary
CC  proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC  binding activity of alphavbeta3 that are necessary for progression of
CC  an alphavbeta3-mediated disease.
XX
XX  Sequence 117 AA;

Query Match      89.0%; Score 81; DB 22; Length 117;
Best Local Similarity 94.1%; Pred. No. 3.5e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 KVSSGGGSTYYPDVTQV 17
Db   50 kvssgggstyyldtvqg 66

RESULT 7
AAG63589
ID  AAG63589 standard; Protein; 117 AA.
XX
XX  AAG63589;
AC
XX
XX  15-OCT-2001 (first entry)
DT
XX
XX  A heavy chain variable region of LM609 antibody.
DE
XX
XX  Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW  chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW  neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW  cancer.
XX
XX  Mus sp.
OS
XX
XX  US2001011125-A1.
PN
XX
XX  02-AUG-2001.
PD

```

```

XX  30-JAN-1997; 97US-0790540.
PF
XX
XX  30-JAN-1997; 97US-0790540.
PR
XX
XX  (HUSE/) HUSE W D.
PA
XX
XX  Huse WD;
PI
XX
XX  WPI; 2001-496171/54.
DR
XX  N-PSDB; AAH74625.
DR
XX
XX  New LM609 grafted antibody exhibiting selective binding affinity to
PT  alphavbeta3, comprising at least one LM609 grafted heavy and light
PT  chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT  disorders or cancer.
XX
XX  Disclosure; Fig 2A; 25pp; English.
PS
XX
XX  The present sequence represents the heavy chain variable region of the
CC  monoclonal antibody LM609. LM609 is a murine antibody which specifically
CC  recognises the integrin alphavbeta3, and inhibits its functional activity.
CC  The specification describes a LM609 grafted antibody which has the
CC  complementarity determining regions (CDRs) substituted into a non-murine
CC  framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC  polypeptides and fragments are useful in diagnostic and therapeutic
CC  purposes, such as in the production of LM609 grafted antibodies and
CC  fragments having binding specificity and inhibitory activity against
CC  the integrin alphavbeta3. The antibody can be used for the diagnosis
CC  or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC  disorders, chronic articular rheumatism, psoriasis, disorders
CC  associated with inappropriate or inopportune invasion of vessels such
CC  as diabetic retinopathy, neovascular glaucoma and capillary
CC  proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC  binding activity of alphavbeta3 that are necessary for progression of
CC  an alphavbeta3-mediated disease.
XX
XX  Sequence 117 AA;

Query Match      89.0%; Score 81; DB 22; Length 117;
Best Local Similarity 94.1%; Pred. No. 3.5e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 KVSSGGGSTYYPDVTQV 17
Db   50 kvssgggstyyldtvqg 66

RESULT 8
AAB61359
ID  AAB61359 standard; protein; 117 AA.
XX
XX  AAB61359;
AC
XX
XX  03-APR-2001 (first entry)
DT
XX
XX  Vitaxin heavy chain variable region protein.
DE
XX
XX  LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
KW  inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX  Unidentified.
OS
XX
XX  WO200078815-A1.
PN
XX
XX  28-DEC-2000.
PD
XX
XX  23-JUN-2000; 2000WO-US17454.
PF
XX
XX  24-JUN-1999; 99US-0339922.
PR
XX
XX  (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA

```

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -

XX Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX Sequence 117 AA;

Query Match 89.0%; Score 81; DB 22; Length 117;
Best Local Similarity 94.1%; Pred. No. 3.5e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSEGGSTYYPTVQG 17
Db 50 kvssggstyyldtvqg 66
|||||

RESULT 9

AB61361
ID AAB61361 standard; protein; 117 AA.

XX AAB61361;

DT 03-APR-2001 (first entry)

XX Antibody LM609 heavy chain variable region protein.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -

XX Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX Sequence 117 AA;

Query Match 89.0%; Score 81; DB 22; Length 117;
Best Local Similarity 94.1%; Pred. No. 3.5e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSEGGSTYYPTVQG 17
Db 50 kvssggstyyldtvqg 66
|||||

RESULT 10

AAY06379
ID AAY06379 standard; Protein; 130 AA.

XX AAY06379;

XX 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 V kappa.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 28..32 /note= "CDR1"

FT Region 47..63 /note= "CDR2"

FT Region 96..103 /note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 49-50; 55pp; English.

XX This sequence represents the light chain V kappa region of murine
CC monoclonal antibody LM609. LM609 is directed to integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 130 AA;

Query Match 89.0%; Score 81; DB 20; Length 130;
 Best Local Similarity 94.1%; Pred. No. 3.9e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGSTYYPDTVOG 17
 DB 47 kvssggstyyldtvvg 63

RESULT 11
 AAE06990
 ID AAE06990 standard; Protein; 87 AA.
 XX
 AC AAE06990;

XX
 DT 16-OCT-2001 (first entry)

XX Mouse germline heavy chain variable (VH) region, VH7183.13.

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioptasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VH; heavy chain variable region.

XX Mus sp.

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US03537.

XX 03-FEB-2000; 2000US-0497625.

XX (MILL-) MILLENNIUM PHARM INC.

XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

XX WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin

XX Disclosure; Page 159; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid

CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline heavy chain variable (VH)
 XX region, VH7183.13.

XX Sequence 87 AA;

Query Match 85.7%; Score 78; DB 22; Length 87;
 Best Local Similarity 81.2%; Pred. No. 7.4e-05;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPDTVOG 17
 DB 40 isngggstyyptvkg 55

RESULT 12
 AAE06978
 ID AAE06978 standard; Protein; 98 AA.

XX AC AAE06978;

XX 16-OCT-2001 (first entry)

XX Mouse germline heavy chain variable (VH) region, V(H) 50.1.

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioptasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VH; heavy chain variable region.

XX Mus sp.

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US03537.

XX 03-FEB-2000; 2000US-0497625.

XX (MILL-) MILLENNIUM PHARM INC.

XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

XX WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin

XX Disclosure; Page 154-155; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin

CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IGE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline heavy chain variable (VH)
 CC region, V(H)50.1.

XX SQ Sequence 98 AA;

Query Match 85.7%; Score 78; DB 22; Length 98;
 Best Local Similarity 81.2%; Pred. No. 8.5e-05;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYPTVQV 17
 :|:|||||||:|
 Db 51 isngggstyptvkg 66

RESULT 13

AAW00240
 ID AAW00240 standard; Protein; 120 AA.

XX AC AAW00240;

XX DT 22-NOV-1996 (first entry)

XX DE EGF receptor chimeric MAb chMint5 VH chain.

XX KW Mouse-human chimeric antibody; monoclonal antibody; chMint5;
 KW epidermal growth factor receptor; EGF-R; diagnosis; therapy;
 KW immunotoxin; immunocytokine; tumour; cancer.

XX OS Mus musculus.

XX FH Key Location/Qualifiers
 FT Region 31..35
 FT /label= CDR1
 FT Region 51..66
 FT /label= CDR2
 FT Region 99..109
 FT /label= CDR3

XX PN W09627010-A1.

XX XX 06-SEP-1996.

XX PF 01-MAR-1996; 96WO-EP00805.

XX PR 01-MAR-1995; 95IT-0FT0036.

XX PA (ITU-Y) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.

XX PI Anastasi AM, Colnaghi MI, De Santis R, Di Massimo AM;
 PI Ferrer Marsal C, Mele A;

XX DR WPI; 1996-412776/41.
 XX DR N-PSDB; AAT33445.

PT Murine/human chimeric monoclonal antibody, chMint5 specific for
 XX EGF-R - shows a lower immunogenicity when administered to humans
 PS Claim 7; Page 15; 28pp; English.

XX CC The amino acid sequence (AAW00240) of the heavy chain variable region
 CC (VH) of the epidermal growth factor receptor (EGF-R)-specific mouse-
 CC human chimeric antibody chMint5 was deduced from a cDNA clone
 CC (AA33445) obtd. by PCR amplification of murine Mint5 hybridoma DSM
 CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused
 CC to human C-gamma1 and CK regions. Constructs were expressed in
 CC CHO cell transfectants. chMint5 shows lower immunogenicity than
 CC Mint5 when administered to humans. It can be used in diagnostic
 CC assays or used to produce immunotoxins or immunocytokines useful
 CC for tumour therapy.

XX SQ Sequence 120 AA;

Query Match 85.7%; Score 78; DB 17; Length 120;
 Best Local Similarity 81.2%; Pred. No. 0.00011;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYPTVQV 17
 :|:|||||||:|
 Db 51 isngggstyptvkg 66

RESULT 14

AAW66099
 ID AAW66099 standard; Protein; 123 AA.

XX AC AAW66099;

XX DT 10-DEC-1998 (first entry)

XX DE anti-CD22 monoclonal antibody heavy chain variable region.

XX KW anti-CD22 monoclonal antibody heavy chain variable region; VL;
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;
 KW malignant B-cell; immunodiagnosis; RFB4 IgG.

XX OS Mammalia.

XX FH Key Location/Qualifiers
 FT Misc-difference 121
 FT /note= "Encoded by gtc"

XX PN W09841641-A1.

XX PD 24-SEP-1998.

XX PF 19-MAR-1998; 98WO-US05453.

XX PR 20-MAR-1997; 97US-0041437.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Fitzgerald D, Kreitman R, Mansfield E, Pastan I;

XX DR WPI; 1998-521227/44.

XX DR N-PSDB; AAV07642.

XX PT Recombinant anti-CD22 antibodies and immuno-conjugates - of
 XX antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin
 XX or a label; for inhibiting malignant B-cells

XX PS Claim 6; Fig 1; 71pp; English.

XX CC The invention claims for a recombinant immunoconjugate comprising
 CC of a therapeutic agent (e.g. Pseudomonas exotoxin) or a detectable
 CC label peptide bonded to a recombinant anti-CD22 antibody (RFB4 IgG)
 CC having the present variable heavy (VH) chain with a cysteine residue

CC at amino acid 44 and a variable light (VL; AAW66098) chain with a
 CC cysteine residue at amino acid 100. The immunconjugate is claimed
 CC to inhibit the growth of malignant B-cells in vivo, such as rodent,
 CC canine or primate B-cells. The anti-CD22 antibody is claimed useful
 CC for detecting CD22 protein in a sample or in vivo in a mammal, and
 CC can be used in diagnostic kits.

SQ Sequence 123 AA;

Query Match 85.7%; Score 78; DB 19; Length 123;
 Best Local Similarity 81.2%; Pred. No. 0.00011;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 VSSGGGTYYPDTVOG 17
 :||||:|||||:
 Db 51 issgggttyypdtvk 66

RESULT 15

AAW11919
 ID AAW11919 standard; Protein; 119 AA.

XX AC AAW11919;

XX DT 24-JUN-1997 (first entry)

XX DE Humanised MAB SK48-E26 heavy chain.

XX KW Interleukin-1 beta; IL-1 beta; recombinant antibody;
 KW humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAB; SK48-E26; inflammation; therapy.

XX OS Chimeric Homo sapiens;.

XX OS Chimeric Mus sp.

XX FH Key Location/Qualifiers

FT Region 1..30

FT /label= FR1

FT /note= "framework region 1"

FT Region 31..35

FT /label= CDR1

FT /note= "complementarity determining region 1
 (Claim 10, page 48)"

FT Region 36..49

FT /label= FR2

FT /note= "framework region 2"

FT Region 50..66

FT /label= CDR2

FT /note= "complementarity determining region 2
 (Claim 10, page 48)"

FT Region 67..98

FT /label= FR3

FT /note= "framework region 3"

FT Region 99..108

FT /label= CDR3

FT /note= "complementarity determining region 3
 (Claim 10, page 48)"

FT Region 109..119

FT /label= FR4

FT /note= "framework region 4"

XX PN WO9501997-A1.

XX PD 19-JAN-1995.

XX PF 07-JUL-1994; 94WO-US07659.

XX PR 09-JUL-1993; 93US-0090534.

XX PR 04-MAR-1994; 94US-0206190.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Gross MS, Hurle MR, Jackson JR, Jonak ZL, Theisen TW;
 PI Young PR;

XX WPI; 1995-066868/09.

DR N-PSDB; AAT51438.

XX Recombinant and humanised chimeric antibodies against human

PT interleukin-1-beta - for preventing and treating

PT interleukin-mediated inflammatory disorders

XX Claim 39; Page 40-41; 62pp; English.

XX The heavy chain variable region (AAW11919) and light chain variable

CC region (AAW11920) of humanised anti-human interleukin-1 beta (IL-1

CC beta) murine monoclonal antibody (MAB) SK48-E26 comprise the

CC complementarity determining regions from MAB SK48-E26 (see also

CC AAW11917-18) grafted into human frameworks. The humanised antibody

CC can be produced in e.g. COS cells transfected with vectors carrying

CC humanised heavy and light chain nucleic acids (AAT51437-39) for use

CC in the treatment and prevention of IL-1 mediated inflammatory

CC disorders.

XX SQ Sequence 119 AA;

Query Match 84.6%; Score 77; DB 16; Length 119;

Best Local Similarity 81.2%; Pred. No. 0.00015;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 VSSGGGTYYPDTVOG 17

Db 51 issgggttyypdtvk 66

Search completed: August 19, 2002, 06:39:12

Job time: 1473 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:40 ; Search time 61.75 Seconds
(without alignments)
6.724 Million cell updates/sec

Title: US-09-339-922A-104

Perfect score: 91
Sequence: 1 KVSQGGSTYPTDVTQVQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	85.7	125	1	US-08-331-398A-65
2	78	85.7	125	2	US-08-331-397B-65
3	78	85.7	125	2	US-08-759-804A-64
4	77	84.6	119	5	PCT-US94-07659-6
5	77	84.6	247	5	PCT-US94-07659-2
6	74	81.3	119	2	US-08-475-000-16
7	74	81.3	119	2	US-08-483-199-16
8	74	81.3	119	2	US-08-484-508-16
9	72	79.1	158	2	US-08-653-402B-6
10	72	79.1	158	2	US-08-653-402B-10
11	65	71.4	32	4	US-08-525-539A-35
12	65	71.4	109	2	US-08-793-490-6
13	65	71.4	116	2	US-08-888-366-10
14	65	71.4	116	2	US-08-888-366-12
15	64	70.3	17	5	PCT-US93-08435-18
16	64	70.3	118	5	PCT-US93-08435-10
17	64	70.3	122	5	PCT-US93-08435-12
18	64	70.3	122	5	PCT-US93-08435-14
19	64	70.3	122	5	PCT-US93-08435-43
20	63	69.2	17	1	US-08-264-093-22
21	63	69.2	118	2	US-08-652-816A-11
22	63	69.2	120	1	US-08-264-093-14
23	62	68.1	118	1	US-08-326-362-2
24	62	68.1	135	4	US-08-579-378A-16
25	62	68.1	135	4	US-08-579-378A-20
26	62	68.1	443	5	PCT-US96-13152-4
27	61	67.0	123	1	US-08-356-272-3

28	61	67.0	300	2	US-08-661-052-4	Sequence 4, Appl
29	61	67.0	300	4	US-09-188-082-4	Sequence 4, Appl
30	61	67.0	301	2	US-08-661-052-14	Sequence 14, Appl
31	61	67.0	301	4	US-09-188-082-14	Sequence 14, Appl
32	61	67.0	553	2	US-08-661-052-16	Sequence 16, Appl
33	61	67.0	553	4	US-09-188-082-16	Sequence 16, Appl
34	60	65.9	120	2	US-08-428-197-20	Sequence 20, Appl
35	60	65.9	120	2	US-08-428-197-22	Sequence 22, Appl
36	60	65.9	120	2	US-08-428-197-24	Sequence 24, Appl
37	60	65.9	120	2	US-08-428-197-26	Sequence 26, Appl
38	60	65.9	120	2	US-08-428-197-28	Sequence 28, Appl
39	60	65.9	120	2	US-08-428-197-30	Sequence 30, Appl
40	60	65.9	120	2	US-08-428-197-32	Sequence 32, Appl
41	60	65.9	120	2	US-08-428-197-34	Sequence 34, Appl
42	60	65.9	120	2	US-08-428-197-40	Sequence 40, Appl
43	60	65.9	120	5	PCT-US93-10555-20	Sequence 20, Appl
44	60	65.9	120	5	PCT-US93-10555-22	Sequence 22, Appl
45	60	65.9	120	5	PCT-US93-10555-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-331-398A-65
; Sequence 65, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: 'Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-1261100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

; NAME/KEY: Region
 ; LOCATION: 1..125
 ; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
 ; OTHER INFORMATION: Heavy chain region"
 US-08-331-397B-65

Query Match 85.7%; Score 78; DB 1; Length 125;
 Best Local Similarity 81.2%; Pred. No. 0.0001;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
 :|:|||||||:|
 Db 51 ISNGGGTYYPDTVKG 66

RESULT 2
 US-08-331-397B-65
 ; Sequence 65, Application US/08331397B
 ; Patent No. 5981726
 ; GENERAL INFORMATION:
 ; APPLICANT: Pastan, Ira
 ; APPLICANT: Benhar, Itai
 ; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
 ; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
 ; NUMBER OF SEQUENCES: 68
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: One Market Plaza, Steuart Street Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105-1492

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/331,397B
 ; FILING DATE: 28-OCT-1994

; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/767,331
 ; FILING DATE: 30-SEP-1991

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/596,289
 ; FILING DATE: 12-OCT-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunter, Tom

; REGISTRATION NUMBER: 38,498
 ; REFERENCE/DOCKET NUMBER: 015280-126120US
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 65:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 125 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear

; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 1..125

; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
 ; OTHER INFORMATION: Heavy chain region"
 US-08-331-397B-65

Query Match 85.7%; Score 78; DB 2; Length 125;
 Best Local Similarity 81.2%; Pred. No. 0.0001;

Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VSSGGGTYYPDTVQG 17
 :|:|||||||:|
 Db 51 ISNGGGTYYPDTVKG 66

RESULT 3
 US-08-759-804A-64
 ; Sequence 64, Application US/08759804A
 ; Patent No. 5990296
 ; GENERAL INFORMATION:
 ; APPLICANT: Pastan, Ira
 ; APPLICANT: Willingham, Mark
 ; APPLICANT: Fitzgerald, David J.
 ; APPLICANT: Brinkmann, Ulrich

; APPLICANT: Pal, Lee
 ; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
 ; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
 ; NUMBER OF SEQUENCES: 68
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/759,804A
 ; FILING DATE: 03-DEC-1996

; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/331,398
 ; FILING DATE: 28-OCT-1994

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/767,331
 ; FILING DATE: 30-SEP-1991
 ; APPLICATION NUMBER: US 07/596,289
 ; FILING DATE: 12-OCT-1990

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Ellen L.
 ; REGISTRATION NUMBER: 32,762
 ; REFERENCE/DOCKET NUMBER: 015280-126140US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 64:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 125 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear

; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 1..125

; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
 ; OTHER INFORMATION: Heavy chain region"
 US-08-759-804A-64

Query Match 85.7%; Score 78; DB 2; Length 125;
 Best Local Similarity 81.2%; Pred. No. 0.0001;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17
 :|:|||||||:|


```
Db 51 ISSGGGTYPTVKG 66
;
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-2

Query Match 84.6%; Score 77; DB 5; Length 247;
Best Local Similarity 81.2%; Pred. No. 0.00029;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGTYPTVQV 17
; :||||| :|||||:
Db 70 ISSGGGTYPTVKG 85

RESULT 6
US-08-475-000-16
; Sequence 16, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424

;
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-6

Query Match 84.6%; Score 77; DB 5; Length 119;
Best Local Similarity 81.2%; Pred. No. 0.00014;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGTYPTVQV 17
; :||||| :|||||:
Db 51 ISSGGGTYPTVKG 66

RESULT 5
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurlle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-6

Query Match 84.6%; Score 77; DB 5; Length 119;
Best Local Similarity 81.2%; Pred. No. 0.00014;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGTYPTVQV 17
; :||||| :|||||:
Db 51 ISSGGGTYPTVKG 66

RESULT 5
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurlle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-475-000-16

```

```

Query Match      81.3%; Score 74; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.00038;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 VSSGGGSTYPTVQ 17
   :||||:||||:|
Db 51 ISSGGNTYPPSVKG 66

```

```

RESULT 7
US-08-483-199-16
; Sequence 16, Application US/08483199
; Patent No. 5849877
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; MOLECULE TYPE: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,199
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-199-16

```

```

Query Match      81.3%; Score 74; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.00038;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 VSSGGGSTYPTVQ 17
   :||||:||||:|
Db 51 ISSGGNTYPPSVKG 66

```

```

RESULT 8
US-08-484-508-16
; Sequence 16, Application US/08484508
; Patent No. 5948647
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; MOLECULE TYPE: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,508
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-508-16

```

```

Query Match      81.3%; Score 74; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.00038;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 VSSGGGSTYPTVQ 17
   :||||:||||:|
Db 51 ISSGGNTYPPSVKG 66

```

```

RESULT 9
US-08-653-402B-6
; Sequence 6, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; MOLECULE TYPE: Immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:

```

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/653,402B
;; FILING DATE: 24-MAY-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95107967.2
;; FILING DATE: 26-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lebovitz, Richard M.
;; REGISTRATION NUMBER: 37,067
;; REFERENCE/DOCKET NUMBER: MERCK 1781
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-243-6333
;; TELEFAX: 703-243-6410
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 158 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-653-402B-6

Query Match 79.1%; Score 72; DB 2; Length 158;
Best Local Similarity 75.0%; Pred. No. 0.001;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYTPDVTQV 17
Db 70 INSGGTYTPDVTKG 85

RESULT 10
US-08-653-402B-10
; Sequence 10, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabeth
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; IMMUNE RESPONSE AGAINST EPIDERMAL GROWTH FACTOR RECEPTOR.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 703-243-6333
;; TELEFAX: 703-243-6410
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 158 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-653-402B-10

Query Match 79.1%; Score 72; DB 2; Length 158;
Best Local Similarity 75.0%; Pred. No. 0.001;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYTPDVTQV 17
Db 70 INSGGTYTPDVTKG 85

RESULT 11
US-08-525-539A-35
; Sequence 35, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A-35

Query Match 71.4%; Score 65; DB 4; Length 32;
Best Local Similarity 68.8%; Pred. No. 0.0021;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTYTPDVTQV 17
Db 2 ISSGGTYTPDVTKG 17

RESULT 12
US-08-793-490-6
; Sequence 6, Application US/08793490
; Patent No. 5968824
; GENERAL INFORMATION:
; APPLICANT: Spruce, Barbara A
; APPLICANT: Prescott, Alan
; APPLICANT: Bottger, Angelika
; APPLICANT: Dewar, Deborah A
; TITLE OF INVENTION: Agents for Inducing Apoptosis and Applications of Said
; FILE REFERENCE: ME A9701
; CURRENT APPLICATION NUMBER: US/08/793,490
; EARLIER FILING DATE: 1997-04-28
; EARLIER APPLICATION NUMBER: GB 9419285.3
; EARLIER FILING DATE: 1994-09-23
; EARLIER APPLICATION NUMBER: GB 9417444.8
; EARLIER FILING DATE: 1994-08-30
; EARLIER APPLICATION NUMBER: PCT/GB95/02037
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoded by anti-proenkephalin immunoglobulin heavy
; OTHER INFORMATION: chain variable domain genes
US-08-793-490-6

Query Match 71.4%; Score 65; DB 2; Length 109;
Best Local Similarity 68.8%; Pred. No. 0.0074;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 VSSGGGTYYPDPVVG 17
:|||||:|||||:|
Db 50 ISSGGGTYYPDSVKG 65

RESULT 13
US-08-888-366-10
; Sequence 10, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.

; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-888-366-10

Query Match 71.4%; Score 65; DB 2; Length 116;
Best Local Similarity 68.8%; Pred. No. 0.0079;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 VSSGGGTYYPDPVVG 17
:|||||:|||||:|
Db 45 ISSGGGTYYPDSVKG 60

RESULT 14
US-08-888-366-12
; Sequence 12, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.

REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-366-12

Query Match 71.4%; Score 65; DB 2; Length 116;
Best Local Similarity 68.8%; Pred. No. 0.0079;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VSSGGGSTYYPDVTQV 17
Db 45 ISSGGSTYYPDSVKG 60

RESULT 15

PCT-US93-08435-18
Sequence 18, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: Smithkline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Conferring Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC F50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-08435-18

Query Match 70.3%; Score 64; DB 5; Length 17;
Best Local Similarity 64.7%; Pred. No. 0.0015;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KVSSGGGSTYYPDVTQV 17
Db 1 EISDGGSTYYPDVTG 17

Search completed: August 19, 2002, 06:34:40
Job time: 1201 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:05 ; Search time 78.53 Seconds
(without alignments)
9.789 Million cell updates/sec

Title: US-09-339-922A-106

Perfect score: 44

Sequence: 1 HLHGSPAS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	84.1	572	2 B48521	bilirubin oxidase
2	36	81.8	1115	2 F86280	protein T5E21.11 [
3	34	77.3	220	2 AE1301	phosphoglycerate d
4	34	77.3	220	2 AE1673	phosphoglycerate d
5	34	77.3	224	2 S37740	transcription fact
6	34	77.3	762	2 B70838	hypothetical prote
7	34	77.3	1294	2 T35044	bacteriophage phiC
8	33	75.0	277	2 F97615	hypothetical prote
9	33	75.0	277	2 AD2838	conserved hypothet
10	33	75.0	346	2 AF3161	phage-related inte
11	33	75.0	413	2 S77339	hypothetical prote
12	33	75.0	761	2 T05299	hypothetical prote
13	33	75.0	796	2 E88029	protein F46F5.11 [
14	32	72.7	95	2 A56644	inverted repeat co
15	32	72.7	208	2 AC2830	pyrazinamidase/nic
16	32	72.7	209	2 E96510	hypothetical prote
17	32	72.7	218	2 AD0711	pyrazinamidase/nic
18	32	72.7	219	1 Q0BCA5	hypothetical 23.4K
19	32	72.7	219	2 C90938	hypothetical prote
20	32	72.7	219	2 G85786	hypothetical prote
21	32	72.7	225	2 H97607	hypothetical prote
22	32	72.7	312	2 D85763	conserved hypothet
23	32	72.7	327	2 T44111	conserved hypothet
24	32	72.7	331	2 T18247	transcription regu
25	32	72.7	335	2 H81662	glyceraldehyde 3-p
26	32	72.7	350	2 AG1407	sorbitol dehydroge
27	32	72.7	350	2 AG1783	sorbitol dehydroge
28	32	72.7	352	2 T07229	photosystem II pro
29	32	72.7	364	2 JQ2268	O-methyltransferas

30 32 72.7 385 2 S56224 hypothetical prote
31 32 72.7 388 2 AC2011 hypothetical prote
32 32 72.7 405 2 S62789 l1beta-hydroxyster
33 32 72.7 444 2 C89768 conserved hypothet
34 32 72.7 449 2 H69862 Na+-transporting A
35 32 72.7 500 2 B83910 hypothetical prote
36 32 72.7 574 1 S11032 5'-nucleotidase (E
37 32 72.7 980 2 T39630 valine-tRNA ligase
38 32 72.7 1104 1 SYBYVT valine--tRNA ligas
39 32 72.7 1603 2 D89407 protein R10E8.6 [i
40 32 72.7 1696 2 T24146 hypothetical prote
41 32 72.7 2121 2 T27406 hypothetical prote
42 31 70.5 98 2 PC6012 thuf protein - Rho
43 31 70.5 178 2 S50637 hypothetical prote
44 31 70.5 222 2 AH0991 cell division ATP-
45 31 70.5 237 2 T07820 hypothetical prote

RESULT 1
B48521
bilirubin oxidase (EC 1.3.3.5) - fungus (Myrothecium verrucaria)
C;Species: Myrothecium verrucaria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: B48521; A48521
R;Koikeda, S.; Ando, K.; Kaji, H.; Inoue, T.; Murao, S.; Takeuchi, K.; Samejima, T.
J. Biol. Chem. 268, 18801-18809, 1993
A;Title: Molecular cloning of the gene for bilirubin oxidase from Myrothecium verruca
A;Reference number: A48521; MUID:93366794
A;Accession: B48521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-572 <KO11>
A;Cross-references: GB:D14081; NID:g436236; PIDN:BA03166.1; PID:g456710
A;Note: sequence extracted from NCBI backbone (NCBIN:136730, NCBI:P:136732)
A;Accession: A48521
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-572 <KO12>
A;Cross-references: GB:D14081; NID:g436236; PIDN:BA03166.1; PID:g456710
A;Note: sequence extracted from NCBI backbone (NCBIN:136728, NCBI:P:136729)
C;Keywords: oxidoreductase

Query Match 84.1%; Score 37; DB 2; Length 572;
Best Local Similarity 85.7%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 1;

Qy 1 HLHGSPA 7
| | | | |
Db 132 HLHGSPS 138

RESULT 2
F86280
protein T5E21.11 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F86280
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: F86280

30 32 72.7 385 2 S56224 hypothetical prote
31 32 72.7 388 2 AC2011 hypothetical prote
32 32 72.7 405 2 S62789 l1beta-hydroxyster
33 32 72.7 444 2 C89768 conserved hypothet
34 32 72.7 449 2 H69862 Na+-transporting A
35 32 72.7 500 2 B83910 hypothetical prote
36 32 72.7 574 1 S11032 5'-nucleotidase (E
37 32 72.7 980 2 T39630 valine-tRNA ligase
38 32 72.7 1104 1 SYBYVT valine--tRNA ligas
39 32 72.7 1603 2 D89407 protein R10E8.6 [i
40 32 72.7 1696 2 T24146 hypothetical prote
41 32 72.7 2121 2 T27406 hypothetical prote
42 31 70.5 98 2 PC6012 thuf protein - Rho
43 31 70.5 178 2 S50637 hypothetical prote
44 31 70.5 222 2 AH0991 cell division ATP-
45 31 70.5 237 2 T07820 hypothetical prote

ALIGNMENTS

RESULT 1
B48521
bilirubin oxidase (EC 1.3.3.5) - fungus (Myrothecium verrucaria)
C;Species: Myrothecium verrucaria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: B48521; A48521
R;Koikeda, S.; Ando, K.; Kaji, H.; Inoue, T.; Murao, S.; Takeuchi, K.; Samejima, T.
J. Biol. Chem. 268, 18801-18809, 1993
A;Title: Molecular cloning of the gene for bilirubin oxidase from Myrothecium verruca
A;Reference number: A48521; MUID:93366794
A;Accession: B48521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-572 <KO11>
A;Cross-references: GB:D14081; NID:g436236; PIDN:BA03166.1; PID:g456710
A;Note: sequence extracted from NCBI backbone (NCBIN:136730, NCBI:P:136732)
A;Accession: A48521
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-572 <KO12>
A;Cross-references: GB:D14081; NID:g436236; PIDN:BA03166.1; PID:g456710
A;Note: sequence extracted from NCBI backbone (NCBIN:136728, NCBI:P:136729)
C;Keywords: oxidoreductase

Query Match 84.1%; Score 37; DB 2; Length 572;
Best Local Similarity 85.7%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 1;

Qy 1 HLHGSPA 7
| | | | |
Db 132 HLHGSPS 138

RESULT 2
F86280
protein T5E21.11 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F86280
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: F86280

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1115 <STO>
C:Cross-references: GB:AE005172; NID:g7527726; PIDN:AAF63175.1; GSPDB:GN00141
C:Genetics:
A:Gene: T5E21.11
A:Map position: 1
C:Superfamily: valine--trna ligase

Query Match 81.8%; Score 36; DB 2; Length 1115;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSPA 7
||| ||
Db 396 HLHGKFA 402

RESULT 3
AE1301
phosphoglycerate dehydrogenase homolog lmo1813 [imported] - Listeria monocytogenes (strain
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1301
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Smoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1301
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99891.1; PTD:gl6411267; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1813

Query Match 77.3%; Score 34; DB 2; Length 220;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSPA 7
||| ||
Db 46 HLHGSPA 52

RESULT 4
AE1673
phosphoglycerate dehydrogenase homolog lin1927 [imported] - Listeria innocua (strain Cl
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1673
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Smoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1673
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97157.1; PTD:gl6414428; GSPDB:GN00178
A:Experimental source: strain Clpil1262
C:Genetics:

A:Gene: lin1927

Query Match 77.3%; Score 34; DB 2; Length 220;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSPA 7
||| ||
Db 46 HLHGSPA 52

RESULT 5
S37740
transcription factor TRF - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: S37740; S29720; S31869; S31871
R:Crowley, T.E.; Hoey, T.; Liu, J.K.; Jan, Y.N.; Jan, L.Y.; Tjian, R.
Nature 361, 557-561, 1993
A:Title: A new factor related to TATA-binding protein has highly restricted expressio
A:Reference number: S29720; MUID:93156846
A:Accession: S37740
A:Molecule type: DNA
A:Residues: 1-224 <CRO1>
A:Cross-references: EMBL:X70838; NID:gl1137; PIDN:CAA50186.1; PID:gl1138
A:Accession: S29720
A:Molecule type: mRNA
A:Residues: 1-224 <CRO2>
A:Cross-references: EMBL:X70837; NID:gl1135; PIDN:CAA50185.1; PID:gl1136
C:Genetics:
A:Gene: FlyBase:Trf
A:Cross-references: FlyBase:FBgn0010287
A:Introns: 52/2
C:Superfamily: transcription initiation factor IID
C:Keywords: DNA binding; transcription factor

Query Match 77.3%; Score 34; DB 2; Length 224;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSPAS 8
|:|:| |:
Db 161 HVHGQFSS 168

RESULT 6
B70838
hypothetical protein Rv0197 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70838
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hollroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987
A:Accession: B70838
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-762 <COL>
A:Cross-references: GB:AL021928; GB:AL123456; NID:g3261522; PIDN:CAAL7319.1; PID:g290
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0197
C:Superfamily: formate dehydrogenase

Query Match 77.3%; Score 34; DB 2; Length 762;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFA 7

Db 326 HLHGSFA 332

RESULT 7

T35044

bacteriophage phiC31 resistance protein pglY - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 01-Dec-2000

C:Accession: T35044; T30203

R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A:Reference number: Z21566

A:Accession: T35044

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1294 <SEE>

A:Cross-references: EMBL:AL031371; PIDN:CAA20546.1; GSPDB:GN00070; SCOEDB:SC4G2.09

A:Experimental source: strain A3(2)

R:Bedford, D.J.; Laity, C.; Buttner, M.J.

J. Bacteriol. 177, 4681-4689, 1995

A>Title: Two genes involved in the phase-variable phi C31 resistance mechanism of Strept

A:Reference number: 220777; MUID:95370146

A:Accession: T30203

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-372, 'N', 374-913, 'I', 915-1002, 'A', 1004-1294 <BED>

A:Cross-references: EMBL:L37531; NID:g576537; PID:g576538; PIDN:AAB00365.1

C:Genetics:

A:Gene: pglY; SCOEDB:SC4G2.09

Query Match

Best Local Similarity 77.3%; Score 34; DB 2; Length 1294;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8

Db 72 YLHGSFGS 79

RESULT 8

F97615

hypothetical protein AGR_C_3868 [Imported] - Agrobacterium tumefaciens (strain C58, Cere

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C:Accession: F97615

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; PMID:11743194

A:Accession: F97615

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-277 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK87879.1; PID:gl515157269; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C_3868

A:Map position: circular chromosome

Query Match

Best Local Similarity 75.0%; Score 33; DB 2; Length 277;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFAS 8

Db 79 LHGSFSS 85

RESULT 8

S77339

hypothetical protein sll1723 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

RESULT 9

AD2838

conserved hypothetical protein Atu2132 [Imported] - Agrobacterium tumefaciens (strain

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C:Accession: AD2838

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam

ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AD2838

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-277 <KUR>

A:Cross-references: GB:AE008688; PIDN:AAL43122.1; PID:gl7740595; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu2132

A:Map position: circular chromosome

Query Match

Best Local Similarity 75.0%; Score 33; DB 2; Length 277;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFAS 8

Db 79 LHGSFSS 85

RESULT 10

AF3161

phage-related integrase [Imported] - Agrobacterium tumefaciens (strain C58, Dupont) p

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C:Accession: AF3161

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam

ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AF3161

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-346 <KUR>

A:Cross-references: GB:AE008687; PIDN:AAL45708.1; PID:gl7743437; GSPDB:GN00188

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: intX

A:Genome: plasmid

Query Match

Best Local Similarity 75.0%; Score 33; DB 2; Length 346;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFAS 8

Db 116 LHGAFA 122

A: Variety: PCC 6803
 C: Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C: Accession: S77339
 R: Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpō, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
 A: Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* s.
 A: Reference number: S74322; MUID: 97061201
 A: Accession: S77339
 A: Status: nucleic acid sequence not shown; translation not shown
 A: Molecule type: DNA
 A: Residues: 1-413 <KAN>
 A: Cross-references: EMBL:D90906; GB:AB001339; NID:gl652492; PTDN:BAAL7442.1; PTD:dl01817
 A: Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 75.0%; Score 33; DB 2; Length 413;
 Best Local Similarity 75.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8
 ||| |||
 Db 128 HLHAHFAS 135

RESULT 12
 T05299
 hypothetical protein F26P21.30 - Arabidopsis thaliana
 C: Species: Arabidopsis thaliana (mouse-ear cress)
 C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 24-Nov-1999
 C: Accession: T05299
 R: Bevan, M.; Terry, N.; Ardiles, W.; Buysschaert, C.; Dasseville, R.; De Clerck, R.; De ewes, H.W.; Mayer, K.F.X.; Schueller, C.
 submitted to the Protein Sequence Database, October 1998
 A: Reference number: Z15407
 A: Accession: T05299
 A: Molecule type: DNA
 A: Residues: 1-761 <BEV>
 A: Cross-references: EMBL:AL031804
 A: Experimental source: cultivar Columbia; BAC clone F26P21
 C: Genetics:
 A: Map position: 4
 A: Introns: 123/2; 167/2; 221/3; 262/3; 281/3; 348/3; 385/3; 398/2; 450/3; 484/3; 492/3;
 A: Note: F26P21.30
 C: Superfamily: Arabidopsis thaliana hypothetical protein F26P21.30

Query Match 75.0%; Score 33; DB 2; Length 761;
 Best Local Similarity 83.3%; Pred. No. 1-7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSF 6
 |||||
 Db 267 HLHGSY 272

RESULT 13
 E88029
 protein F46F5.11 [imported] - Caenorhabditis elegans
 C: Species: Caenorhabditis elegans
 C: Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C: Accession: E88029
 R: anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A: Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biolog
 A: Reference number: A75000; MUID: 99069613; PMID: 9851916
 A: Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
 A: Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A: Accession: E88029
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-796 <STO>

A: Cross-references: GB:chr_II; PTDN:AC78189.1; PID:g3886038; GSPDB:GN00020; CESP:F46F
 C: Genetics:
 A: Gene: F46F5.11
 A: Map position: 2

Query Match 75.0%; Score 33; DB 2; Length 796;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSF 6
 |||||
 Db 601 HLHGSY 606

RESULT 14
 A56644
 inverted repeat component hypothetical protein IR3 - equine herpesvirus 1
 C: Species: equine herpesvirus 1
 C: Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 08-Oct-1999
 C: Accession: A56644
 R: Holden, V.R.; Harty, R.N.; Yalamanchili, R.R.; O'Callaghan, D.J.
 DNA Seq. 3, 143-152, 1992
 A: Title: The IR3 gene of equine herpesvirus type 1: a unique gene regulated by sequen
 A: Reference number: A56644; MUID: 93112995
 A: Accession: A56644
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-95 <HOL>
 A: Cross-references: GB:M92043; NID:g330912; PTDN:AAA68888.1; PID:g330913
 A: Note: sequence extracted from NCBI backbone (NCBIN:121461, NCBI:P:121462)
 C: Genetics:
 A: Gene: IR3

Query Match 72.7%; Score 32; DB 2; Length 95;
 Best Local Similarity 75.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8
 ||| |||
 Db 20 HLHALFAS 27

RESULT 15
 AC2830
 pyrazinamidase/nicotinamidase [imported] - Agrobacterium tumefaciens (strain C58, Dup
 C: Species: Agrobacterium tumefaciens
 C: Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C: Accession: AC2830
 R: Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A: Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
 ster, E.W.
 A: Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A: Reference number: AB2577; PMID: 11743193
 A: Accession: AC2830
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-208 <KUR>
 A: Cross-references: GB:AE008688; PTDN:AAL43057.1; PID:gl7740524; GSPDB:GN00186
 A: Experimental source: strain C58 (Dupont)
 C: Genetics:
 A: Gene: pncA
 A: Map position: circular chromosome

Query Match 72.7%; Score 32; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HGSFAS 8
| | | | |
Db 54 HGSFAS 59

Search completed: August 19, 2002, 05:36:07
Job time: 1288 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:09 ; Search time 51.81 seconds
(without alignments)
5.979 Million cell updates/sec

Title: US-09-339-922A-106

Perfect score: 44

Sequence: 1 HLHGSFAS 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	84.1	572	1 BLRO_MYRVE	Q12737 myrothecium
2	36	81.8	1107	1 SYV_ARATH	P93736 arabidopsis
3	35	79.5	394	1 IPOUL_DROME	P24350 drosophila
4	34	77.3	358	1 YC07_KLEPN	Q48453 klebsiella
5	32	72.7	213	1 PNCA_ECOLI	P21369 escherichia
6	32	72.7	222	1 SDHB_PEPAS	P33074 peptostrept
7	32	72.7	335	1 G3P_CHLMU	Q9pjn6 chlamydia m
8	32	72.7	352	1 PSBD_CHLVU	P56319 chlorella v
9	32	72.7	364	1 ZRP4_MAIZE	P47917 zea mays (m
10	32	72.7	385	1 YF00_YEAST	P43567 saccharomyc
11	32	72.7	400	1 DH12_RAT	P50233 rattus norv
12	32	72.7	405	1 DH12_HUMAN	P80365 homo sapien
13	32	72.7	574	1 SNTD_HUMAN	P21589 homo sapien
14	32	72.7	980	1 SYV_SCHPO	O75005 schizosacch
15	32	72.7	1104	1 SYV_YEAST	P07806 saccharomyc
16	31	70.5	178	1 YEW4_YEAST	P40081 saccharomyc
17	31	70.5	887	1 YLX8_CAEEL	P46504 caenorhabdi
18	30	68.2	176	1 TRAF_AGRT5	Q44350 agrobacteri
19	30	68.2	176	1 TRAF_AGRT6	Q44364 agrobacteri
20	30	68.2	176	1 TRAF_AGRT9	P15595 agrobacteri
21	30	68.2	197	1 EGG5_FASHE	P07915 fasciola he
22	30	68.2	244	1 T2FC_YEAST	P35189 saccharomyc
23	30	68.2	272	1 MCBC_ECOLI	P23185 escherichia
24	30	68.2	317	1 YDC1_YEAST	Q02896 saccharomyc
25	30	68.2	376	1 CYB_PLABE	O99253 plasmodium
26	30	68.2	376	1 CYB_PLACH	O99256 plasmodium
27	30	68.2	376	1 CYB_PLAFA	Q02768 plasmodium
28	30	68.2	382	1 CYB_PLAVS	O63696 plasmodium
29	30	68.2	427	1 AROA_STRPN	Q9s400 streptococc
30	30	68.2	445	1 GLNA_LACDE	P45627 lactobacill
31	30	68.2	529	1 ENP3_HUMAN	O75355 homo sapien
32	30	68.2	768	1 LEM3_RAT	P98106 rattus norv
33	30	68.2	906	1 FOX2_CANTR	P22414 candida tro

ALIGNMENTS

```

RESULT 1
BLRO_MYRVE
ID BLRO_MYRVE STANDARD; PRT; 572 AA.
AC Q12737;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Bilirubin oxidase precursor (EC 1.3.3.5).
OS Myrothecium verrucaria.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.
OX NCBI_TaxID=5532;
RN [1]
RC STRAIN=MT-1;
RX MEDLINE=93366794; PubMed=8360171;
RA Koikeda S., Ando K., Kaji H., Inoue T., Murao S., Takeuchi K.,
RA Samejima T.;
RT "Molecular cloning of the gene for bilirubin oxidase from Myrothecium
RT verrucaria and its expression in Yeast.";
RL J. Biol. Chem. 268:18801-18809(1993).
CC -|- FUNCTION: OXIDATION OF BILIRUBIN AND OTHER TETRAPYRROLES.
CC -|- CATALYTIC ACTIVITY: Bilirubin + O(2) -> biliverdin + H(2)O.
CC -|- CONTAINER: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH
CC -|- CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2
CC OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR. CONTAINS 2 BLUE COPPER
CC ATOMS PER MOLECULE.
CC -|- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -|- SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; D14081; BAA03166.1; -
CC EMBL; D12579; BAA02123.1; -
CC InterPro; IPR001117; Cu-oxidase.
CC Pfam; PF00394; Cu-oxidase; 1.
CC Signal; Copper; Metal-binding; Oxidoreductase; Glycoprotein; Repeat.
CC SIGNAL 1 19 PROBABLE.
CC PROPEP 20 38
CC CHAIN 39 572
CC DOMAIN 98 194
CC FT DOMAIN 404 526 PLASTOCYANIN-LIKE 2.
CC FT METAL 132 132 COPPER (TYPE 2) (BY SIMILARITY).
CC FT METAL 134 134 COPPER (TYPE 3) (BY SIMILARITY).
CC FT METAL 172 172 COPPER (TYPE 3) (BY SIMILARITY).
CC FT METAL 174 174 COPPER (TYPE 3) (BY SIMILARITY).
CC FT METAL 436 436 COPPER (TYPE 1) (BY SIMILARITY).
CC FT METAL 439 439 COPPER (TYPE 2) (BY SIMILARITY).
CC FT METAL 441 441 COPPER (TYPE 3) (BY SIMILARITY).
CC FT METAL 494 494 COPPER (TYPE 3) (BY SIMILARITY).
CC FT METAL 495 495 COPPER (TYPE 1) (BY SIMILARITY).

```

```

34 30 68.2 946 1 YIN7_YEAST P40462 saccharomyc
35 30 68.2 963 1 ATC4_HUMAN O75185 homo sapien
36 30 68.2 970 1 Y277_MYCGE Q49409 mycoplasma
37 30 68.2 1584 1 BAIL_HUMAN O14514 homo sapien
38 30 68.2 3122 1 DPO2_MOUSE Q61493 mus musculus
39 30 68.2 3130 1 DPO2_HUMAN O60673 homo sapien
40 29 65.9 126 1 VATG_CAEEL P91303 caenorhabdi
41 29 65.9 196 1 WBBJ_ECOLI P37750 escherichia
42 29 65.9 221 1 TRPF_HALVO P52563 halobacteri
43 29 65.9 231 1 ARAD_ECOLI P08203 escherichia
44 29 65.9 231 1 ARAD_SALTY P6190 salmonella
45 29 65.9 231 1 SGBE_ECOLI P37680 escherichia

```

```

FT METAL 496 496 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 500 500 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 503 503 COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 510 510 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 572 AA; 63947 MW; 5842D641303E5EFF CRC64;

Query Match 84.1%; Score 37; DB 1; Length 572;
Best Local Similarity 85.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLHGSFA 7
    |||||
Db 132 HLHGSFS 138

RESULT 2
SYV_ARATH STANDARD; PRT; 1107 AA.
AC P93736;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VAL1-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).
GN VALRS.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=97352801; PubMed=9207094;
RA Zhang J.Z., Somerville C.R.;
RT "Suspensor-derived polyembryony caused by altered expression of
RL valyl- tRNA synthetase in the tw2 mutant of Arabidopsis.";
Proc. Natl. Acad. Sci. U.S.A. 94:7349-7355(1997).
CC -|- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -|- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U89986; AAB49704.1; -.
CC EMBL; U93308; AAB51589.1; -.
CC HSP; P96142; IGX.
CC InterPro; IPR002300; tRNA-synt_la.
CC InterPro; IPR001412; tRNA-synt_I.
CC InterPro; IPR002303; tRNA-synt_val.
CC Pfam; PF00133; tRNA-synt_1; 1.
CC PRINTS; PR00986; TRNASYNTHAL.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SITE 177 187 "HIGH" REGION.
FT SITE 694 698 "KMSKS" REGION.
FT BINDING 697 697 ATP (BY SIMILARITY).
SQ SEQUENCE 1107 AA; 125894 MW; ED71F237DF24E51B CRC64;

Query Match 81.8%; Score 36; DB 1; Length 1107;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLHGSFA 7
    |||||

```

```

Db 388 HLHGKFA 394

RESULT 3
IPOU_DROME STANDARD; PRT; 394 AA.
AC P24350; Q26465; O77214;
DT 01-MAR-1992 (Rel. 21, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Inhibitory POU protein (I-POU) (Abnormal chemosensory jump 6 protein).
GN IPOU OR ACJ6.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I-POU).
RX MEDLINE=91204052; PubMed=1673230;
RA Treacy M.N., He X., Rosenfeld M.G.;
RT "I-POU: a POU-domain protein that inhibits neuron-specific gene
RT activation.";
RL Nature 350:577-584(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM TI-POU).
RC STRAIN=CANTON-S;
RA Clyne P.J., Certel S., de Bruyne M., Zaslavsky L., Johnson W.,
RA Carlson J.R.;
RT "The odor-specificities of a subset of olfactory receptor neurons are
RT governed by Acj6, a POU domain transcription factor.";
Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 318-375 FROM N.A. (ISOFORM TI-POU).
RX MEDLINE=92154665; PubMed=1346754;
RA Treacy M.N., Neilson L.I., Turner E.E., He X., Rosenfeld M.G.;
RT "Twin of I-POU: a two amino acid difference in the I-POU homeodomain
RT distinguishes an activator from an inhibitor of transcription.";
Cell 68:491-505(1992).
RN [4]
RP DNA-BINDING.
RX MEDLINE=97140288; PubMed=8986770;
RA Turner E.E.;
RT "Similar DNA recognition properties of alternatively spliced
RT Drosophila POU factors.";
Proc. Natl. Acad. Sci. U.S.A. 93:15097-15101(1996).
CC -|- FUNCTION: MODULATES GENE TRANSCRIPTION.
CC -|- SUBCELLULAR LOCATION: Nuclear.
CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; I-POU (SHOWN HERE) AND TI-
CC POU/TWIN-OF-I-POU; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -|- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE CENTRAL NERVOUS
CC SYSTEM.
CC -|- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
CC TO CLASS-4 POU.
CC -|- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT THAT I-POU HOMEOBOX IS
CC UNABLE TO BIND DNA BECAUSE IT LACKS TWO N-TERMINAL BASIC RESIDUES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X58436; CAA41342.1; -.
CC EMBL; AF086816; AAC35369.1; -.
CC EMBL; S82271; AAB21441.1; -.
CC EMBL; S82267; AAB21441.1; JOINED.
CC FTR; S14795; S14795.
CC HSSP; P14859; IOCT.
CC TRANSFAC; T01898; -.
CC Flybase; FBgn0000028; acj6.

```


entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; M26934; AAA23447.1; -
DR EMBL; AE000271; AAC74838.1; ALT_INIT.
DR EMBL; D90820; BAA15559.1; -
DR EMBL; D90821; BAA15566.1; -
DR PIR; J00048; QOECAS.
DR EcGene; EG11135; pncA.
DR InterPro; IPR000868; Isochorismatase.
DR Pfam; PF00857; Isochorismatase; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 213 AA; 23362 MW; B9F8D946FA18433F CRC64;

Query Match 72.7%; Score 32; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HGSFAS 8
Db 58 HGSFAS 63

RESULT 6

SDHB_PEPAS
ID SDHB_PEPAS STANDARD; PRT; 222 AA.
AC P33074;
DT 01-OCT-1993 (Rel. 27, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE L-serine dehydratase, beta chain (EC 4.2.1.13) (L-serine deaminase) (SDH) (L-SD).
GN SDHB.
OS Peptostreptococcus asaccharolyticus (Peptococcus asaccharolyticus).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Peptoniphilus.
ON NCBI_TaxID=1258;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14963;
RX MEDLINE=97386436; PubMed=9244285;
RA Holmester A.E., Textor S., Buckel W.;
RT "Cloning and expression of the genes coding for the L-serine dehydratase from Peptostreptococcus asaccharolyticus: relationship of the iron-sulfur protein to both L-serine dehydratases from Escherichia coli.";
RT J. Bacteriol. 179:4937-4941(1997).
RN [2]
RP SEQUENCE OF 4-19.
RC STRAIN=ATCC 14963;
RX MEDLINE=91293139; PubMed=2065681;
RA Grabowski R., Buckel W.;
RT "Purification and properties of an iron-sulfur-containing and pyridoxal-phosphate-independent L-serine dehydratase from Peptostreptococcus asaccharolyticus.";
RT Eur. J. Biochem. 199:89-94(1991).
RL -1- CATALYTIC ACTIVITY: L-serine + H(2)O -> pyruvate + NH(3) + H(2)O.
CC -1- COFACTOR: IRON-SULFUR (4FE-4S).
CC -1- PATHWAY: GLUCONEOGENESIS FROM SERINE.
CC -1- SUBUNIT: HETEROCTAMER OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
CC -1- SIMILARITY: BELONGS TO THE IRON-SULFUR DEPENDENT L-SERINE DEHYDRATASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; U76260; AAC45545.1; -

DR PIR; S16376; S16376.
DR InterPro; IPR002912; ACT.
DR Pfam; PF01842; ACT; 1.
KW Lyase; Iron-sulfur; 4Fe-4S; Gluconeoegenesis.
SQ SEQUENCE 222 AA; 24151 MW; 3A2A624EC3104C08 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFA 7
Db 47 LHGSFA 52

RESULT 7

G3P_CHLMU
ID G3P_CHLMU STANDARD; PRT; 335 AA.
AC Q9PJN6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glyceralddehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
GN GAP OR TC0792.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nig9;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S., White O., Hickey E.K., Peterson J., Utterback T., Bowan C., Dodson R., Linher K., Weidman J., Khouri H., Craven B., McClarty G., Salzberg S.L., Winn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- CATALYTIC ACTIVITY: D-glyceralddehyde 3-phosphate + phosphate + NAD(+) -> 3-phospho-D-glyceroyl phosphate + NADH.
CC -1- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; AE002347; AAF39595.1; -
DR TIGR; TC0792;
DR InterPro; IPR000173; GAP_DH.
DR Pfam; PF00044; gpdh; 1.
DR Pfam; PF02800; gpdh_C; 1.
DR PRINTS; PR00078; G3PDHGRNAS.
DR PROSITE; PS00071; GAPDH; 1.
KW Glycolysis; NAD; Oxidoreductase; Complete proteome.
FT BINDING 151 151
FT GLYCERALDEHYDE 3-PHOSPHATE (BY
FT SIMILARITY).
FT ACT_SITE 178 178
FT ACTIVATES THIOL GROUP DURING CATALYSIS
FT (BY SIMILARITY).
SQ SEQUENCE 335 AA; 36240 MW; BE1CF546FB17FD2 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HGSFAS 8
| | | | |
DB 50 HGSFAS 55

RESULT 8
PSBD_CHLVU STANDARD; PRT; 352 AA.
AC P56319;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II D2 protein (Photosystem Q(A) protein) (PSII D2
protein).
GN PSBD.

OS Chlorella vulgaris.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-IAM C-27 / TANIYA;
RX MEDLINE=97303241; PubMed=9159184;
RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
RA Inamura A., Yoshinaga K., Sugiura M.;
RT "Complete nucleotide sequence of the chloroplast genome from the
RT green alga Chlorella vulgaris: the existence of genes possibly
RT involved in chloroplast division";
RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).

CC -!- FUNCTION: THIS IS ONE OF THE TWO REACTION CENTER PROTEINS OF PSII,
CC D2 PROTEIN IS NEEDED FOR ASSEMBLY OF A STABLE PSII COMPLEX.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
CC thylakoid membrane.
CC -!- SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA /
CC PSBD FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; AB001684; BAA57876.1; -.
DR HSP; P02955; IDOP.
DR InterPro; IPR000484; Photo_RC.
DR Pfam; PF00124; photoRC; 1.
DR ProDom; PD000551; Photo_RC; 1.
DR PROSITE; PS00244; REACTION_CENTER; 1.
KW Transmembrane; Electron transport; Thylakoid; Photosystem II;
KW Chloroplast; Iron.
FT TRANSMEM 35 56 POTENTIAL.
FT TRANSMEM 108 128 POTENTIAL.
FT TRANSMEM 141 163 POTENTIAL.
FT TRANSMEM 191 217 POTENTIAL.
FT TRANSMEM 266 286 POTENTIAL.
FT METAL 214 214 IRON (NON HEME).
FT METAL 224 224 IRON (NON HEME).
FT METAL 268 268 IRON (NON HEME).
SQ SEQUENCE 352 AA; 39429 MW; 0F8FD072C9FD139 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFA 7
| | | | |

DB 116 LHGSFA 121

RESULT 9
ZRP4_MAIZE STANDARD; PRT; 364 AA.
AC P47917;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT).
GN ZRP4.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=CV. NKH31; TISSUE=Root;
RX MEDLINE=94105316; PubMed=8278520;
RA Held B.M., Wang H., John I., Wurtele E.S., Colbert J.T.;
RT "An mRNA putatively coding for an O-methyltransferase accumulates
RT preferentially in maize roots and is located predominantly in the
RT region of the endodermis";
RL Plant Physiol. 102:1001-1008(1993).
CC -!- FUNCTION: MAY BE INVOLVED IN THE O-METHYLATION OF SUBERIN
CC PHENYLPROPANOID PRECURSORS.
CC -!- TISSUE SPECIFICITY: ACCUMULATES PREFERENTIALLY IN THE ROOTS AND IS
CC LOCATED PREDOMINANTLY IN THE REGION OF THE ENDODERMIS, LOW LEVELS
CC ARE SEEN IN THE LEAVES, STEMS, AND OTHER SHOOT ORGANS.
CC -!- SIMILARITY: TO OTHER OMTS REQUIRING S-ADENOSYL-L-METHIONINE AS
CC SUBSTRATE.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; L14063; AAA18532.1; -.
DR MaizeDB; 63528; -.
DR InterPro; IPR001601; Meth-transf.
DR InterPro; IPR001077; Methyltransf_2.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF00891; Methyltransf_2; 1.
KW Transferase; Methyltransferase.
SQ SEQUENCE 364 AA; 39583 MW; FB8AD93AD5A6611D CRC64;

Query Match 72.7%; Score 32; DB 1; Length 364;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8
| | | | |
DB 46 HLHGSFAS 53

RESULT 10
YFD0_YEAST STANDARD; PRT; 385 AA.
ID YFD0_YEAST
AC P43567;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 41.9 kDa protein in HAC1-CAK1 intergenic region.
GN YFL030W.

OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

```

OX NCBI_TaxID=4932;
RN SEQUENCE FROM N.A.
RC MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.";
RL Nat. Genet. 10:261-268(1995).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D50617; BAA09208.1; -.
DR SGD; S0001864; YFL030M.
DR InterPro; IPR000192; AminoTransf_class_V.
DR Pfam; PF00266; aminotran_5; 1.
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KW Hypothetical protein; Pyridoxal phosphate.
FT BINDING 201 201 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 385 AA; 41907 MW; 460D5DCCAB8FDF79F CRC64;

Query Match 72.7%; Score 32; DB 1; Length 385;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8
DB 230 HVHGFSS 237
|:|:| |

RESULT 11
DH12_RAT
ID DH12_RAT STANDARD; PRT; 400 AA.
AC P50233;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Corticosteroid 11-beta-dehydrogenase, isozyme 2 (EC 1.1.1.146) (11-
DE DH2) (11-beta-hydroxysteroid dehydrogenase 2) (11-beta-HSD2) (NAD-
DE dependent 11-beta-hydroxysteroid dehydrogenase).
GN HSD11B2 OR HSD11K.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Kidney;
RX MEDLINE=95377198; PubMed=7649078;
RA Zhou M.Y., Gomez-Sanchez E.P., Cox D.L., Cosby D.,
RA Gomez-Sanchez C.E.;
RT "Cloning, expression, and tissue distribution of the rat nicotinamide
RT adenine dinucleotide-dependent 11 beta-hydroxysteroid
RT dehydrogenase.";
RL Endocrinology 136:3729-3734(1995).
CC -!- FUNCTION: HAS A ROLE IN MODULATING GLUCOCORTICOID ACTIVITY BOTH AT
CC THE LEVEL OF THE MINERALOCORTICOID RECEPTOR AND THE GLUCOCORTICOID
CC RECEPTOR. USES NADH WHILE 11-DH1 USES NADPH. CATALYZES NON
CC REVERSIBLY THE CONVERSION OF CORTISOL TO THE INACTIVE METABOLITE
CC CORTISONE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: A 11-BETA-HYDROXYSTEROID + NAD(+) = A

```

```

CC 11-OXOSTEROID + NADH.
CC -!- SUBCELLULAR LOCATION: Mitochondrion.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U22424; AAA87007.1; -.
DR HSP; P14061; IFDU.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; Mitochondrion.
FT NE_BIND 82 111 NAD (BY SIMILARITY).
FT ACT_SITE 232 232 BY SIMILARITY.
SQ SEQUENCE 400 AA; 43726 MW; A1BAAA328E2F189D CRC64;

Query Match 72.7%; Score 32; DB 1; Length 400;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSF 6
DB 302 HLHGF 307
|:|:| |

RESULT 12
DH12_HUMAN
ID DH12_HUMAN STANDARD; PRT; 405 AA.
AC P80365; Q13194;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Corticosteroid 11-beta-dehydrogenase, isozyme 2 (EC 1.1.1.146) (11-
DE DH2) (11-beta-hydroxysteroid dehydrogenase 2) (11-beta-HSD2) (NAD-
DE dependent 11-beta-hydroxysteroid dehydrogenase).
GN HSD11B2 OR HSD11K.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95163772; PubMed=7859916;
RA Albiston A.L., Obeyesekere V.R., Smith R.E., Krozowski Z.S.;
RT "Cloning and tissue distribution of the human 11 beta-hydroxysteroid
RT dehydrogenase type 2 enzyme.";
RL Mol. Cell. Endocrinol. 105:R11-R17(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96079108; PubMed=8530071;
RA Agarwal A.K., Rogerson F.M., Mune T., White P.C.;
RT "Gene structure and chromosomal localization of the human HSD11K gene
RT encoding the kidney (type 2) isozyme of 11 beta-hydroxysteroid
RT dehydrogenase.";
RL Genomics 29:195-199(1995).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96190749; PubMed=8611140;
RA Brown R.W., Chapman K.E., Kotelevtsev Y., Yau J.L., Lindsay R.S.,
RA Brett L., Leckie C., Murad P., Lyons V., Mullins J.J.,
RA Edwards C.R.W., Seckl J.R.;
RT "Cloning and production of antisera to human placental 11 beta-

```


RT hydroxysteroid dehydrogenase type 2.";
 RL Biochem. J. 313:1007-1017(1996).
 RN [4]
 RP VARIANT'S AME CYS-208 AND CYS-213.
 RX MEDLINE=95400319; PubMed=7670488;
 RA Mune T., Rogerson F.M., Nikkila H., Agarwal A.K., White P.C.;
 RT "Human hypertension caused by mutations in the kidney isozyme of 11
 beta-hydroxysteroid dehydrogenase.";
 RL Nat. Genet. 10:394-399(1995).
 CC -|- FUNCTION: HAS A ROLE IN MODULATING GLUCOCORTICOID ACTIVITY BOTH AT
 CC THE LEVEL OF THE MINERALOCORTICOID RECEPTOR AND THE GLUCOCORTICOID
 CC RECEPTOR. USES NADH WHILE 11-DH1 USES NADPH. CATALYZES NON
 CC REVERSIBLY THE CONVERSION OF CORTISOL TO THE INACTIVE METABOLITE
 CC CORTISONE.
 CC -|- CATALYTIC ACTIVITY: A 11-BETA-HYDROXYSTEROID + NAD(+) = A
 CC 11-OXOSTEROID + NADH.
 CC -|- SUBCELLULAR LOCATION: Mitochondrial.
 CC -|- TISSUE SPECIFICITY: FOUND IN PLACENTA, KIDNEY, PANCREAS, PROSTATE,
 CC OVARY, SMALL INTESTINE AND COLON.
 CC -|- DISEASE: DEFECTS IN HSD11B2 ARE THE CAUSE OF A POTENTIALLY FATAL
 CC FORM OF CHILDHOOD HYPERTENSION TERMED APPARENT MINERALOCORTICOID
 CC EXCESS (AME). IT IS THOUGHT THAT INACTIVATION OF HSD11B2 PERMITS
 CC CORTISOL TO OCCUPY THE RENAL MINERALOCORTICOID RECEPTOR AND
 CC THEREBY CAUSE SODIUM RETENTION AND HYPERTENSION.
 CC -|- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U14631; AAA91969.1; -;
 DR EMBL; U27317; AAB48544.1; -;
 DR EMBL; U26726; AAC50356.1; -;
 DR HSSP; P14061; IFDW.
 DR MIM; 218030; -;
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PROSITE; PS00061; adh_short; 1.
 KW Oxidoreductase; NAD; Microsome; Disease mutation.
 FT NP_BIND 82 111 NAD (BY SIMILARITY).
 FT ACT_SITE 232 232 BY SIMILARITY.
 FT VARIANT 208 208 R -> C (IN AME).
 FT VARIANT 213 213 /FTIG=VAR_006958.
 FT VARIANT 213 213 R -> C (IN AME).
 FT CONFLICT 148 148 L -> F (IN REF. 2).
 FT CONFLICT 148 148 L -> V (IN REF. 3).
 FT SEQUENCE 405 AA; 44140 MW; 4AB7538269913F24 CRC64;
 SQ
 Query Match 72.7%; Score 32; DB 1; Length 405;
 Best Local Similarity 83.3%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 HLHGSF 6
 Db 302 HLHGQF 307
 RESULT 13
 ID 5NTD_HUMAN STANDARD; PRT; 574 AA.
 AC P21589; O75520;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 5'-nucleotidase precursor (EC 3.1.3.5) (ecto-5'-nucleotidase) (5'-NT)
 DE (CD73 antigen).

GN NT5 OR NTE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=90361037; PubMed=2129526;
 RA Misumi Y., Ogata S., Ohkubo K., Hirose S., Ikehara Y.;
 RT "Primary structure of human placental 5'-nucleotidase and
 RT identification of the glycolipid anchor in the mature form.";
 RL Eur. J. Biochem. 191:563-569(1990).
 RN [2]
 RP SEQUENCE OF 1-113 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=96144293; PubMed=8566797;
 RA Hansen K.R., Resta R., Webb C.F., Thompson L.F.;
 RT "Isolation and characterization of the promoter of the human 5'-
 RT nucleotidase (CD73)-encoding gene.";
 RL Gene 167:307-312(1995).
 RN [3]
 RP SEQUENCE OF 359-489 FROM N.A.
 RC TISSUE=Leukocyte;
 RA Zanoni L., Rosi F., Pagani R., Marinello E.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 27-40.
 RC TISSUE=Placenta;
 RX MEDLINE=91058583; PubMed=2173922;
 RA Klemens M.R., Sherman W.R., Holmberg N.J., Ruedi J.M., Low M.G.,
 RA Thompson L.F.;
 RT "Characterization of soluble vs membrane-bound human placental 5'-
 RT nucleotidase.";
 RL Biochem. Biophys. Res. Commun. 172:1371-1377(1990).
 RN [5]
 RP DISEASE.
 RX MEDLINE=98313134; PubMed=9651114;
 RA Rosi F., Agostinho A.B., Carlucci F., Zanoni L., Porcelli B.,
 RA Marinello E., Galleni P., Tabucchi A.;
 RT "Behaviour of human lymphocytic isoenzymes of 5'-nucleotidase.";
 RL Life Sci. 62:2257-2266(1998).
 CC -|- FUNCTION: HYDROLYZES EXTRACELLULAR NUCLEOTIDES INTO MEMBRANE
 CC PERMEABLE NUCLEOSIDES.
 CC -|- CATALYTIC ACTIVITY: A 5'-ribonucleotide + H(2)O = a ribonucleoside
 CC + phosphate.
 CC -|- COFACTOR: ZINC.
 CC -|- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -|- DISEASE: THERE IS A DECREASE IN THE ACTIVITY OF NT5 IN B-CELL
 CC CHRONIC LYMPHOCYTIC LEUKEMIA.
 CC -|- SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.
 CC -|- DATABASE: NAME=PROW; NOTE=CD guide CD73 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd73.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X55740; CAA39271.1; -;
 DR EMBL; U21730; AAA96950.1; -;
 DR EMBL; AF069067; AAC98672.1; -;
 DR PIR; S11032; S11032.
 DR HSSP; P07024; ZUSH.
 DR MIM; 129190; -;
 DR InterPro; IPR002224; 5_nucleotidase.
 DR InterPro; IPR000934; Ser_thr_phosphatse.
 DR Pfam; PF01009; 5_nucleotidase; 1.
 DR Pfam; PF02872; 5_nucleotidase; 1.

DR PROSITE: PS00785; 5_NUCLEOTIDASE_1; 1.
 DR PROSITE: PS00786; 5_NUCLEOTIDASE_2; 1.
 KW Hydrolase: Signal; GPI-anchor; Glycoprotein; Zinc.
 FT SIGNAL 1 26
 FT CHAIN 27 549 5'-NUCLEOTIDASE.
 FT PROPEP 550 574 REMOVED IN MATURE FORM.
 FT LIPID 549 549 GPI-ANCHOR.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 376 376 T -> A (IN REF. 3).
 SQ SEQUENCE 574 AA; 63367 MW; A99AF170AB7EAECE CRC64;

Query Match 72.7%; Score 32; DB 1; Length 574;
 Best Local Similarity 71.4%; Pred. No. 55;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
 | | | | |
 Db 553 HCHGSFS 559

RESULT 14
 SYV_SCHPO STANDARD; PRT; 980 AA.
 AC 075005;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable valyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.9)
 DE (Valine--tRNA ligase) (VALRS).
 GN SPBC1709.02C OR SPBC1734.18C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Rajandream M.A., Barrell B.G., Rieger M.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
 CC + L-valyl-tRNA(Val).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Probable).
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AL031856; CAA21312.1; -.
 CC EMBL; AL031852; CAA21241.1; -.
 CC HSSP; P96142; LGAX.
 DR InterPro; IPR002300; tRNA-synt_la.
 DR InterPro; IPR001412; tRNA-synt_I.
 DR InterPro; IPR002303; tRNA-synt_val.
 DR Pfam; PF001133; tRNA-synt.1; 1.
 DR PRINTS; PR00986; TRNASYNTHAL.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 KW Hypothetical protein; Aminoacyl-tRNA synthetase; Protein biosynthesis;
 KW Ligase: ATP-binding; Mitochondrion; Transit peptide.
 FT TRANSIT 1 ?
 FT CHAIN 1 980 PROBABLE VALYL-TRNA SYNTHETASE.
 FT SITE 139 149 "HIGH" REGION.
 FT SITE 652 656 "KMSKS" REGION.
 FT BINDING 655 655 ATP (BY SIMILARITY).

SQ SEQUENCE 980 AA; 111316 MW; BB91FAF976030C3C CRC64;

Query Match 72.7%; Score 32; DB 1; Length 980;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSF 6
 | | | | |
 Db 351 HLHGKF 356

RESULT 15
 SYV_YEAST STANDARD; PRT; 1104 AA.
 AC P07806;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Valyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.9)
 DE (Valine--tRNA ligase) (VALRS).
 GN VAS1 OR YGR094W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87222321; PubMed=3294828;
 RA Jordana X., Chatton B., Paz-Weisshaar M., Buhler J.-M., Cramer F.,
 RA Ebel J.-P., Fasiolo F.;
 RT "Structure of the yeast valyl-tRNA synthetase gene (VASI) and the
 RT homology of its translated amino acid sequence with Escherichia coli
 RT isoleucyl-tRNA synthetase.";
 RL J. Biol. Chem. 262:7189-7194(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wedler H., Scharfe M., Wedler E., Wambutt R.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hernandez K., Weber N., Wipfli P., Schmidheini T.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-78 FROM N.A.
 RX MEDLINE=88087140; PubMed=3275649;
 RA Chatton B., Walter P., Ebel J.-P., Lacroite F., Fasiolo F.;
 RT "The yeast VAS1 gene encodes both mitochondrial and cytoplasmic
 RT valyl-tRNA synthetases.";
 RL J. Biol. Chem. 263:52-57(1988).
 CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
 CC + L-valyl-tRNA(Val).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
 CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J02719; AAA35207.1; -.
 CC EMBL; 272879; CAA37097.1; -.
 CC EMBL; M18392; AAA35205.1; -.
 CC EMBL; M18392; AAA35206.1; -.
 CC PIR; A29871; SYBVYT.
 CC HSSP; P96142; LGAX.
 CC SGD; S0003326; VAS1.
 CC InterPro; IPR002300; tRNA-synt_la.

DR InterPro; IPR001412; trna-synt_I.
DR InterPro; IPR002303; trna-synt_val.
DR Pfam; PF00133; trna-synt_1; 1.
DR PRINTS; PR00986; TRNASYNTHVAL.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Mitochondrion; Transit peptide; Alternative initiation.
FT TRANSIT 1 47 MITOCHONDRION.
FT CHAIN 48 1104 VALYL-TRNA SYNTHETASE, MITOCHONDRIAL
FT ISOFORM.
FT CHAIN 47 1104 VALYL-TRNA SYNTHETASE, CYTOPLASMIC
FT ISOFORM.
FT INIT_MET 47 47 FOR CYTOPLASMIC ISOFORM.
FT SITE 190 200 "HIGH" REGION.
FT SITE 703 707 "KMSKS" REGION.
FT BINDING 706 706 ATP (BY SIMILARITY).
FT CONFLICT 147 147 A -> G (IN REF. 1).
FT CONFLICT 540 540 R -> K (IN REF. 1).
SQ SEQUENCE 1104 AA; 125769 MW; 6493AEF37ECD4A7C CRC64;

Query Match 72.7%; Score 32; DB 1; Length 1104;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSF 6
| | | | |
Db 402 HLHGKF 407

Search completed: August 19, 2002, 06:59:10
Job time: 1375 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:13 ; Search time 140.4 Seconds
(without alignments)
9.857 Million cell updates/sec

Title: US-09-339-922A-106

Perfect score: 44

Sequence: 1 HLHGSFAS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertibrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	84.1	254	10 O82093	O82093 prunus arne
2	37	84.1	254	10 O9FUM3	O9FUM3 prunus aviu
3	37	84.1	602	3 O9P8C3	O9P8C3 acronium
4	36	81.8	105	10 Q42273	Q42273 arabidopsis
5	36	81.8	214	10 Q9FE97	Q9FE97 arabidopsis
6	36	81.8	240	10 Q9FUT0	Q9FUT0 arabidopsis
7	36	81.8	1115	10 Q9MA22	Q9MA22 arabidopsis
8	35	79.5	389	5 O9VXW1	O9VXW1 arabidopsis
9	35	79.5	494	10 Q9LSH2	Q9LSH2 arabidopsis
10	35	79.5	581	5 Q9V509	Q9V509 drosophila
11	34	77.3	83	4 Q9H374	Q9H374 homo sapien
12	34	77.3	220	16 Q92AJ5	Q92AJ5 listeria in
13	34	77.3	224	5 Q27896	Q27896 drosophila
14	34	77.3	762	16 O53648	O53648 mycobacteri
15	34	77.3	1294	2 O86682	O86682 streptomyc
16	34	77.3	1294	2 O53942	O53942 streptomyc

17	33	75.0	81	2	O50075	Q50075 mycobacteri
18	33	75.0	192	10	O9FUQ9	O9FUQ9 oryza meyer
19	33	75.0	219	10	O9FN71	O9FN71 arabidopsis
20	33	75.0	322	10	O9SPK6	O9SPK6 haematococc
21	33	75.0	413	16	P73402	P73402 synechocyst
22	33	75.0	527	12	Q91SH3	Q91SH3 guinea pig
23	33	75.0	710	2	O936V8	Q936V8 prochloroco
24	33	75.0	713	10	O9ASW9	O9ASW9 arabidopsis
25	33	75.0	761	10	O82634	O82634 arabidopsis
26	33	75.0	796	5	O9TXK9	O9TXK9 caenorhabdi
27	33	75.0	1413	5	O9VJ38	O9VJ38 drosophila
28	33	75.0	1424	5	O9VJ39	O9VJ39 drosophila
29	32	72.7	95	12	O05535	O05535 equine herp
30	32	72.7	105	12	O9Q911	O9Q911 avian adeno
31	32	72.7	209	10	O9SX97	O9SX97 arabidopsis
32	32	72.7	286	2	O93IC9	O93IC9 staphylococ
33	32	72.7	294	13	O98S10	O98S10 brachydanio
34	32	72.7	299	8	O9TNI8	O9TNI8 adiantum ca
35	32	72.7	306	2	O9RIV6	O9RIV6 streptomyc
36	32	72.7	312	16	O99XE0	O99XE0 staphylococ
37	32	72.7	315	13	O9YCT8	O9YCT8 brachydanio
38	32	72.7	329	13	O98S11	O98S11 brachydanio
39	32	72.7	331	3	O94066	O94066 candida alb
40	32	72.7	350	16	O927H5	O927H5 listeria in
41	32	72.7	368	5	O9VKF7	O9VKF7 drosophila
42	32	72.7	442	2	O9S0L8	O9S0L8 staphylococ
43	32	72.7	443	2	O93AC9	O93AC9 pseudomonas
44	32	72.7	444	16	O99XC5	O99XC5 staphylococ
45	32	72.7	449	16	O31658	O31658 bacillus su

ALIGNMENTS

RESULT 1

O82093	ID	O82093	PRELIMINARY;	PRT;	254 AA.
AC	O82093;				
DT	01-NOV-1998	(TREMBlrel. 08, Created)			
DT	01-NOV-1998	(TREMBlrel. 08, Last sequence update)			
DT	01-DEC-2001	(TREMBlrel. 19, Last annotation update)			
DE	EXPANSIN.				
GN	PA-EXPL.				
OS	Prunus armeniaca (Apricot).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid1; Rosales; Rosaceae; Amygdaloideae; Prunus.				
OX	NCBI_TaxID=36596;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BERGERON; TISSUE=MESOCARP PLUS EXOCARP;				
RA	Mbeguile-A-Mbeguile D., Gomez R.-M., Fills-Lycaon B.;				
RT	"Molecular cloning and nucleotide sequence of expansin 1 (PA-Exp1)				
RT	from apricot fruit";				
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; U93167; AAC33529.1; -				
DR	InterPro; IPR000882; Pollen_allergen.				
DR	Pfam; PF01357; Pollen_allergen; 1.				
DR	PRINTS; PR01225; EXPANSIN.FAMILY.				
DR	ProDom; PD002179; Pollen_allergen; 1.				
SQ	SEQUENCE 254 AA; 27264 MW; 88068D75932FD0E1 CRC64;				

Query Match 84.1%; Score 37; DB 10; Length 254;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HLHGSFA 7

Db 21 HLHGAFA 27

RESULT 2

```

Q9FUM3
ID Q9FUM3 PRELIMINARY; PRT; 254 AA.
AC Q9FUM3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EXPANSIN 1.
GN EXP1 OR EXP2.
OS Prunus avium (Cherry), and
OS Prunus cerasus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=42229, 140311;
[1]
RN SEQUENCE FROM N.A.
RC SPECIES=P.avium;
RA Wu Z., Wiersma P.A.;
RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry
(R Prunus avium L.) During Fruit Ripening.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC SPECIES=P.cerasus; TISSUE=RIPENING FRUIT;
RA yoo S.-D., Gao Z., Cantini C., Loeschner W., van Nocker S.;
RT "Coordinated expression of genes encoding expansins and other cell
wall-modifying enzymes is associated with pectin-related changes in
the cell wall during ripening of cherry (P. cerasus) fruit.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF297521; AAG13982.1; -.
DR EMBL; AF350937; AAK48846.1; -.
DR InterPro; IPR000882; Pollen_allergen.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMILY.
DR ProDom; PD02179; Pollen_allergen; 1.
SQ SEQUENCE 254 AA; 27278 MW; 953A7EB2491FD0E1 CRC64;

Query Match 84.1%; Score 37; DB 10; Length 254;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
Db 21 HLHGAF 27
|||||

RESULT 3
Q9P8C3 PRELIMINARY; PRT; 602 AA.
AC Q9P8C3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE POLYPHENOL OXIDASE PRECURSOR.
GN PPOA.
OS Acremonium murorum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acremonium.
OX NCBI_TaxID=45278;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=CBS 157.72;
RX MEDLINE=21268855; PubMed=11375170;
RA Gouka R.J., van der Heiden M., Swarthoff T., Verrips C.T.;
RT "Cloning of a phenol oxidase gene from Acremonium murorum and its
expression in Aspergillus awamori.";
RL Appl. Environ. Microbiol. 67:2610-2616(2001).
DR EMBL; AJ271104; CAB75422.1; -.
KW Signal.
RN SIGNAL.
FT SIGNAL.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 602 AA; 66920 MW; 0303D991405228A3 CRC64;

```

```

Query Match 84.1%; Score 37; DB 3; Length 602;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
Db 154 HLHGSFS 160
|||||

RESULT 4
Q42273 PRELIMINARY; PRT; 105 AA.
AC Q42273;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HSP26A HOMOLOGUE (FRAGMENT).
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=DRY SEEDS OF A.THALIANA ECOTYPE COLUMBIA;
RA Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z34012; CAA03973.1; -.
DR InterPro; IPR004045; GST_N.
DR Pfam; PF02798; GST_N; 1.
FT NON_TER 105
SQ SEQUENCE 105 AA; 12376 MW; 7FDC76BEC069ECD4 CRC64;

Query Match 81.8%; Score 36; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFAS 8
Db 11 LHGSFAS 17
|||||

RESULT 5
Q9FE97 PRELIMINARY; PRT; 214 AA.
AC Q9FE97;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLUTATHIONE S-TRANSFERASE-LIKE PROTEIN.
GN GST14B.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=99087489; PubMed=9872454;
RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
RT Sequence features of the regions of 1,013,767 bp covered by sixteen
RT physically assigned pl and TAC clones.";
RL DNA Res. 5:297-308(1998).
[2]
RN SEQUENCE FROM N.A.
RC Wagner U., Mauch F.;
RT "Analysis of the glutathione S-transferase family in Arabidopsis

```

RT thaliana.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB015469; BAB11498.1; -;
 DR EMBL; AF288180; AAG30129.1; -;
 KW Transferase.
 SQ SEQUENCE 214 AA; 24673 MW; 644A7B5E201D30D3 CRC64;

Query Match 81.8%; Score 36; DB 10; Length 214;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LHGSFAS 8
 |||||
 Db 11 LHGSFAS 17

RESULT 6
 Q9FUT0 PRELIMINARY; PRT; 240 AA.

AC Q9FUT0:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GLUTATHIONE S-TRANSFERASE.
 GN GSTL4.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.

RA Wagner U., Mauch F.;
 RT "Analysis of the glutathione S-transferase family in Arabidopsis thaliana";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF288179; AAG30128.1; -;
 DR InterPro; IPR004045; GST_N.
 KW Transferase.
 SQ SEQUENCE 240 AA; 27612 MW; D0872464356EA2FB CRC64;

Query Match 81.8%; Score 36; DB 10; Length 240;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LHGSFAS 8
 |||||
 Db 11 LHGSFAS 17

RESULT 7
 Q9MA22 PRELIMINARY; PRT; 1115 AA.

AC Q9MA22:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE T5E21.11.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
 RA Shinn P., Tambunga G., Altafi H., Bei Q., Chin C., Chiou J., Choi E.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Torlumi M., Vaysberg M., Yu G., Federspiel N.A.,

RA Theologis A., Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC T5E21 from chromosome I";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC010657; AAF63175.1; -;
 DR HSSP; P96142; IGAX.
 DR InterPro; IPR002300; tRNA-synt_1a.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR002301; tRNA-synt_1le.
 DR InterPro; IPR002303; tRNA-synt_val.
 DR Pfam; PF00133; tRNA-synt_1; 1.
 DR PRINTS; PR00986; TRNASYNTHAL.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 SQ SEQUENCE 1115 AA; 126675 MW; 4F383F79B656B0D1 CRC64;

Query Match 81.8%; Score 36; DB 10; Length 1115;
 Best Local Similarity 85.7%; Pred. No. 98;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 HLHGSPA 7
 |||||
 Db 396 HLHGKFA 402

RESULT 8
 Q9VXW1 PRELIMINARY; PRT; 389 AA.

AC Q9VXW1:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CG9151 PROTEIN.
 GN ACJ6 OR CG9151.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kaulush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Pittman K.A., Nixon K., Nusskern D.R., Pacled J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
 "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: WITH OTHER HOMEBOX PROTEINS.
 DR EMBL; AE003498; AAF48447.1; -.
 DR HSSP; P10037; 1AU7.
 DR FlyBase; FBgn0000028; acj6.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF00157; pou; 1.
 DR PRINTS; PR00028; POU DOMAIN.
 DR ProDom; PD000583; POU; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00352; POU; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 DR PROSITE; PS00035; POU_1; 1.
 DR PROSITE; PS00465; POU_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 389 AA; 42844 MW; 4AAB56FD4F07721 CRC64;

Query Match 79.5%; Score 35; DB 5; Length 389;
 Best Local Similarity 75.0%; Pred. No. 51;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HLHGSFAS 8
 Db 165 HLHGSYHS 172
 |||||: |

RESULT 9
 ID Q9LSH2 PRELIMINARY; PRT; 494 AA.
 AC Q9LSH2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GLUTAMATE DECARBOXYLASE.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
 CC TYRDC).
 DR EMBL; AB026646; BAB02870.1; -.
 DR InterPro; IPR002129; Pyridoxal_dec.
 DR Pfam; PF00282; Pyridoxal_dec; 1.
 KW Decarboxylase; Lyase; Pyridoxal phosphate.
 SQ SEQUENCE 494 AA; 55770 MW; 7985F175E54DF262 CRC64;

Query Match 79.5%; Score 35; DB 10; Length 494;
 Best Local Similarity 75.0%; Pred. No. 66;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HLHGSFAS 8
 Db 12 HLHSTFAS 19
 ||||: |||

RESULT 10
 ID Q9VS09 PRELIMINARY; PRT; 581 AA.
 AC Q9VS09;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CG8645 PROTEIN.
 GN CG8645.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
 "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003560; AAF50621.1; -.
 DR HSSP; P39061; IKOE.
 DR FlyBase; FBgn0035732; CG8645.
 DR InterPro; IPR000087; Collagen.
 DR InterPro; IPR002088; PPTA.
 DR Pfam; PF01391; Collagen; 3.

DR PROSITE; PS00904; PPTA; UNKNOWN1.
SQ SEQUENCE 581 AA; 60772 MW; 19EC1E48CB477FE7 CRC64;

Query Match 79.5%; Score 35; DB 5; Length 581;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLKGSFAS 8
||| |||||

DB 507 HLKGSFAS 514

RESULT 11
Q9H374
ID Q9H374 PRELIMINARY; PRT; 83 AA.
AC Q9H374;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PRO1102.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,
RA Xu W., Gao F., Liu M., He F.;

RT "Functional prediction of the coding sequences of 75 new genes deduced
RT by analysis of cDNA clones from human fetal liver."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF130105; AAG35530.1; -
SQ SEQUENCE 83 AA; 9799 MW; 6F76AF9B9BDBD4B5 CRC64;

Query Match 77.3%; Score 34; DB 4; Length 83;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLKGSFA 7
||| ||| |

DB 14 HLKGSIA 20

RESULT 12
Q92AJ5
ID Q92AJ5 PRELIMINARY; PRT; 220 AA.
AC Q92AJ5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LIN1927 PROTEIN.
GN LIN1927.

OS Listeria innocua.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.

OX NCBI_TaxID=1642;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CLIP 11262 / SEROVAR 6A;

RX PubMed=11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Ectian K.-D., Fshi H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkut G.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of *Listeria* species."; Science 294:849-852(2001).
RL EMBL; AL596170; CAC97157.1; -.
DR L1stlist; LIN01927; -.
KW Complete proteome.
SQ SEQUENCE 220 AA; 23860 MW; F50CDC3E026F97AE CRC64;

Query Match 77.3%; Score 34; DB 16; Length 220;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
||| |||||

DB 46 HLHGSFA 52

RESULT 13
Q27896
ID Q27896 PRELIMINARY; PRT; 224 AA.
AC Q27896;
DT 01-JAN-1999 (TREMBLrel. 09, Created)
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TBP-RELATED FACTOR.
DE TRP OR CG7562.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC STRAIN=CANTON-S; TISSUE=TESTIS;

RX MEDLINE=93156846; PubMed=8429912;

RA Crowley T.E., Hoey T., Liu J.-K., Jan Y.N., Jan L.Y., Tjian R.;

RT "A new factor related to TATA-binding protein has highly restricted

RL expression patterns in *Drosophila*."

RN Nature 361:557-561(1993).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,

RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
SC Science 287:2183-2195(2000).
CC -1- FUNCTION: ACTS AS A TRANSCRIPTION FACTOR. BINDS TO THE TATA BOX
CC PROMOTER ELEMENT WHICH LIES CLOSE TO THE POSITION OF TRANSCRIPTION
CC INITIATION.
CC -1- FUNCTION: MAY BE ESSENTIAL FOR EMBRYONIC DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: PRIMARY SPERMATOCYTES IN THE ADULT TESTIS AND
CC IN A SUBSET OF CELLS IN THE DORSAL MEDIAL REGION OF THE EMBRYONIC
CC CENTRAL NERVOUS SYSTEM.
CC -1- SIMILARITY: WEAK, WITH BACTERIAL POLYMERASE SIGMA-FACTORS. HIGH,
CC WITH TBP.
DR EMBL: X70837; CAA50185.1; -;
DR EMBL: X70838; CAA50186.1; -;
DR EMBL: AE003619; AAF52600.1; -;
DR HSSP: P20226; 1TGH.
DR FlyBase: FBgn0010287; Trf.
DR InterPro: IPR000814; TFIID.
DR Pfam: PF00352; TBP; 2.
DR PRINTS; PR00686; TIFACTORIID.
DR PROSITE; PS00351; TFIID; 2.
KW Transcription regulation; DNA-binding; Nuclear protein; Repeat.
FT DOMAIN 51 218 2 X TFIID REPEATS.
FT REPEAT 51 127 1.
FT REPEAT 141 218 2.
FT SEQUENCE 224 AA; 25455 MW; CA619BE4BA726460 CRC64;

Query Match 77.3%; Score 34; DB 5; Length 224;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSPFAS 8
|:|:| |:
DB 161 HVHGQFSS 168

RESULT 14
O53648 PRELIMINARY; PRT; 762 AA.
AC O53648
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 82.6 KDA PROTEIN.
GN RV0197 OR MTV033.05.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
DR EMBL: AL021928; CAA17319.1; -;

DR TuberculList: Rv0197; -;
DR InterPro: IPR001467; Molybdopterin.
DR Pfam: PF00384; molybdopterin; 3.
DR Pfam: PF01568; molybdop_binding; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 762 AA; 82571 MW; 73PFF9DD5D14BCCE CRC64;

Query Match 77.3%; Score 34; DB 16; Length 762;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSEFA 7
|:|:| |:
DB 326 HLHSSFA 332

RESULT 15
O86682 PRELIMINARY; PRT; 1294 AA.
AC O86682
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BACTERIOPHAGE (PHIC31) RESISTANCE GENE PGLY.
GN PGLY.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL031371; CAA20546.1; -;
SQ SEQUENCE 1294 AA; 141187 MW; 5515825E3087B4F1 CRC64;

Query Match 77.3%; Score 34; DB 2; Length 1294;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSPFAS 8
|:|:| |:
DB 72 YLHGSPGS 79

Search completed: August 19, 2002, 06:58:15
Job time: 1405 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On: August 19, 2002, 06:39:12 ; Search time 180.34 Seconds
(without alignments)
4.927 Million cell updates/sec

Title: US-09-339-922A-106

Perfect score: 44

Sequence: 1 HLHSPAS 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

```

1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	8	22	AA61401
2	37	84.1	10	19	AAW76037
3	37	84.1	10	22	AA61395
4	37	84.1	21	22	AA81503
5	37	84.1	21	22	AA20098
6	37	84.1	572	14	AA40843
7	37	84.1	578	22	AA81506
8	37	84.1	583	22	AA81505
9	37	84.1	583	22	AA20097
10	37	84.1	602	21	AA69204
11	36	81.8	240	21	AAG42074

12	36	81.8	242	21	AAG54727	Arabidopsis thalia
13	35	79.5	95	21	AAG47207	Arabidopsis thalia
14	35	79.5	97	21	AAG11600	Arabidopsis thalia
15	35	79.5	389	22	AB84263	Drosophila melanog
16	35	79.5	494	21	AAG13764	Arabidopsis thalia
17	35	79.5	507	21	AAG13763	Arabidopsis thalia
18	35	79.5	581	22	AB60799	Drosophila melanog
19	34	77.3	112	22	AAE01420	Human secreted pro
20	34	77.3	224	22	AB63359	Drosophila melanog
21	34	77.3	736	22	ABG17921	Novel human diagno
22	33	75.0	10	19	AAW76020	LM609 grafted anti
23	33	75.0	10	22	AB61378	Mutant VH CDR3 pep
24	33	75.0	99	22	AAU45647	Propionibacterium
25	33	75.0	187	22	AAU45960	Propionibacterium
26	33	75.0	322	21	AA11111	H. pluvialis carot
27	33	75.0	1413	22	AB60857	Drosophila melanog
28	33	75.0	1424	22	AB60854	Drosophila melanog
29	32	72.7	31	20	AA80315	Glucagon peptide-1
30	32	72.7	66	22	AB17631	Human nervous syst
31	32	72.7	66	22	AA23960	Human EST encoded
32	32	72.7	157	22	AA01883	Human polypeptide
33	32	72.7	176	21	AAG12100	Arabidopsis thalia
34	32	72.7	198	21	AAG12099	Arabidopsis thalia
35	32	72.7	208	21	AAG39024	Arabidopsis thalia
36	32	72.7	209	21	AAG36752	Arabidopsis thalia
37	32	72.7	215	22	AA93514	Human polypeptide
38	32	72.7	226	21	AAG36751	Arabidopsis thalia
39	32	72.7	330	22	AAG75161	Human colon cancer
40	32	72.7	346	22	ABG24308	Novel human diagno
41	32	72.7	368	22	AB61162	Drosophila melanog
42	32	72.7	405	18	AAW18677	Human 11-beta-hydr
43	32	72.7	451	22	ABG24306	Novel human diagno
44	32	72.7	475	21	AA53985	Amino acid sequenc
45	32	72.7	493	22	ABG29667	Novel human diagno

ALIGNMENTS

```

RESULT 1
AA61401
ID   AAB61401 standard; peptide; 8 AA.
XX
AC   AAB61401;
XX
DT   03-APR-2001 (first entry)
XX
DE   Enhanced LM609 VH CDR3 peptide.
XX
KW   LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW   inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS   Unidentified.
XX
PN   WO200078815-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-US17454.
XX
PR   24-JUN-1999; 99US-0339922.
XX
(MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
Huse WD, Wu H;
XX
WPI; 2001-050110/06.
XX
Enhanced LM609 grafted antibodies exhibiting selective binding affinity
to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
osteoporosis -
XX

```

PS Claim 1; Page 45; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 44; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8
 | | | | | | |
 Db 1 hlhgsfas 8

RESULT 2

AAW76037
 ID AAW76037 standard; Protein; 10 AA.

XX AAW76037;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #13.

XX Vitaxin; antibody; variable region; heavy chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49874.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 43; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 84.1%; Score 37; DB 19; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.63;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8
 | | | | | | |
 Db 3 hnhgsfas 10

RESULT 3

AAAB61395
 ID AAB61395 standard; peptide; 10 AA.

XX AAB61395;

XX 03-APR-2001 (first entry)

XX Multiple mutant VH CDR3 #1.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Page 42; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX SQ Sequence 10 AA;

Query Match 84.1%; Score 37; DB 22; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.63;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8
 | | | | |
 Db 3 hnhgsfas 10

RESULT 4
 AAB81503
 ID AAB81503 standard; peptide; 21 AA.
 XX AC AAB81503;
 XX DT 18-JUN-2001 (first entry)
 XX DE Stachybotrys chartarum phenol oxidising enzyme peptide #1.
 XX KW Stachybotrys chartarum; phenol oxidising enzyme; detergent;
 KW paper production; pulp production; textile; food industry; bleaching.
 XX OS Stachybotrys chartarum.
 XX PN WO200121748-A1.
 XX PD 29-MAR-2001.
 XX PF 06-SEP-2000; 2000WO-EP08840.
 XX PR 22-SEP-1999; 99EP-0203120.
 XX PA (UNIL) UNILEVER NV.
 PA (UNIL) UNILEVER PLC.
 PA (HIND-) HINDUSTAN LEVER LTD.
 XX PI Convents D, Doornink M, De Vries CH, Wang H;
 XX WPI; 2001-273462/28.
 XX DR New detergent compositions comprising a phenol oxidizing enzyme useful
 PT in detergent or cleaning compositions, fiber treatment, processing,
 PT finishing or production, paper and pulp production, or in starch
 PT processing applications -
 XX PS Example 2; Page 27; 46pp; English.
 XX CC The present sequence is a fragment of the Stachybotrys chartarum
 CC phenol oxidising enzyme. It was obtained by subjecting the enzyme to SDS
 CC polyacrylamide gel electrophoresis, treating the isolated fraction
 CC with urea and iodoacetamide, and digesting with enzyme endoLysC.
 CC The invention relates to detergent compositions comprising one or more
 CC surfactants and a phenol oxidising enzyme having at least 68% identity to
 CC the Stachybotrys chartarum phenol oxidising enzyme. Phenol oxidising
 CC enzymes may be used in the detergent, paper, pulp, textile and food
 CC industries. They are used for preventing the transfer of dyes in solution
 CC from one textile to another during detergent washing, or in modifying the
 CC colour associated with dyes and coloured compounds having different
 CC chemical structures, such as in pulp and paper bleaching, bleaching the
 CC colour of stains on fabric and in detergent and textile applications.

QY 1 HLHGSFA 7
 | | | | |
 Db 14 hlhgsfs 20

Sequence 21 AA;
 Query Match 84.1%; Score 37; DB 22; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.4;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
 | | | | |
 Db 14 hlhgsfs 20

RESULT 5
 AAB20098
 ID AAB20098 standard; Peptide; 21 AA.

XX AAB20098;
 AC 23-APR-2001 (first entry)
 DT Stachybotrys chartarum phenol oxidase B peptide.
 DE Phenol oxidising enzyme; phenol oxidase B; bleach; pulp; paper;
 KW textile; detergent.
 XX OS Stachybotrys chartarum.
 XX PN US6168936-B1.
 XX PD 02-JAN-2001.
 XX PF 22-SEP-1999; 99US-0401476.
 XX PR 22-SEP-1999; 99US-0401476.
 XX PA (GEMV) GENENCOR INT INC.
 XX PI Wang H;
 XX WPI; 2001-136715/14.
 XX DR New phenol oxidizing enzyme, also useful in the detergent, paper and
 PT pulp, textile or food industries, especially in modifying the colour
 PT associated with dyes and coloured compounds, as well as in anti-dye
 PT transfer applications -
 XX PS Example 2; Column 13; 23pp; English.
 XX CC The present sequence is that of an isolated peptide of the
 CC phenol oxidase B enzyme of Stachybotrys chartarum M0CL 38898. The
 CC peptide was isolated from purified enzyme by endoLysC digestion
 CC and HPLC separation. A primer (see AAF30030) based on the peptide
 CC was used in the PCR amplification of the S. chartarum phenol
 CC oxidase B gene (spob, see AAF30029). The invention provides phenol
 CC oxidising enzymes such as S. chartarum phenol oxidase B (see
 CC AAB20097), or enzymes having at least 68% identity to it, nucleic
 CC acids encoding them, expression vectors, filamentous fungus and
 CC yeast host cells, and methods for the recombinant production of the
 CC enzymes. The phenol oxidising enzymes are useful for bleaching
 CC pulp and paper, fabric stains, and in detergent and textile
 CC applications.
 XX CC Sequence 21 AA;
 QY 1 HLHGSFA 7
 | | | | |
 Db 14 hlhgsfs 20

Query Match 84.1%; Score 37; DB 22; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.4;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
 | | | | |
 Db 14 hlhgsfs 20

RESULT 6
 AAR40843
 ID AAR40843 standard; Protein; 572 AA.
 XX AC AAR40843;
 XX DT 24-FEB-1994 (first entry)
 XX DE Bilirubin oxidase.
 XX KW Bilirubin; oxidase; analytical; BO; expression vector; PCR;
 KW polymerase chain reaction.
 XX OS Myrothecium verrucaria.

```

XX Key Location/Qualifiers
FT Peptide 1..38
FT /label= sig_peptide
FT Protein 39..534
FT /label= mat_protein
XX
XX JF05199882-A.
XX
XX
XX 10-AUG-1993.
XX
XX 24-JAN-1992; 92JP-00341126.
XX
XX 24-JAN-1992; 92JP-00341126.
XX
XX (AMAN ) AMANO PHARM KK.
XX
XX WPI; 1993-284681/36.
XX
XX N-PSDB; AAQ47790.
XX
XX Bilirubin oxidase prepn. useful as an analytical enzyme - by
XX culturing bilirubin oxidase in transformant culture
XX
XX Claim 1; Page 29-32; 32pp; Japanese.
XX
XX The sequence encodes bilirubin oxidase. The protein produced has a
XX 38 amino acid signal peptide which is removed to give the mature
XX protein (AAR40843).
XX
XX Sequence 572 AA;

Query Match 84.1%; Score 37; DB 14; Length 572;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
Db 132 hlhgsfs 138

RESULT 7
AAB81506
ID AAB81506 standard; Protein; 578 AA.
XX
XX AAB81506;
XX
XX 18-JUN-2001 (first entry)
XX
XX Bilirubin oxidase.
XX
XX Bilirubin oxidase; phenol oxidising enzyme; phenol oxidase B;
XX detergent; paper production; pulp production; textile; food industry;
XX bleaching.
XX
XX Unidentified.
XX
XX WO200121748-A1.
XX
XX 29-MAR-2001.
XX
XX 06-SEP-2000; 2000WO-EP08840.
XX
XX 22-SEP-1999; 99EP-0203120.
XX
XX (UNIL ) UNILEVER NV.
XX
XX (UNIL ) UNILEVER PLC.
XX
XX (HIND-) HINDUSTAN LEVER LTD.
XX
XX Convents D, Doornink M, De Vries CH, Wang H;
XX
XX WPI; 2001-273462/28.
XX

New detergent compositions comprising a phenol oxidizing enzyme useful
in detergent or cleaning compositions, fiber treatment, processing,
finishing or production, paper and pulp production, or in starch
processing applications -
Example 4; Fig 2; 46pp; English.

The present sequence was used for comparison with the Stachybotrys
chartarum phenol oxidising enzyme. The invention relates to detergent
compositions comprising one or more surfactants and a phenol oxidising
enzyme having at least 68% identity to the Stachybotrys chartarum phenol
oxidising enzyme. Phenol oxidising enzymes may be used in the detergent,
paper, pulp, textile and food industries. They are used for preventing
the transfer of dyes in solution from one textile to another during
detergent washing, or in modifying the colour associated with dyes and
coloured compounds having different chemical structures, such as in pulp
and paper bleaching, bleaching the colour of stains on fabric and in
detergent and textile applications.

Sequence 578 AA;

Query Match 84.1%; Score 37; DB 22; Length 578;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
Db 135 hlhgsfs 141

RESULT 8
AAB81505
ID AAB81505 standard; Protein; 583 AA.
XX
XX AAB81505;
XX
XX 18-JUN-2001 (first entry)
XX
XX stachybotrys chartarum phenol oxidase B enzyme.
XX
XX stachybotrys phenol oxidase B; spoB; phenol oxidising enzyme;
XX detergent; paper production; pulp production; textile; food industry;
XX bleaching.
XX
XX stachybotrys chartarum.
XX
XX WO200121748-A1.
XX
XX 29-MAR-2001.
XX
XX 06-SEP-2000; 2000WO-EP08840.
XX
XX 22-SEP-1999; 99EP-0203120.
XX
XX (UNIL ) UNILEVER NV.
XX
XX (UNIL ) UNILEVER PLC.
XX
XX (HIND-) HINDUSTAN LEVER LTD.
XX
XX Convents D, Doornink M, De Vries CH, Wang H;
XX
XX WPI; 2001-273462/28.
XX
XX N-PSDB; AAF82586.
XX
XX New detergent compositions comprising a phenol oxidizing enzyme useful
XX in detergent or cleaning compositions, fiber treatment, processing,
XX finishing or production, paper and pulp production, or in starch
XX processing applications -
XX Claim 1; Fig 2; 46pp; English.
XX
XX The present sequence is a Stachybotrys chartarum phenol oxidising
XX enzyme. The invention relates to detergent compositions comprising one or
XX

```

CC more surfactants and a phenol oxidising enzyme having at least 68%
 CC identity to the Stachybotrys chartarum phenol oxidising enzyme. Phenol
 CC oxidising enzymes may be used in the detergent, paper, pulp, textile and
 CC food industries. They are used for preventing the transfer of dyes in
 CC solution from one textile to another during detergent washing, or in
 CC modifying the colour associated with dyes and coloured compounds having
 CC different chemical structures, such as in pulp and paper bleaching,
 CC bleaching the colour of stains on fabric and in detergent and textile
 CC applications.

XX SQ Sequence 583 AA;

Query Match 84.1%; Score 37; DB 22; Length 583;
 Best Local Similarity 85.7%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSPA 7
 Db 135 hlhgfs 141
 |||||:

RESULT 9
 AAB20097
 ID AAB20097 standard; Protein; 583 AA.
 XX AC AAB20097;

DT 23-APR-2001 (first entry)

XX Stachybotrys chartarum phenol oxidase B.

XX Phenol oxidising enzyme; phenol oxidase B; spoB gene; bleach;
 KW pulp; paper; textile; detergent.

XX Stachybotrys chartarum.

XX US6168936-B1.

XX 02-JAN-2001.

XX 22-SEP-1999; 99US-0401476.

XX 22-SEP-1999; 99US-0401476.

XX (GEMV) GENENCOR INT INC.

XX Wang H;

XX WPI; 2001-136715/14.

DR N-PSDB; AAF30028, AAF20029.

XX New phenol oxidizing enzyme, also useful in the detergent, paper and
 PT pulp, textile or food industries, especially in modifying the colour
 PT associated with dyes and coloured compounds, as well as in anti-dye
 PT transfer applications.

XX Claim 1; Fig 2; 23pp; English.

XX The present sequence is that of Stachybotrys chartarum MUCL 38898
 CC phenol oxidase B, as deduced from isolated genomic DNA (see
 CC AAF30028). The invention provides phenol oxidising enzymes such
 CC as phenol oxidase B, or enzymes having at least 68% identity to
 CC it, nucleic acids encoding them, expression vectors, filamentous
 CC fungus and yeast host cells, and methods for the recombinant
 CC production of the phenol oxidising enzymes. The enzymes are useful
 CC for bleaching pulp and paper, fabric stains, and in detergent and
 CC textile applications. They show optimal activity at pH range 5-11,
 CC 7-10.5 or 8-10, and at 20-60 or 20-40 degree C.

XX SQ Sequence 583 AA;

Query Match 84.1%; Score 37; DB 22; Length 583;
 Best Local Similarity 85.7%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSPA 7
 Db 135 hlhgfs 141
 |||||:

RESULT 10
 AAY69204
 ID AAY69204 standard; Protein; 602 AA.
 XX AC AAY69204;

DT 30-MAY-2000 (first entry)

XX Amino acid sequence of a phenol oxidising enzyme.

XX Phenol oxidizing enzyme; fungus; redox reaction; detergent; bleaching;
 KW fabric; pulp; paper; decolourisation; plant-derived food product;
 KW coloured compound; porphyrin; tannin; polyphenol; carotenoid;
 KW anthocyanin; Maillard reaction product.

XX Acremonium murorum.

XX WO200005349-A1.

XX 03-FEB-2000.

XX 13-JUL-1999; 99WO-EP04922.

XX 21-JUL-1998; 98EP-0202454.

XX (UNIL) UNILEVER NV.

XX (UNIL) UNILEVER PLC.

XX (HIND-) HINDUSTAN LEVER LTD.

XX Convents D, Gouka RJ, Van Der Heiden M, Swarthoff T, Verrips CT;

XX WPI; 2000-195101/17.

XX N-PSDB; AA61243.

XX Phenol-oxidizing enzyme from Acremonium, used in detergent compositions
 PT for bleaching stains on fabrics

XX Claim 5; Page 41-43; 45pp; English.

XX The present sequence represents a phenol oxidizing enzyme from the
 CC fungus Acremonium murorum. The enzyme has the CBS accession number
 CC 157.72. The enzyme catalyses redox reactions and is specific for
 CC molecular oxygen as the electron acceptor. The phenol oxidising enzyme
 CC is specifically used in detergents for bleaching strains on fabrics,
 CC but also for bleaching pulp and paper and for decolourisation of
 CC plant-derived food products. The enzyme has a pH optimum in the
 CC alkaline to neutral range and can bleach a wide variety of coloured
 CC compounds, e.g. porphyrins, tannins, polyphenols, carotenoids,
 CC anthocyanins and Maillard reaction products.

XX SQ Sequence 602 AA;

Query Match 84.1%; Score 37; DB 21; Length 602;
 Best Local Similarity 85.7%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSPA 7
 Db 154 hlhgfs 160
 |||||:

RESULT 11
 AAG42074

ID AAG42074 standard; Protein; 240 AA.
AC AAG42074;
XX 18-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52426.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 29-MAR-1999; 99US-0126264.
PR 01-APR-1999; 99US-0126785.
PR 06-APR-1999; 99US-0127462.
PR 08-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0129845.
PR 21-APR-1999; 99US-0130077.
PR 23-APR-1999; 99US-0130449.
PR 28-APR-1999; 99US-0130510.
PR 30-APR-1999; 99US-0130891.
PR 04-MAY-1999; 99US-0131449.
PR 05-MAY-1999; 99US-0132048.
PR 06-MAY-1999; 99US-0132407.
PR 07-MAY-1999; 99US-0132484.
PR 11-MAY-1999; 99US-0132485.
PR 14-MAY-1999; 99US-0132486.
PR 14-MAY-1999; 99US-0132487.
PR 18-MAY-1999; 99US-0132487.
PR 19-MAY-1999; 99US-0132863.
PR 20-MAY-1999; 99US-0134256.
PR 21-MAY-1999; 99US-0134218.
PR 24-MAY-1999; 99US-0134219.
PR 25-MAY-1999; 99US-0134221.
PR 27-MAY-1999; 99US-0134370.
PR 28-MAY-1999; 99US-0134768.
PR 01-JUN-1999; 99US-0134941.
PR 03-JUN-1999; 99US-0135124.
PR 04-JUN-1999; 99US-0135353.
PR 07-JUN-1999; 99US-0135629.
PR 08-JUN-1999; 99US-0136021.
PR 10-JUN-1999; 99US-0136392.
PR 10-JUN-1999; 99US-0136782.
PR 14-JUN-1999; 99US-0137222.
PR 16-JUN-1999; 99US-0137528.
PR 17-JUN-1999; 99US-0137724.
PR 18-JUN-1999; 99US-0138094.
PR 18-JUN-1999; 99US-0138540.
PR 18-JUN-1999; 99US-0138847.
PR 18-JUN-1999; 99US-0139119.
PR 18-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 23-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.

PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 03-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0158059.
PR 07-OCT-1999; 99US-0158079.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161932.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 81.8%; Score 36; DB 21; Length 240;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFAS 8
| | | | |
Db 11 lhgsfas 17

RESULT 12

AAG54727
ID AAG54727 standard; Protein; 242 AA.

XX AC AAG54727;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 69855.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX OS
XX EP1033405-A2.
XX PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 09-JUL-1999; 99US-0142803.
PR 12-JUL-1999; 99US-0142920.
PR 13-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.

PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 81.8%; Score 36; DB 21; Length 242;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHGSPAS 8

Db 11 lhgsfas 17

RESULT 13

AAG47207

ID AAG47207 standard; Protein; 95 AA.

XX AAG47207;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 59473.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX

PN	EP1033405-A2.		
XX	06-SEP-2000.	PR	01-JUL-1999;
PD		PR	02-JUL-1999;
XX		PR	06-JUL-1999;
PF		PR	08-JUL-1999;
XX	25-FEB-2000; 2000EP-0301439.	PR	09-JUL-1999;
		PR	12-JUL-1999;
		PR	13-JUL-1999;
		PR	14-JUL-1999;
		PR	15-JUL-1999;
		PR	16-JUL-1999;
		PR	16-JUL-1999;
		PR	16-JUL-1999;
		PR	19-JUL-1999;
		PR	19-JUL-1999;
		PR	19-JUL-1999;
		PR	19-JUL-1999;
		PR	19-JUL-1999;
		PR	20-JUL-1999;
		PR	20-JUL-1999;
		PR	21-JUL-1999;
		PR	21-JUL-1999;
		PR	21-JUL-1999;
		PR	22-JUL-1999;
		PR	22-JUL-1999;
		PR	22-JUL-1999;
		PR	23-JUL-1999;
		PR	23-JUL-1999;
		PR	23-JUL-1999;
		PR	26-JUL-1999;
		PR	27-JUL-1999;
		PR	27-JUL-1999;
		PR	28-JUL-1999;
		PR	02-AUG-1999;
		PR	02-AUG-1999;
		PR	02-AUG-1999;
		PR	03-AUG-1999;
		PR	04-AUG-1999;
		PR	04-AUG-1999;
		PR	05-AUG-1999;
		PR	05-AUG-1999;
		PR	06-AUG-1999;
		PR	06-AUG-1999;
		PR	09-AUG-1999;
		PR	09-AUG-1999;
		PR	10-AUG-1999;
		PR	11-AUG-1999;
		PR	12-AUG-1999;
		PR	13-AUG-1999;
		PR	13-AUG-1999;
		PR	16-AUG-1999;
		PR	17-AUG-1999;
		PR	18-AUG-1999;
		PR	20-AUG-1999;
		PR	20-AUG-1999;
		PR	20-AUG-1999;
		PR	23-AUG-1999;
		PR	23-AUG-1999;
		PR	25-AUG-1999;
		PR	26-AUG-1999;
		PR	27-AUG-1999;
		PR	27-AUG-1999;
		PR	30-AUG-1999;
		PR	31-AUG-1999;
		PR	01-SEP-1999;
		PR	07-SEP-1999;
		PR	13-SEP-1999;
		PR	15-SEP-1999;
		PR	16-SEP-1999;
		PR	99US-0142154.
		PR	99US-0142055.
		PR	99US-0142390.
		PR	99US-0142803.
		PR	99US-0142920.
		PR	99US-0142977.
		PR	99US-0143542.
		PR	99US-0143624.
		PR	99US-0144005.
		PR	99US-0144085.
		PR	99US-0144086.
		PR	99US-0144325.
		PR	99US-0144331.
		PR	99US-0144332.
		PR	99US-0144333.
		PR	99US-0144334.
		PR	99US-0144335.
		PR	99US-0144352.
		PR	99US-0144632.
		PR	99US-0144884.
		PR	99US-0144814.
		PR	99US-0145086.
		PR	99US-0145088.
		PR	99US-0145085.
		PR	99US-0145087.
		PR	99US-0145089.
		PR	99US-0145192.
		PR	99US-0145145.
		PR	99US-0145218.
		PR	99US-0145224.
		PR	99US-0145276.
		PR	99US-0145313.
		PR	99US-0145919.
		PR	99US-0145919.
		PR	99US-0145951.
		PR	99US-0146386.
		PR	99US-0146388.
		PR	99US-0146389.
		PR	99US-0147038.
		PR	99US-0147204.
		PR	99US-0147302.
		PR	99US-0147192.
		PR	99US-0147260.
		PR	99US-0147303.
		PR	99US-0147416.
		PR	99US-0147493.
		PR	99US-0147935.
		PR	99US-0148171.
		PR	99US-0148319.
		PR	99US-0148341.
		PR	99US-0148565.
		PR	99US-0148684.
		PR	99US-0149368.
		PR	99US-0149175.
		PR	99US-0149426.
		PR	99US-0149722.
		PR	99US-0149723.
		PR	99US-0149929.
		PR	99US-0149902.
		PR	99US-0149930.
		PR	99US-0150566.
		PR	99US-0150884.
		PR	99US-0151065.
		PR	99US-0151066.
		PR	99US-0151080.
		PR	99US-0151303.
		PR	99US-0151438.
		PR	99US-0151930.
		PR	99US-0152363.
		PR	99US-0153070.
		PR	99US-0153758.
		PR	99US-0154018.
		PR	99US-0154039.

```
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 23-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 03-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 23-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161932.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 79.58; Score 35; DB 21; Length 95;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSEA 7
Db 69 hlhgfa 75

RESULT 14
AAG11600
ID AAG11600 standard; Protein; 97 AA.
XX
AC AAG11600;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10376.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 23-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR
```

```
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR
```

PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 01-SEP-1999; 99US-0152363.
PR 07-SEP-1999; 99US-0153070.
PR 10-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.

PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 18-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 79.5%; Score 35; DB 21; Length 97;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
||| |
Db 71 hlhgrfa 77

RESULT 15

ABB64263
ID ABB64263 standard; Protein; 389 AA.

XX
AC ABB64263;

XX
DT 26-MAR-2002 (first entry)

XX
DE Drosophila melanogaster polypeptide SEQ ID NO 19581.

XX
DE Drosophila; developmental biology; cell signalling; insecticide;

XX
KW pharmaceutical.

XX
OS Drosophila melanogaster.

XX
WO200171042-A2.

XX
PD 27-SEP-2001.

XX
PF 23-MAR-2001; 2001WO-US09231.

XX
PR 23-MAR-2000; 2000US-191637P.

XX
PR 11-JUL-2000; 2000US-0614150.

XX
PA (PEKE) PE CORP NY.

XX
PI Venter JC, Adams M, Li PWD, Myers EW;

XX
DR WPI; 2001-656860/75.

DR
N-PSDB; ABL08366.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure; SEQ ID NO 19581; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 389 AA;

Query Match 79.5%; Score 35; DB 22; Length 389;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLHGSFAS 8
| | | | |
Db 165 hlhgsyhs 172

Search completed: August 19, 2002, 06:39:14
Job time: 1475 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:40 ; Search time 61.75 Seconds
(without alignments)
3.164 Million cell updates/sec

Title: US-09-339-922A-106

Perfect score: 44

Sequence: 1 HLHGSPAS 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	84.1	21	4	US-09-401-476-5
2	37	84.1	572	4	US-09-401-476-4
3	37	84.1	583	4	US-09-401-476-2
4	32	72.7	213	2	US-08-653-821-16
5	32	72.7	405	2	US-08-519-081-2
6	32	72.7	405	2	US-08-754-369-2
7	31	70.5	384	2	US-08-637-759B-375
8	31	70.5	384	3	US-08-871-355A-375
9	31	70.5	384	4	US-09-201-945-375
10	30	68.2	249	2	US-09-154-802-1
11	30	68.2	249	3	US-09-373-029-1
12	30	68.2	346	2	US-08-702-153-2
13	30	68.2	346	2	US-08-702-153-4
14	30	68.2	529	4	US-09-240-639-4
15	30	68.2	2595	4	US-09-036-987A-2
16	30	68.2	2595	4	US-09-370-700-2
17	29	65.9	14	3	US-08-946-329A-4
18	29	65.9	14	4	US-08-567-357A-4
19	29	65.9	14	4	US-08-729-743A-4
20	29	65.9	14	4	US-08-349-498-4
21	29	65.9	14	5	PCT-US95-15463-4
22	29	65.9	14	5	PCT-US95-15923-4
23	29	65.9	231	3	US-08-926-842B-20
24	29	65.9	240	3	US-08-926-842B-21
25	29	65.9	271	1	US-07-914-282D-4
26	29	65.9	271	1	US-08-276-887A-4
27	29	65.9	271	5	PCT-US93-02460-4

```

28      29      65.9      402      4      US-09-025-578-2      Sequence 2, Appli
29      29      65.9      625      1      US-08-365-981-13      Sequence 13, Appli
30      29      65.9      893      4      US-09-514-302-4      Sequence 4, Appli
31      29      65.9      1065      3      US-08-630-172-9      Sequence 9, Appli
32      29      65.9      1065      4      US-09-375-419-9      Sequence 9, Appli
33      29      65.9      1170      2      US-08-789-078-2      Sequence 2, Appli
34      29      65.9      1170      2      US-08-752-633-2      Sequence 2, Appli
35      29      65.9      1170      2      US-08-476-062A-42      Sequence 2, Appli
36      29      65.9      1170      5      PCT-US95-04886-2      Sequence 2, Appli
37      29      65.9      1170      5      PCT-US96-01314-42      Sequence 2, Appli
38      29      65.9      1257      1      US-08-049-783-2      Sequence 2, Appli
39      29      65.9      1257      1      US-08-158-232-6      Sequence 6, Appli
40      29      65.9      1257      1      US-08-304-626-6      Sequence 6, Appli
41      29      65.9      1257      1      US-08-316-301A-6      Sequence 6, Appli
42      29      65.9      1257      2      US-08-611-928-6      Sequence 6, Appli
43      29      65.9      1257      3      US-09-173-891-6      Sequence 6, Appli
44      29      65.9      1257      4      US-09-076-137-6      Sequence 6, Appli
45      29      65.9      1257      5      PCT-US92-03624-6      Sequence 6, Appli

```

ALIGNMENTS

```

RESULT 1
US-09-401-476-5
; Sequence 5, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-401-476-5

```

```

Query Match      84.1%; Score 37; DB 4; Length 21;
Best Local Similarity 85.7%; Pred. No. 0.42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 HLHGSEA 7
DB      14 HLHGSES 20

```

```

RESULT 2
US-09-401-476-4
; Sequence 4, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Stachybotrys charatum
US-09-401-476-4

```

```

Query Match      84.1%; Score 37; DB 4; Length 572;

```

Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
| | | | |
Db 132 HLHGSFS 138

RESULT 3
US-09-401-476-2
; Sequence 2, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401.476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-401-476-2

Query Match 84.1%; Score 37; DB 4; Length 583;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7
| | | | |
Db 135 HLHGSFS 141

RESULT 4
US-08-655-821-16
; Sequence 16, Application US/08655821
; Patent No. 5846718
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ying
; TITLE OF INVENTION: IDENTIFICATION OF PYRAZINAMIDE-RESISTANT
; TITLE OF INVENTION: MYCOBACTERIA AND METHODS FOR TREATING
; TITLE OF INVENTION: MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,821
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07662/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids

; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-655-821-16

Query Match 72.7%; Score 32; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HGSFAS 8
| | | | |
Db 58 HGSFAS 63

RESULT 5
US-08-519-081-2
; Sequence 2, Application US/08519081
; Patent No. 5883240
; GENERAL INFORMATION:
; APPLICANT: Baker Medical Research, Institute
; TITLE OF INVENTION: Genetic sequences encoding
; TITLE OF INVENTION: glucocorticoid dehydrogenases and uses therefor
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,081
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-519-081-2

Query Match 72.7%; Score 32; DB 2; Length 405;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSF 6
| | | | |
Db 302 HLHGSF 307

RESULT 6
US-08-754-369-2
; Sequence 2, Application US/08754369
; Patent No. 5965372
; GENERAL INFORMATION:
; APPLICANT: Baker Medical Research, Institute
; TITLE OF INVENTION: Genetic sequences encoding
; TITLE OF INVENTION: glucocorticoid dehydrogenases and uses therefor
; NUMBER OF SEQUENCES: 3

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham LLP
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/754,369
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 278-0400
;; TELEFAX: (212) 391-0525
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 405 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-754-369-2

Query Match 72.7%; Score 32; DB 2; Length 405;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLHGSF 6
Db 302 HLHGQF 307

RESULT 7
US-08-637-759B-375
; Sequence 375, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (404) 873-8794
;; TELEFAX: (404) 873-8795
;; INFORMATION FOR SEQ ID NO: 375:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 384 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; US-08-637-759B-375

Query Match 70.5%; Score 31; DB 2; Length 384;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLHGSEA 7
Db 154 YLHGAF 160

RESULT 8
US-08-871-355A-375
; Sequence 375, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-871-355A-375

Query Match 70.5%; Score 31; DB 3; Length 384;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 7
; :|||:|
Db 154 YLHGAF 160

RESULT 9

US-09-201-945-375
; Sequence 375, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201.945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
US-09-201-945-375

Query Match 70.5%; Score 31; DB 4; Length 384;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 7
; :|||:|
Db 154 YLHGAF 160

RESULT 10

US-09-154-802-1
; Sequence 1, Application US/09154802
; Patent No. 5989822
; GENERAL INFORMATION:
; APPLICANT: Y. Tom Tang
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: ATP SYNTHASE SUBUNIT HOMOLOG
; FILE REFERENCE: PF-0596 US
; CURRENT APPLICATION NUMBER: US/09/154.802

; CURRENT FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1887516
US-09-154-802-1

Query Match 68.2%; Score 30; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 5
; :|||:|
Db 27 HLHGSA 31

RESULT 11

US-09-373-029-1
; Sequence 1, Application US/09373029
; Patent No. 6036954
; GENERAL INFORMATION:
; APPLICANT: Y. Tom Tang
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: ATP SYNTHASE SUBUNIT HOMOLOG
; FILE REFERENCE: PF-0596 US
; CURRENT APPLICATION NUMBER: US/09/373.029
; CURRENT FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 09/154,802
; EARLIER FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1887516
US-09-373-029-1

Query Match 68.2%; Score 30; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 5
; :|||:|
Db 27 HLHGSA 31

RESULT 12

US-08-702-153-2
; Sequence 2, Application US/08702153
; Patent No. 5955332
; GENERAL INFORMATION:
; APPLICANT: PREVOTS, Fabien
; APPLICANT: TOLOU, Sandrine
; APPLICANT: DALOYAU, Marl ne
; TITLE OF INVENTION: Nucleic acid sequences and plasmids
; TITLE OF INVENTION: comprising at least one phage resistance mechanism,
; TITLE OF INVENTION: bacteria containing them, and their use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,153
FILING DATE: 23-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 09980
FILING DATE: 22-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16781/625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-153-2

Query Match 68.2%; Score 30; DB 2: Length 346;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGS 5
|||||
Db 194 HLHGS 198

RESULT 13
US-08-702-153-4
Sequence 4, Application US/08702153
Patent No. 595332
GENERAL INFORMATION:
APPLICANT: PREVOTS, Fabien
APPLICANT: TOLOU, Sandrine
APPLICANT: DALOYAU, Marl ne
TITLE OF INVENTION: Nucleic acid sequences and plasmids
TITLE OF INVENTION: comprising at least one phage resistance mechanism,
TITLE OF INVENTION: bacteria containing them, and their use
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,153
FILING DATE: 23-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 09980
FILING DATE: 22-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16781/625

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-153-4

Query Match 68.2%; Score 30; DB 2: Length 346;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGS 5
|||||
Db 194 HLHGS 198

RESULT 14
US-09-240-639-4
Sequence 4, Application US/09240639
Patent No. 6350447
GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 529
TYPE: PRT
ORGANISM: Homo sapiens
US-09-240-639-4

Query Match 68.2%; Score 30; DB 4: Length 529;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGS 5
|||||
Db 127 HLHGS 131

RESULT 15
US-09-036-987A-2
Sequence 2, Application US/09036987A
Patent No. 6143526
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana

; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2595 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-036-987A-2

Query Match 68.2%; Score 30; DB 4; Length 2595;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGS 5
|
|
|
|
|
Db 1100 HLHGS 1104

Search completed: August 19, 2002, 06:34:42
Job time: 1203 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:07 ; Search time 78.53 Seconds
(without alignments)
13.460 Million cell updates/sec

Title: US-09-339-922A-108

Perfect score: 56

Sequence: 1 QASQISNHLH 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	46	82.1	106	2	PL0267
2	46	82.1	123	2	S35479
3	45	80.4	102	2	S26346
4	45	80.4	104	2	B43413
5	45	80.4	107	2	B45722
6	45	80.4	107	2	A45722
7	45	80.4	138	2	A26471
8	44	78.6	107	2	C45722
9	42	75.0	107	2	S32188
10	41	73.2	96	2	G33730
11	41	73.2	103	2	S19375
12	39	69.6	62	2	S42265
13	39	69.6	87	2	I52592
14	39	69.6	88	2	S34088
15	39	69.6	88	2	S34087
16	39	69.6	95	2	PH0862
17	39	69.6	108	2	S19674
18	39	69.6	110	2	S44118
19	39	69.6	117	2	S43528
20	39	69.6	117	2	S42263
21	39	69.6	127	2	S40367
22	39	69.6	129	1	K1HOWK
23	39	69.6	129	2	S52789
24	37	66.1	106	2	PC4282
25	37	66.1	122	2	S40370
26	37	66.1	1085	2	H82511
27	37	66.1	10787	2	T30192
28	36	64.3	115	1	K3HUCI
29	36	64.3	115	2	A30553

```

30      36      64.3      117      1      K4RBF2      Ig kappa chain pre
31      36      64.3      122      2      S40314      Ig kappa chain - h
32      36      64.3      506      2      A81191      hypothetical prote
33      36      64.3      833      2      F81989      hypothetical prote
34      35.5      63.4      93      2      S17634      Ig kappa chain v r
35      35      62.5      92      1      KVRB38      Ig kappa chain v r
36      35      62.5      93      2      S38564      Ig kappa chain v r
37      35      62.5      107      2      B28044      Ig kappa chain v r
38      35      62.5      107      2      B28044      Ig kappa chain v r
39      35      62.5      107      2      D48677      Ig kappa chain v-J
40      35      62.5      107      2      B49026      Ig kappa chain v r
41      35      62.5      107      2      S69901      Ig kappa chain (cl
42      35      62.5      107      2      S69906      Ig kappa chain (cl
43      35      62.5      108      1      KVM5AR      Ig kappa chain v r
44      35      62.5      108      2      C26405      Ig kappa chain v r
45      35      62.5      108      2      PL0282      Ig kappa chain v r

```

ALIGNMENTS

RESULT 1

PL0267

Ig kappa chain V region (anti-DNA, Dp12VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: PL0267

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A>Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618

A:Accession: PL0267

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

```

Query Match      82.1%; Score 46; DB 2; Length 106;
Best Local Similarity 81.8%; Pred.No. 0.098;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 QASQISNHLH 11

Db 24 RASQISNYLH 34

RESULT 2

S35479

Ig kappa chain precursor V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: S35479

R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.

Nucleic Acids Res. 20, 4099, 1992

A>Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from

A:Reference number: S35479; MUID:92375706

A:Accession: S35479

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-123 <TAK>

A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148

C:Genetics:

A:Map position: 6

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 46; DB 2; Length 123;
Best Local Similarity 81.8%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0

QY 1 QASQSISNHLH 11
:|||||:||
Db 36 RASQSISNHLH 46

RESULT 3
S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421
A:Accession: S26346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 102;
Best Local Similarity 81.8%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0

QY 1 QASQSISNHLH 11
:|||||:||
Db 22 RASQSISNHLH 32

RESULT 4
B43413
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B43413
R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kun
J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
A:Reference number: A43413; MUID:92388177
A:Accession: B43413
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <TOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 104;
Best Local Similarity 81.8%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0

QY 1 QASQSISNHLH 11
:|||||:||
Db 21 RASQSISNHLH 31

RESULT 5
B45722

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A:Reference number: A45722; MUID:93100833
A:Accession: B45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0

QY 1 QASQSISNHLH 11
:|||||:||
Db 24 RASQSISNHLH 34

RESULT 6
A45722

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A:Reference number: A45722; MUID:93100833
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0

QY 1 QASQSISNHLH 11
:|||||:||
Db 24 RASQSISNHLH 34

RESULT 7
A26471

Ig kappa chain precursor V region (MAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
A:Reference number: A91572; MUID:87248058
A:Accession: A26471
A:Molecule type: mRNA
A:Residues: 1-138 <BUCA>
A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 80.4%; Score 45; DB 2; Length 138;
 Best Local Similarity 81.8%; Pred. No. 0.21;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSTSNHLH 11
 :|||||:|
 Db 44 RASQSTSNLH 54

RESULT 8

C45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse (f
 C;Species: Mus musculus (house mouse)
 C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C;Accession: C45722
 R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
 J. Virol. 67, 489-496, 1993
 A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
 A;Reference number: A45722; MUID:93100833
 A;Accession: C45722
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-107 <SIM>
 A;Note: sequence extracted from NCBI backbone (NCBIP:120591)
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 44; DB 2; Length 107;
 Best Local Similarity 72.7%; Pred. No. 0.24;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSTSNHLH 11
 :|||||:|
 Db 24 RASQSVSNLH 34

RESULT 9

S32188
 Ig kappa chain V region - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C;Accession: S32188
 R;izul, S.
 submitted to the EMBL Data Library, February 1993
 A;Reference number: S32188
 A;Accession: S32188
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-107 <IZU>
 A;Cross-References: EMBL:X70090; NID:g288253; PIDN:CAA49695.1; PID:g288254
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 42; DB 2; Length 107;
 Best Local Similarity 72.7%; Pred. No. 0.59;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSTSNHLH 11
 :||| |||:|
 Db 24 RASQSTSNLH 34

RESULT 10

G33730
 immunoglobulin V region; immunoglobulin homology

Ig kappa chain V region (23.32) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
 C;Accession: G33730
 R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
 Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
 A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u
 A;Reference number: A33730; MUID:89367325
 A;Accession: G33730
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-96 <LAW>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 96;
 Best Local Similarity 72.7%; Pred. No. 0.82;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSTSNHLH 11
 :|||||:|
 Db 24 RASQSTSNLH 34

RESULT 11

S19975
 Ig kappa chain V region (M-7408) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C;Accession: S19975
 R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
 submitted to the EMBL Data Library, March 1992
 A;Description: Structural characterization of CD4 mAb.
 A;Reference number: S19963
 A;Accession: S19975
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-103 <WEI>
 A;Cross-References: EMBL:X65097; NID:g52296; PIDN:CAA46225.1; PID:g52297
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F:11-85/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 103;
 Best Local Similarity 72.7%; Pred. No. 0.89;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSTSNHLH 11
 :|||||:|
 Db 19 RASQSTSNLH 29

RESULT 12

S42265
 Ig kappa chain V region (018) - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
 C;Accession: S42265
 R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.;
 J. Immunol. 147, 4007-4013, 1991
 A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus
 A;Reference number: S42263; MUID:92043792
 A;Accession: S42265
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-62 <SCO>
 A;Cross-References: EMBL:M64856
 C;Genetics:
 C;Introns: 19/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 69.6%; Score 39; DB 2; Length 62;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
|||||:|:|:
Db 24 QASQDISNYLN 34

RESULT 13

Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I52592
R:Wagner, S.D.; Martinelli, V.; Luzzatto, L.
Blood 83, 3647-3653, 1994
A:Title: Similar patterns of V kappa gene usage but different degrees of somatic mutation
A:Reference number: I52592; MUID:94264318
A:Accession: I52592
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-87 <RES>
A:Cross-references: GB:S71057; NID:547053; PIDN:AAB30971.1; PID:g547054
C:Genetics:
A:Gene: IgKV
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 39; DB 2; Length 87;
Best Local Similarity 72.7%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
|||||:|:|:
Db 17 QASQDISNYLN 27

RESULT 14

Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34088
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387
A:Accession: S34088
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <WAG>
A:Cross-references: EMBL:X67172
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 39; DB 2; Length 88;
Best Local Similarity 72.7%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
|||||:|:|:
Db 17 QASQDISNYLN 27

RESULT 15

Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34087
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387
A:Accession: S34087
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <WAG>
A:Cross-references: EMBL:X67171
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34087
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387
A:Accession: S34087
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <WAG>
A:Cross-references: EMBL:X67171
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 39; DB 2; Length 88;
Best Local Similarity 72.7%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
|||||:|:|:
Db 17 QASQDISNYLN 27

Search completed: August 19, 2002, 06:36:07
Job time: 1288 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:10 ; Search time 51.81 Seconds
(without alignments)
8.221 Million cell updates/sec

Title: US-09-339-922A-108

Perfect score: 56

Sequence: 1 QASQSISNHLH 11

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	69.6	129	1 KVIW_HUMAN	P04431 homo sapien
2	36	64.3	129	1 KVIW_RABIT	P01691 oryctolagus
3	36	64.3	129	1 KVJH_HUMAN	P04207 homo sapien
4	35	62.5	92	1 KV09_RABIT	P01690 oryctolagus
5	35	62.5	108	1 KV5K_MOUSE	P01644 mus musculus
6	35	62.5	108	1 KV5L_MOUSE	P01645 mus musculus
7	35	62.5	108	1 KV5M_MOUSE	P01646 mus musculus
8	35	62.5	455	1 NH55_CAEEL	O16962 caenorhabdi
9	34	60.7	108	1 KVIH_HUMAN	P01594 homo sapien
10	34	60.7	108	1 KVIQ_HUMAN	P01609 homo sapien
11	34	60.7	108	1 KV5U_MOUSE	P04946 mus musculus
12	34	60.7	379	1 FLIP_BUCAI	P57184 buchnera ap
13	34	60.7	446	1 CLUS_PIG	Q29549 sus scrofa
14	34	60.7	746	1 YUV1_CAEEL	P54073 caenorhabdi
15	34	60.7	866	1 MYSP_SCHJA	Q05870 schistosoma
16	34	60.7	866	1 MYSP_SCHMA	P06198 schistosoma
17	33	58.9	108	1 KVIH_HUMAN	P01600 homo sapien
18	33	58.9	108	1 KV5J_MOUSE	P01643 mus musculus
19	33	58.9	111	1 KVI2_RABIT	P01693 oryctolagus
20	33	58.9	157	1 HMAA_SCHGR	P29556 schistocerc
21	33	58.9	447	1 CLUS_RABIT	Q9xsc5 oryctolagus
22	33	58.9	494	1 YPCI_CAEEL	Q11178 caenorhabdi
23	33	58.9	553	1 ASN8_ECOLI	P22106 escherichia
24	33	58.9	594	1 Y410_ARATH	P16128 arabidopsis
25	33	58.9	708	1 GIT2_MOUSE	Q9j1q2 mus musculus
26	33	58.9	759	1 GIT2_HUMAN	Q14161 homo sapien
27	33	58.9	886	1 ORC1_KLULA	P54788 kluveromyc
28	33	58.9	1581	1 ACC8_CRICR	Q09427 cricetus cr
29	33	58.9	1581	1 ACC8_RAT	Q09429 rattus norv
30	33	58.9	1900	1 STH4_YEAST	P37297 saccharomyc
31	32	57.1	108	1 KV5N_MOUSE	P01647 mus musculus
32	32	57.1	108	1 KV5O_MOUSE	P01648 mus musculus
33	32	57.1	109	1 KV3F_HUMAN	P01624 homo sapien

34 32 57.1 115 1 KVIW_HUMAN P04431 homo sapien
35 32 57.1 237 1 MINC_NEIMA Q91x17 neisseria m
36 32 57.1 237 1 MINC_NEIMB Q9k110 neisseria m
37 32 57.1 277 1 MCRA_ECOLI P24200 escherichia
38 32 57.1 308 1 RIBF_HAEIN P44957 haemophilus
39 32 57.1 308 1 YPER_ECOLI P77500 escherichia
40 32 57.1 349 1 PERM_HAEIN P43969 haemophilus
41 32 57.1 398 1 DAP3_HUMAN P51398 homo sapien
42 32 57.1 432 1 MUC6_RICCN Q92gr5 rickettsia
43 32 57.1 445 1 ML64_HUMAN Q14849 homo sapien
44 32 57.1 451 1 YQEV_BACSU P54462 bacillus su
45 32 57.1 471 1 HH_DROME Q02936 drosophila

ALIGNMENTS

RESULT 1
KVIW_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X00965; CAA25477.1; ALT_TERM.
CC PIR: A01883; K1HUWK.
CC HSP: P01607; IREI.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 22
CC CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
CC DOMAIN 23 45 FRAMEWORK-1.
CC DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 57 71 FRAMEWORK-2.
CC DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 79 110 FRAMEWORK-3.
CC DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 120 129 FRAMEWORK-4.
CC DISULFID 45 110 BY SIMILARITY.
CC NON_TER 129 129
CC SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 69.6%; Score 39; DB 1; Length 129;
Best Local Similarity 72.7%; Pred. No. 0.64;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 QASQSISNHLH 11
:|||||:|


```

Db 46 RASQISISNVLN 56

RESULT 2
KV10_RABIT
ID KV10_RABIT STANDARD; PRT; 117 AA.
AC P01691;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region 12F2 precursor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83273646; PubMed=6410392;
RA Dreher K.L., Emorine L., Kindt T.J., Max E.E.;
RT "cDNA clone encoding a complete rabbit immunoglobulin kappa light
chain of b4 allotype."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4489-4493(1983).
CC -1- MISCELLANEOUS: THIS CLONE WAS DERIVED FROM THE RABBIT-MOUSE
HYBRIDOMA 12F2; THE CHAIN PRODUCED IS A MONOCLONAL ANTIBODY
AGAINST STREPTOCOCCAL GROUP C VACCINE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01358; AAB59259.1; ALT_TERM.
DR PIR; A01954; K4RBF2.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma; Signal.
FT CHAIN 1 117
FT SIGNAL <1 6
FT CHAIN 7 117 IG KAPPA CHAIN V REGION 12F2.
FT DOMAIN 7 29 FRAMEWORK-1.
FT DOMAIN 30 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 29 86 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12288 MW; E24A7582389E4439 CRC64;

Query Match 64.3%; Score 36; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 2.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISISNHL 10
|||||:|
Db 30 QASQISISTYL 39

RESULT 3
KV3H_HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

```

DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
light-chain gene."
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M12740; AAA58992.1; -.
DR PIR; A01898; K3HUCL.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 64.3%; Score 36; DB 1; Length 129;
Best Local Similarity 70.0%; Pred. No. 2.6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISISNHL 10
|||||:|
Db 44 RASQSVSNL 53

RESULT 4
KV09_RABIT
ID KV09_RABIT STANDARD; PRT; 92 AA.
AC P01690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region 3381 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=75176905; PubMed=1094456;
RA Margolies M.N., Cannon L.E. III, Strosberg A.D., Haber E.;
RT "Diversity of light chain variable region sequences among rabbit
antibodies elicited by the same antigens."
RL Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III

```

CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.

DR PIR: A01953; KVRB38.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig: 1.
 DR SMART; SM00406; IGV: 1.
 KW Immunoglobulin V region.

FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 >92
 FT NON_TER 92 92
 SQ SEQUENCE 92 AA; 9730 MW; 9A36B15913CB3BEE CRC64;

Query Match 62.5%; Score 35; DB 1; Length 92;
 Best Local Similarity 80.0%; Pred. No. 2.7;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSISNHL 10
 :|||:|||||
 Db 24 QASESISNWL 33

RESULT 5

ID KV5K_MOUSE STANDARD; PRT; 108 AA.
 AC P01644;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region HP R16.7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.

RC STRAIN=A/J;

RX MEDLINE=82150934; PubMed=6801658;

RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
 RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 RL -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

CC PIR: A01927; KVM5AR.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig: 1.

DR SMART; SM00406; IGV: 1.

KW Immunoglobulin V region; Antiarsenate antibody.

FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 BY SIMILARITY.

SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 62.5%; Score 35; DB 1; Length 108;
 Best Local Similarity 63.6%; Pred. No. 3.3;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSISNHL 11
 :|||:|||||
 Db 24 RASQDISNYLN 34

RESULT 6

ID KV5L_MOUSE STANDARD; PRT; 108 AA.
 AC P01645;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region HP 93G7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.

RC STRAIN=A/J;

RX MEDLINE=82150934; PubMed=6801658;

RA Siegelman M., Capra J.D.;

RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
 RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 RL -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

CC PIR: A01927; KVM5AR.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig: 1.

DR SMART; SM00406; IGV: 1.

KW Immunoglobulin V region; Antiarsenate antibody.

FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 BY SIMILARITY.

SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 62.5%; Score 35; DB 1; Length 108;
 Best Local Similarity 63.6%; Pred. No. 3.3;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSISNHL 11
 :|||:|||||
 Db 24 RASQDISNYLN 34

RESULT 7

ID KV5M_MOUSE STANDARD; PRT; 108 AA.
 AC P01646;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region HP 123E6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.

RC STRAIN=A/J;

RX MEDLINE=82150934; PubMed=6801658;

RA Siegelman M., Capra J.D.;

RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
 RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 RL -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

```
DR PIR; A01927; KVMGAR.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
KW Immunoglobulin V region; Antiarsonate antibody.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 108 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON_TER 108 108  
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;  
  
Query Match 62.5%; Score 35; DB 1; Length 108;  
Best Local Similarity 63.6%; Pred. No. 3.3;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QASQISNHLH 11  
Db 24 RASQDISNYLN 34  
:::|::|:  
  
RESULT 8  
NH55_CAEEL STANDARD; PRT; 455 AA.  
AC O16962; Q9GTF7; Q9GTF8;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Nuclear hormone receptor family member nhr-55.  
GN NHR-55 OR T01G6.7  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RA Jones K., Bradshaw H., Graves T.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
[2]  
PP SEQUENCE OF 103-455 FROM N.A.  
RA Boran A., Maiba C.V., Yamamoto K., Cohen F., Sluder A.E.;  
RT "Caenorhabditis elegans nuclear receptor sequences exhibit biophysical compatibility with the ligand-binding domain fold."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ORPHAN NUCLEAR RECEPTOR.  
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
-----  
CC EMBL; AF022978; AAG24179.1; -  
CC EMBL; AF273801; AAG15150.1; -  
CC EMBL; AF273802; AAG15151.1; -  
CC WormPep; T01G6.7; CEL3002.  
DR InterPro; IPR000536; Hormone_rec_lig.  
DR InterPro; IPR001628; zf-C4.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00047; STROIDFINGER.  
DR SMART; SM00430; HOLI; 1.  
DR SMART; SM00399; Znf_C4; 1.  
  
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; FALSE_NEG.  
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
KW Zinc-finger. 59 124 NUCLEAR RECEPTOR-TYPE.  
FT DNA_BIND 59 124 C4-TYPE.  
FT ZN_FING 59 86 C4-TYPE.  
FT ZN_FING 95 119 C4-TYPE.  
FT DOMAIN 34 40 POLY-SER.  
FT DOMAIN 43 50 POLY-SER.  
SQ SEQUENCE 455 AA; 52956 MW; B56CEFA00D6B1A3 CRC64;  
  
Query Match 62.5%; Score 35; DB 1; Length 455;  
Best Local Similarity 62.5%; Pred. No. 18;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 QSISNHLH 11  
Db 389 ETLNHLH 396  
:::|::|:  
  
RESULT 9  
KV1B_HUMAN STANDARD; PRT; 108 AA.  
ID KV1B_HUMAN  
AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region AU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72189444; PubMed=5028201;  
RA Schiechl H., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT Immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
RT protein Au).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehlinhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
RA Schwager P., Steigemann W., Schramm H.J.;  
RT "The structure determination of the variable portion of the  
RT Bence-Jones protein Au."  
RL Biophys. Struct. Mech. 1:139-146(1975).  
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
CC REGION OF THE KAPPA CHAIN REI.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01862; KIHUAV.  
DR HSP; P01607; IREI.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON_TER 108 108  
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6FB9 CRC64;  
  
Query Match 60.7%; Score 34; DB 1; Length 108;
```

j:

```
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 QASQDISNYL 34

RESULT 10
KV1Q_HUMAN STANDARD; PRT; 108 AA.
AC KV1Q_HUMAN
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Scw.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059271; PubMed=4435756;
RA Eulitz M., Hilschmann N.;
RT "The primary structure of a human immunoglobulin L-chain of
kappa-type (Bence-Jones protein Scw.); II: The chymotryptic peptides
and the complete amino acid sequence.";
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01875; KIHUSW.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DISULFID 98 107 COMPLEMENTARITY-DETERMINING-3.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 QASQDIRKHL 34

RESULT 11
KV5U_MOUSE STANDARD; PRT; 108 AA.
AC KV5U_MOUSE
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region NQ5-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 60.7%; Score 34; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 QASQDIRKHL 34

RESULT 11
KV5U_MOUSE STANDARD; PRT; 108 AA.
AC KV5U_MOUSE
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region NQ5-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 60.7%; Score 34; DB 1; Length 108;
Best Local Similarity 70.0%; Pred. No. 5.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQISNHLH 11
Db 25 ASQDISNYL 34

RESULT 12
FLIP_BUCAI STANDARD; PRT; 379 AA.
AC P57184;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Flagellar biosynthetic protein flip.
GN FLIP OR BU082.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: PLAYS A ROLE IN THE FLAGELLUM-SPECIFIC TRANSPORT SYSTEM
(BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
```

CC entitles requires a license agreement (See <http://www.isb-sib.ch/announcement/>)
CC or send an email to license@isb-sib.ch.
CC -----

DR EMBL; AP001118; BAB12802.1; -
DR InterPro: IPR002039; FlIP.
DR Pfam; PF00813; FlIP; 1.
DR PRINTS; PR01302; TYPE3IMPPROT.
DR PRODOM; PD002586; FlIP; 1.
DR PROSITE; PS01060; FlIP.1; FALSE_NEG.
DR PROSITE; PS01061; FlIP.2; 1.
KW Flagella; Transmembrane; Complete proteome.
FT TRANSMEM 23 43 POTENTIAL.
FT TRANSMEM 140 160 POTENTIAL.
FT TRANSMEM 178 198 POTENTIAL.
FT TRANSMEM 222 242 POTENTIAL.
FT TRANSMEM 319 339 POTENTIAL.
FT TRANSMEM 357 377 POTENTIAL.
SQ SEQUENCE 379 AA; 43192 MW; DE6E1F040DA825B0 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 379;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QSISNHLH 11
|||||

Db 8 QSISNSLH 15
|||||

RESULT 13

CLUS_PIG
ID CLUS_PIG STANDARD; PRT; 446 AA.
AC Q29549;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Clusterin precursor (Complement cytotoxic inhibitor) (CLI).
GN CLI.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92184774; PubMed=1544909;
RA Diemer V., Hoyle M., Baglioni C., Millis A.J.;
RT "Expression of porcine complement cytotoxic inhibitor mRNA in
RT cultured aortic smooth muscle cells. Changes during differentiation
RT in vitro.";
RL J. Biol. Chem. 267:5257-5264(1992).
CC -!- FUNCTION: NOT YET CLEAR, IT IS KNOWN TO BE EXPRESSED IN A VARIETY
CC OF TISSUES AND IT SEEMS TO BE ABLE TO BIND TO CELLS, MEMBRANES,
CC AND HYDROPHOBIC PROTEINS. IT HAS BEEN ASSOCIATED WITH PROGRAMMED
CC CELL DEATH (BY SIMILARITY).
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED HETERODIMER (BY
CC SIMILARITY).
CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND LIVER; LOWER
CC LEVELS ARE DETECTED IN OTHER TISSUES, INCLUDING THE AORTA.
CC -!- SIMILARITY: BELONGS TO THE CLUSTERIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>)
CC or send an email to license@isb-sib.ch.
CC -----
DR EMBL; M84639; AAA31013.1; -
DR InterPro: IPR000753; Clusterin.
DR Pfam; PF01093; Clusterin; 1.
DR SMART; SM00035; CLA; 1.
DR SMART; SM00030; CLB; 1.

DR PROSITE; PS00492; CLUSTERIN_1; 1.
DR PROSITE; PS00493; CLUSTERIN_2; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 446 CLUSTERIN.
FT CHAIN 29 446 BETA-CHAIN (A CHAIN).
FT CHAIN 228 446 ALPHA-CHAIN (B CHAIN).
FT DISULFID 102 312 INTERCHAIN (BY SIMILARITY).
FT DISULFID 113 304 INTERCHAIN (BY SIMILARITY).
FT DISULFID 116 301 INTERCHAIN (BY SIMILARITY).
FT DISULFID 121 294 INTERCHAIN (BY SIMILARITY).
FT DISULFID 129 284 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 373 373 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 446 AA; 51774 MW; BID5B434B668E3AA CRC64;

Query Match 60.7%; Score 34; DB 1; Length 446;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QASQSIHSLH 11
|||||

Db 253 QAQAMDAHLH 263
|||||

RESULT 14

YUV1-CAEEL
ID YUV1-CAEEL STANDARD; PRT; 746 AA.
AC P54073; Q20418;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 86.9 kDa protein F44G4.1 in chromosome II precursor.
GN F44G4.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Sims M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Durbin R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: SOME, TO YEAST YHR088W AND IMP4.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>)
CC or send an email to license@isb-sib.ch.
CC -----
DR EMBL; Z49910; CAA90124.2; -
DR EMBL; Z70034; CAA90124.2; JOINED.
DR WormPep; F44G4.1; CE23730.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR001270; CLP_AB.
DR InterPro; IPR002799; IMP4.
DR Pfam; PF01945; IMP4; 1.
DR PRINTS; PR00300; CLPPROTEASEA.
DR SMART; SM00382; AAA; 1.
KW Hypothetical protein; Signal.

```
FT SIGNAL      1 18 POTENTIAL.
FT CHAIN       19 746 HYPOTHETICAL 86.9 KDA PROTEIN F44G4.1.
SQ SEQUENCE    746 AA; 86929 MW; 84333162C34A70C6 CRC64;

Query Match
Best Local Similarity 60.7%; Score 34; DB 1; Length 746;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNHL 10
   I I I I I I I I
DB 254 QMSLISNHL 263

RESULT 15
MYP_SCHJA STANDARD; PRT; 866 AA.
AC Q05870; Q26510; Q26518;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Paramyosin (Antigen SJ97).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
OC Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;
OC Neodermata; Trematoda; Digenea; Strigeldida; Schistosomatoidae;
OC Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHILIPPINE;
RX MEDLINE=95407380; PubMed=7676905;
RA Becker M.M., Kallina B.H., Yang W., Harrop S.A., Scott J.C.,
RA Wayne G.J., Kurtis J.D., McManus D.P.;
RT "Gene cloning and complete nucleotide sequence of philippine
RL Schistosoma japonicum paramyosin.";
RN Acta Trop. 59:143-147(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JAPANESE;
RX MEDLINE=95034466; PubMed=7947464;
RA Nara T., Matsumoto N., Jancharut T., Matsuda H., Yamamoto K.,
RA Iimura T., Nakamura K.I., Aikawa M., Oswald I., Sher A., Kita K.,
RA Kojima S.;
RT "Demonstration of the target molecule of a protective IgE antibody in
RL secretory glands of Schistosoma japonicum larvae.";
RN Int. Immunol. 6:963-971(1994).
RN [3]
RP SEQUENCE OF 171-559 FROM N.A.
RX MEDLINE=93138870; PubMed=1487380;
RA Yang W., Wayne G.J., Sculley D.G., Liu X., McManus D.P.;
RT "Cloning and partial nucleotide sequence of Schistosoma japonicum
RL paramyosin: a potential vaccine candidate against schistosomiasis.";
RN Int. J. Parasitol. 22:1187-1191(1992).
CC -!- FUNCTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT OF
CC MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC -!- DEVELOPMENTAL STAGE: MAY BE INCORPORATED INTO THE TEGUMENT DURING
CC THE DEVELOPMENT OF SCHISTOSOMA, THUS BECOMING A TARGET FOR
CC PROTECTIVE IMMUNITY DURING THE MIGRATORY PHASE OF THE PARASITE.
CC -!- SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; U11825; AAA81003.1; -.
DR EMBL; D28811; BAA05972.1; -.
```

```
DR EMBL; M90492; -; NOT_ANNOTATED_CDS.
DR InterPro; IPR002928; Myosin_tail.
DR Pfam; PF01576; Myosin_tail; 1.
KW Coiled coil; Muscle protein; Thick filament; Myosin; Antigen.
FT DOMAIN 1 22 NONHELICAL REGION (POTENTIAL).
FT DOMAIN 23 839 COILED COIL (POTENTIAL).
FT DOMAIN 840 866 NONHELICAL REGION (POTENTIAL).
FT DISULFID 750 750 INTERCHAIN (POTENTIAL).
FT CONFLICT 371 371 E -> D (IN REF. 1).
FT CONFLICT 559 559 E -> K (IN REF. 3).
SQ SEQUENCE 866 AA; 100541 MW; 37D7BDF2CF32775D CRC64;
```

Query Match
Best Local Similarity 60.7%; Score 34; DB 1; Length 866;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNHL 10
 I I I I I I I I
DB 475 QASQAALNHL 484

Search completed: August 19, 2002, 06:59:11
Job time: 1376 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:15 ; Search time 140.4 seconds
(without alignments)
13.554 Million cell updates/sec

Title: US-09-339-922A-108

Perfect score: 56

Sequence: 1 QASQISINHLH 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	42	75.0	116	4 Q96PF6	Q96pf6 homo sapien
2	42	75.0	431	5 Q966H7	Q966h7 caenorhabdi
3	41	73.2	414	5 Q966H8	Q966h8 caenorhabdi
4	39	69.6	107	4 Q9UL81	Q9ul81 homo sapien
5	38	67.9	401	5 Q9VM04	Q9vm04 drosophila
6	38	67.9	417	13 P79751	P79751 fugu rubrip
7	37	66.1	1085	16 Q9KNE5	Q9kne5 vibrio chol
8	37	66.1	1574	16 Q92M45	Q92m45 rhizobium m
9	37	66.1	1581	2 Q9ZFB9	Q9zfb9 rhizobium e
10	37	66.1	10797	3 Q94116	Q94116 aureobasidi
11	36	64.3	506	16 Q9KOS2	Q9kos2 neisseria m
12	36	64.3	833	2 Q9JPE1	Q9jpe1 neisseria m
13	36	64.3	833	16 Q9JQR5	Q9jqr5 neisseria m
14	35	62.5	38	13 Q9PV38	Q9pv38 channa sp.
15	35	62.5	234	11 Q91WF8	Q91wf8 mus musculu
16	35	62.5	293	10 Q49020	Q49020 gossypium h

17	35	62.5	293	10 Q94JN5	Q94jn5 gossypium h
18	35	62.5	293	10 Q94JN4	Q94jn4 gossypium h
19	35	62.5	388	5 Q9VMB3	Q9vmb3 drosophila
20	35	62.5	452	5 Q9UL00	Q9ul00 leishmania
21	35	62.5	464	16 Q99W16	Q99w16 staphylococ
22	35	62.5	2630	12 Q55319	Q55319 acyrthosiph
23	34	60.7	107	4 Q96SA9	Q96sa9 homo sapien
24	34	60.7	108	4 Q9UL77	Q9ul77 homo sapien
25	34	60.7	108	4 Q9UL70	Q9ul70 homo sapien
26	34	60.7	193	12 Q9YW53	Q9yhw53 melanoplus
27	34	60.7	200	17 Q9HHY3	Q9hh3 halobacteri
28	34	60.7	305	16 Q9KFT1	Q9kft1 bacillus ha
29	34	60.7	313	2 Q9RN71	Q9rn71 streptomyce
30	34	60.7	334	8 Q33795	Q33795 emericelia
31	34	60.7	349	10 Q9SQL0	Q9sql0 lycopersico
32	34	60.7	350	5 Q95NY6	Q95ny6 caenorhabdi
33	34	60.7	356	5 Q95NU5	Q95nu5 caenorhabdi
34	34	60.7	375	8 Q9TL10	Q9tl10 nephroselmi
35	34	60.7	435	2 Q86899	Q86899 sphingomona
36	34	60.7	443	5 Q26507	Q26507 schistosoma
37	34	60.7	443	5 Q26508	Q26508 schistosoma
38	34	60.7	449	6 Q29482	Q29482 equus caball
39	34	60.7	458	10 Q9AY47	Q9ay47 oryza sativ
40	34	60.7	487	10 Q9SY94	Q9sy94 adiantum ca
41	34	60.7	527	5 Q33762	Q33762 caenorhabdi
42	34	60.7	560	10 Q49896	Q49896 arabidopsis
43	34	60.7	566	10 Q9ZQK5	Q9zqk5 arabidopsis
44	34	60.7	578	2 Q9ZG94	Q9z994 pseudomonas
45	34	60.7	866	5 Q9UAS3	Q9uas3 schistosoma

ALIGNMENTS

RESULT 1

Q96PF6 ID Q96PF6 PRELIMINARY; PRT; 116 AA.

AC Q96PF6; Q96PF6; PRELIMINARY; PRT; 116 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).

GN SDNK1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21361171; PubMed=11468171;

RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;

RT "The tropism of organ involvement in primary systemic amyloidosis:

RT contributions of Ig V(L) germ line gene use and clonal plasma cell

RT burden."

RL Blood 98:714-720(2001).

DR EMBL; AF361758; AAK51465.1; -.

FT NON_TER 1 116

FT SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 75.0%; Score 42; DB 4; Length 116;

Best Local Similarity 72.7%; Pred. No. 1.3;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINHLH 11

|||||:

Db 24 QASQDIANHLN 34

RESULT 2

Q966H7 ID Q966H7 PRELIMINARY; PRT; 431 AA.

Q966H7;
 AC 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN M02H5.3.
 GN M02H5.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Bradshaw-Cordum H.;
 RT "The sequence of C. elegans cosmid M02H5.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006675; AAK84553.1; --
 SQ SEQUENCE 431 AA; 50490 MW; E026D36A14019BD2 CRC64;

Query Match 75.0%; Score 42; DB 5; Length 431;
 Best Local Similarity 72.7%; Pred. No. 5;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QASQSISNHLH 11
 I |
 Db 361 QLQDSISNHLH 371

RESULT 3
 Q966H8
 ID Q966H8 PRELIMINARY; PRT; 414 AA.
 AC Q966H8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN M02H5.4.
 GN M02H5.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Bradshaw-Cordum H.;
 RT "The sequence of C. elegans cosmid M02H5.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;

RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006675; AAK84554.1; --
 SQ SEQUENCE 414 AA; 48113 MW; 34E312692E3B30A0 CRC64;

Query Match 73.2%; Score 41; DB 5; Length 414;
 Best Local Similarity 72.7%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QASQSISNHLH 11
 I |
 Db 344 QFQDSISNHLH 354

RESULT 4
 Q9UL81
 ID Q9UL81 PRELIMINARY; PRT; 107 AA.
 AC Q9UL81;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
 DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035033; AAD56269.1; --
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 69.6%; Score 39; DB 4; Length 107;
 Best Local Similarity 72.7%; Pred. No. 4.4;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASQSISNHLH 11
 I |
 Db 24 RASQSISNHLN 34

RESULT 5
 Q9VW04
 ID Q9VW04 PRELIMINARY; PRT; 401 AA.
 AC Q9VW04;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CG9295 PROTEIN.
 GN CG9295.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.


```

RX STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balwle R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003516; AAF49151.1; -.
DR FlyBase; FBgn0036880; CG9295.
DR InterPro; IPR000618; Insect_cuticle.
DR Pfam; PF00379; Insect_cuticle; 1.
DR PRINTS; PR00947; CUTICLE.
DR PROSITE; PS00233; CUTICLE; 1.
SQ SEQUENCE 401 AA; 45863 MW; CD2341B6F9715308 CRC64;

Query Match 67.9%; Score 38; DB 5; Length 401;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 Q5ISNHLH 11
Db 277 ESISNHH 284

RESULT 6 PRELIMINARY; PRT; 417 AA.
ID P79751
AC P79751;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IKAROS-LIKE.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=99177347; PubMed=10077531;
RA Gellner K., Brenner S.;
RT "Analysis of 148 kb of genomic DNA around the wnt1 locus of Fugu
RT rubripes."
RL Genome Res. 9:251-258(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF056116; AAC34387.1; -.
DR HSPSP; P15822; IBB0.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR PRINTS; PR00048; ZINC_FINGER.
DR SMART; SM00355; Znf_C2H2; 6.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SQ SEQUENCE 417 AA; 45664 MW; 8A4E4AA806946D74 CRC64;

Query Match 67.9%; Score 38; DB 13; Length 417;
Best Local Similarity 72.7%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QASOSISNHLH 11
Db 322 QISTSNHLH 332

RESULT 7
ID Q9KNE5 PRELIMINARY; PRT; 1085 AA.
AC Q9KNE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN VCA0020.
VCA0020.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AE004345; AAF95934.1; -.
DR TIGR; VCA0020; -.
DR InterPro; IPR001917; AminoTransf_2.
DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
KW Hypothetical protein; Complete proteome
SQ SEQUENCE 1085 AA; 121042 MW; D176D85571729945 CRC64;

Query Match 66.1%; Score 37; DB 16; Length 1085;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASOSISNHLH 10
Db 497 QANQAINHHI 506

RESULT 8
Q92M45

```

```

ID Q92M45 PRELIMINARY; PRT; 1574 AA.
AC Q92M45;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PROBABLE GLUTAMATE SYNTHASE NADPH LARGE CHAIN PROTEIN (EC
DE 1.4.1.13)
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cloux A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gowie S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
RA Vorholter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti."
RL Science 293:668-672(2001).
KW EMBL; AL591791; CAC47390.1; -.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 1574 AA; 172198 MW; 6D2EBBECE0BA0E29 CRC64;

Query Match 66.1%; Score 37; DB 16; Length 1574;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QSISNHLH 11
Db 1521 QLISNHLH 1528

RESULT 9
Q92FB9 PRELIMINARY; PRT; 1581 AA.
AC Q92FB9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GLUTAMATE SYNTHASE LARGE SUBUNIT (EC 1.4.1.13).
GN GLTB.
OS Rhizobium etli.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RX MEDLINE=20340966; PubMed=10878127;
RA Castillo A., Taboada H., Mendoza A., Valderrama B., Encarnacion S.,
RA Mora J.;
RT "Role of GOGAT in carbon and nitrogen partitioning in Rhizobium
etli."
RL Microbiology 146:1627-1637(2000).
DR EMBL; AF107264; AAC97376.1; -.
DR HSP; P01175; 1LCO.
DR InterPro; IPR002489; DUF14.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR002932; Glu_synthase.
DR Pfam; PF01493; DUF14; 1.
DR Pfam; PF01645; Glu_synthase; 1.
KW Oxidoreductase.
SQ SEQUENCE 1581 AA; 171437 MW; 87AB88A9AB590F3C CRC64;

Query Match 66.1%; Score 37; DB 16; Length 1574;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QSISNHLH 11
Db 1521 QLISNHLH 1528

RESULT 9
Q92FB9 PRELIMINARY; PRT; 1581 AA.
AC Q92FB9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GLUTAMATE SYNTHASE LARGE SUBUNIT (EC 1.4.1.13).
GN GLTB.
OS Rhizobium etli.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RX MEDLINE=20340966; PubMed=10878127;
RA Castillo A., Taboada H., Mendoza A., Valderrama B., Encarnacion S.,
RA Mora J.;
RT "Role of GOGAT in carbon and nitrogen partitioning in Rhizobium
etli."
RL Microbiology 146:1627-1637(2000).
DR EMBL; AF107264; AAC97376.1; -.
DR HSP; P01175; 1LCO.
DR InterPro; IPR002489; DUF14.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR002932; Glu_synthase.
DR Pfam; PF01493; DUF14; 1.
DR Pfam; PF01645; Glu_synthase; 1.
KW Oxidoreductase.
SQ SEQUENCE 1581 AA; 171437 MW; 87AB88A9AB590F3C CRC64;

Query Match 66.1%; Score 37; DB 2; Length 1581;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QSISNHLH 11
Db 1528 QLISNHLH 1535

RESULT 10
Q94116 PRELIMINARY; PRT; 10797 AA.
AC Q94116;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PEPTIDE SYNTHETASE.
OS Aureobasidium pullulans.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothyriomycetes incertae sedis; Dothioraceae;
OC mitosporic Dothioraceae; Aureobasidium.
OX NCBI_TaxID=5580;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R106;
RA Peery R.B., Thornevell S.J., Tobin M.B., Skatrud P.L.;
RT "Discovery of an MDR-like gene adjacent to a peptide synthetase in
Aureobasidium pullulans."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U85909; AAD00581.1; -.
DR HSP; P14687; IAMU.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; DUF4.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR003880; Phosphopant_attach.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00501; AMP-binding; 9.
DR Pfam; PF00668; Condensation; 11.
DR Pfam; PF00550; pp-binding; 12.
DR PROSITE; PS00075; ACP_DOMAIN; 12.
DR PROSITE; PS00455; AMP_BINDING; 4.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_10.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Phosphopantetheine.
SQ SEQUENCE 10797 AA; 1190733 MW; 9EDB1A3E0A13A2D0 CRC64;

Query Match 66.1%; Score 37; DB 3; Length 10797;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
Db 8268 KASESVKNNLH 8278

RESULT 11
Q9K0S2 PRELIMINARY; PRT; 506 AA.
AC Q9K0S2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN NMB0506.
GN NMB0506.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;

```

```

RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citron H., Clark E.B.,
RA Cotton M.D., Uckerback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RA "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AE002407; AAF40938.1; -.
DR TIGR: NMB0506; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 506 AA; 52695 MW; A45ECDEA04046B5C CRC64;

Query Match 64.3%; Score 36; DB 16; Length 506;
Best Local Similarity 45.5%; Pred. No. 86;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11
Db 131 QAAEAVSKHFH 141

RESULT 12
Q9JPE1 PRELIMINARY; PRT; 833 AA.
AC Q9JPE1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 88.4 KDA PROTEIN.
GN RTW4.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_taxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FAM18;
RX MEDLINE=20187481; PubMed=10722605;
RA Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
RA Tinsley C.R.;
RT "Molecular and biological analysis of eight genetic islands that
RT distinguish neisseria meningitidis from the closely related pathogen
RT neisseria gonorrhoeae."
RL Infect. Immun. 68:2082-2095(2000).
DR EMBL: AJ31284; CAB72083.1; -.
DR EMBL: AJ391284; CAB72083.1; -.
KW Hypothetical protein.
SQ SEQUENCE 833 AA; 88396 MW; B967C8422CD71A12 CRC64;

Query Match 64.3%; Score 36; DB 2; Length 833;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11
Db 458 QAAEAVSKHFH 468

RESULT 13
Q9JQR5 PRELIMINARY; PRT; 833 AA.
AC Q9JQR5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN NMA0692.
GN NMA0692 OR RTW4.
OS Neisseria meningitidis (serogroup A), and
```

```

OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_taxID=63699; 487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20187481; PubMed=10722605;
RA Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
RA Tinsley C.R.;
RT "Molecular and biological analysis of eight genetic islands that
RT distinguish neisseria meningitidis from the closely related pathogen
RT neisseria gonorrhoeae."
RL Infect. Immun. 68:2082-2095(2000).
DR EMBL: ALJ62753; CAB83978.1; -.
DR EMBL: AJ391255; CAB71949.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 833 AA; 88713 MW; DBC9914A375114C9 CRC64;

Query Match 64.3%; Score 36; DB 16; Length 833;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11
Db 458 QAAEAVSKHFH 468

RESULT 14
Q9PV38 PRELIMINARY; PRT; 38 AA.
AC Q9PV38;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DYSTROPHIN (FRAGMENT).
GN DYST.
OS Channa sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Channoidae;
OC Channidae; Channa.
OX NCBI_taxID=94222;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF137157; AAD53434.1; -.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4342 MW; AAC53B3FF62C025C CRC64;

Query Match 62.5%; Score 35; DB 13; Length 38;
Best Local Similarity 70.0%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 QASQISNHL 10
 || |||||
Db 20 QAQPSISNHV 29

RESULT 15

Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 25.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC015292; AAH15292.1; -
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6E7812D2 CRC64;

Query Match 62.5%; Score 35; DB 11; Length 234;
Best Local Similarity 63.6%; Pred. No. 60;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
 ||| |||:
Db 44 RASQDISNYLN 54

Search completed: August 19, 2002, 06:58:18
Job time: 1408 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:14 ; Search time 180.34 Seconds
(without alignments)
6.775 Million cell updates/sec

Title: US-09-339-922A-108
Perfect score: 56
Sequence: 1 QASQISNHLH 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*

1:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT.*
13:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	11	22	AAW7456
2	56	100.0	13	19	AAW76011
3	56	100.0	13	22	AAW76011
4	56	100.0	107	19	AAW76006
5	56	100.0	107	19	AAW76002
6	56	100.0	107	19	AAW76004
7	56	100.0	107	22	AAW76004
8	56	100.0	107	22	AAW76004
9	56	100.0	107	22	AAW76004
10	56	100.0	107	22	AAW76004
11	56	100.0	107	22	AAW76004

12	52	92.9	105	20	AAW7456
13	52	92.9	105	20	AAW7458
14	52	92.9	107	20	AAW84098
15	52	92.9	108	20	AAW84094
16	52	92.9	109	20	AAW06380
17	52	92.9	112	20	AAW84100
18	47	83.9	11	22	AAW61403
19	47	83.9	13	19	AAW76031
20	47	83.9	13	22	AAW61389
21	45	80.4	107	13	AAW25729
22	45	80.4	107	15	AAW54319
23	45	80.4	107	17	AAW01287
24	45	80.4	107	21	AAW95139
25	45	80.4	107	21	AAW98248
26	45	80.4	107	22	AAW69677
27	45	80.4	107	22	AAW69678
28	45	80.4	107	22	AAW69690
29	45	80.4	108	12	AAW15438
30	45	80.4	109	20	AAW89176
31	45	80.4	127	15	AAW54093
32	45	80.4	127	22	AAW59687
33	45	80.4	240	12	AAW15443
34	43	76.8	108	17	AAW00241
35	43	76.8	259	21	AAW09775
36	42	75.0	88	21	AAW56654
37	42	75.0	124	21	AAW56719
38	42	75.0	127	21	AAW32405
39	42	75.0	127	21	AAW32407
40	41	73.2	11	15	AAW52526
41	41	73.2	107	14	AAW38601
42	41	73.2	107	19	AAW58482
43	41	73.2	107	20	AAW30203
44	41	73.2	107	20	AAW30205
45	41	73.2	107	21	AAW71240

ALIGNMENTS

RESULT 1
AAB61402
ID AAB61402 standard; peptide; 11 AA.
XX AAB61402;
XX 03-APR-2001 (first entry)
XX Enhanced 6H6LH light chain CDRI.
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX inflammatory; cancer; retina; restenosis; osteoporosis.
XX Unidentified.
XX WO200078815-A1.
XX 28-DEC-2000.
XX 23-JUN-2000; 2000WO-US17454.
XX 24-JUN-1999; 99US-0339922.
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX Huse WD, Wu H;
XX WPI; 2001-050110/06.
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis--

Jk gene product.
Humanised anti-alp
Murine vitronectin
Murine monoclonal
Vitronectin alpha-
Enhanced LM609 VH
LM609 grafted anti
Mutant VL CDRI pep
Humanised VL regio
Anti-HIV gp120 imm
VL region of HIV n
Anti-gp120 antibod
Anti-gp120 antibod
Murine CMV5 antibo
Humanised CMV5 ant
Human WOI antibody
Light chain variab
Anti-p53 monoclon
Sequence of mouse
Murine CMV5 antibo
Single chain Fv fr
EGF receptor chime
TWV 30K movement p
Partial peptide fr
Amino acid sequenc
Mouse anti-verotox
Mouse anti-verotox
306 light chain co
HYH light chain.
Murine HYH antibod
The variable light
The variable light
Humanised antibody

PS Claim 4; Page 46; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 11 AA;

Query Match 100.0%; Score 56; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00041;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASQSTSNHLH 11
 |||||
 Db 1 qasqsisnhlh 11

RESULT 2

AAW76011
 ID AAW76011 standard; Protein; 13 AA.

AC AAW76011;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-L region CDR1 protein fragment #1.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

OS Mus sp.

PN W09833919-A2.

PD 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49848.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Disclosure; Page 40; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

SQ Sequence 13 AA;

Query Match 100.0%; Score 56; DB 19; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00049;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASQSTSNHLH 11
 |||||
 Db 1 qasqsisnhlh 11

RESULT 3

AAB61369
 ID AAB61369 standard; peptide; 13 AA.

XX AAB61369;

XX 03-APR-2001 (first entry)

XX LM609 VL CDR1 peptide.

DE LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX W0200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 13 AA;

Query Match 100.0%; Score 56; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00049;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
 Db 1 qasqsisnhlh 11

RESULT 4
 AAW76006
 ID AAW76006 standard; Protein; 107 AA.
 XX AC AAW76006;
 XX DT 02-NOV-1998 (first entry)
 XX DE LM609 grafted antibody light chain variable region protein fragment.
 XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX OS Mus sp.
 XX FH Key Location/Qualifiers
 FT Misc-difference 49 /label= Arg, Met
 XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX DR WPI; 1998-437472/37.
 XX DR N-PSDB; AAV49843.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 angiogenesis or restenosis
 XX Claim 19; Fig 7; 129pp; English.
 XX This sequence represents a LM609 grafted antibody variable light chain
 region. LM609 and the antibody vitaxin bind selectively to integrin
 alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand
 and thus block integrin-mediated signal transduction. This is useful in
 the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
 specifically angiogenesis and restenosis (but also e.g. (non-)immune
 inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 etc.). The antibodies contain non-murine framework regions so are
 suitable for use in humans. Enhanced types of LM609 have affinity
 more than 90 times greater than that of parent the parent antibody.
 XX Sequence 107 AA;

Query Match 100.0%; Score 56; DB 19; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
 Db 24 qasqsisnhlh 34

RESULT 5
 AAW76002
 ID AAW76002 standard; Protein; 107 AA.
 XX AC AAW76002;
 XX DT 02-NOV-1998 (first entry)
 XX DE Vitaxin antibody light chain variable region protein fragment.
 XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX OS Mus sp.
 XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX DR WPI; 1998-437472/37.
 XX DR N-PSDB; AAV49821.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 angiogenesis or restenosis
 XX Claim 1; Fig 1b; 129pp; English.
 XX This sequence represents the vitaxin antibody variable light chain
 region. Vitaxin and the antibody LM609 bind selectively to integrin
 alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a
 ligand and thus block integrin-mediated signal transduction. This is
 useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated
 disease, specifically angiogenesis and restenosis (but also e.g.
 (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 osteoporosis etc.). The antibodies contain non-murine framework regions
 so are suitable for use in humans. Enhanced types of LM609 have affinity
 more than 90 times greater than that of parent the parent antibody.
 XX Sequence 107 AA;

Query Match 100.0%; Score 56; DB 19; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
 Db 24 qasqsisnhlh 34

RESULT 6
 AAW76004
 ID AAW76004 standard; Protein; 107 AA.
 XX AC AAW76004;
 XX DT 02-NOV-1998 (first entry)
 XX

DE LM609 antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAW76004.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 46; Fig 2b; 129pp; English.

XX This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 107 AA;

Query Match 100.0%; Score 56; DB 19; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.0058;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNHLH 11

Db 24 qasqsishlh 34

RESULT 7

AAG63588

ID AAG63588 standard; Protein; 107 AA.

XX AAG63588;

XX 15-OCT-2001 (first entry)

XX A light chain variable region of LM609 grafted antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.

XX Synthetic.

OS Mus sp.

OS Mus sp.

XX

FH

Key

Misc-difference 49

FT

FT

XX

XX

PN

XX

XX

PD

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Location/Qualifiers

/note= "unspecified residue encoded by MKK"

US2001011125-A1.

02-AUG-2001.

30-JAN-1997; 97US-0790540.

30-JAN-1997; 97US-0790540.

(HUSE/) HUSE W D.

Huse WD;

WPI; 2001-496171/54.

N-PSDB; AAH74624.

New LM609 grafted antibody exhibiting selective binding affinity to

alphavbeta3, comprising at least one LM609 grafted heavy and light

chain polypeptide, useful for diagnosing and treating e.g. inflammatory

disorders or cancer

Claim 1; Fig 1b; 25pp; English.

The present sequence represents the light chain variable region of the

grafted monoclonal antibody LM609. LM609 is a murine antibody which

specifically recognises the integrin alphavbeta3, and inhibits is

functional activity. The LM609 grafted antibody has the

complementarity determining regions (CDRs) substituted into a non-murine

framework. Nucleic acids encoding LM609 grafted heavy and light chain

polypeptides and fragments are useful in diagnostic and therapeutic

purposes, such as in the production of LM609 grafted antibodies and

fragments having binding specificity and inhibitory activity against

the integrin alphavbeta3. The antibody can be used for the diagnosis

or treatment of alphavbeta3-mediated diseases (e.g. inflammatory

disorders, chronic articular rheumatism, psoriasis, disorders

associated with inappropriate or inopportune invasion of vessels such

as diabetic retinopathy, neovascular glaucoma and capillary

proliferation in atherosclerotic plaques, or cancers), and to inhibit

binding activity of alphavbeta3 that are necessary for progression of

an alphavbeta3-mediated disease.

Sequence 107 AA;

Query Match 100.0%; Score 56; DB 22; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.0058;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNHLH 11

Db 24 qasqsishlh 34

RESULT 8

AAG63590

ID AAG63590 standard; Protein; 107 AA.

XX AAG63590;

XX 15-OCT-2001 (first entry)

XX A light chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;

KW chronic articular rheumatism; psoriasis; diabetic retinopathy;

KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;

KW cancer.

XX Synthetic.

OS Mus sp.

OS Mus sp.

XX PN US2001011125-A1.
 XX PD 02-AUG-2001.
 XX PF 30-JAN-1997; 97US-0790540.
 XX PR 30-JAN-1997; 97US-0790540.
 XX PA (HUSE/) HUSE W D.
 XX PI Huse WD;
 XX DR WPI: 2001-496171/54.
 XX DR N-PSDB: AAH74626.
 XX PT New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX PS Disclosure: Fig 2B; 25pp; English.
 XX CC The present sequence represents the light chain variable region of the
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.
 CC The specification describes a LM609 grafted antibody which has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.
 XX SQ Sequence 107 AA;
 Query Match 100.0%; Score 56; DB 22; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QASQISNHLH 11
 Db 24 qasqsisnhlh 34
 RESULT 9
 AAB61360
 ID AAB61360 standard; protein; 107 AA.
 XX AC AAB61360;
 XX PD 03-APR-2001 (first entry)
 XX DE Vitaxin light chain variable region protein.
 XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 XX inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI: 2001-050110/06.
 XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX SQ Sequence 107 AA;
 Query Match 100.0%; Score 56; DB 22; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QASQISNHLH 11
 Db 24 qasqsisnhlh 34
 RESULT 10
 AAB61362
 ID AAB61362 standard; protein; 107 AA.
 XX AC AAB61362;
 XX DT 03-APR-2001 (first entry)
 XX DE Antibody LM609 light chain variable region protein.
 XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 XX inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI: 2001-050110/06.
 XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI: 2001-050110/06.
 XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX PS Disclosure: Fig 1; 132pp; English.
 XX CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX SQ Sequence 107 AA;
 Query Match 100.0%; Score 56; DB 22; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QASQISNHLH 11
 Db 24 qasqsisnhlh 34
 RESULT 10
 AAB61362
 ID AAB61362 standard; protein; 107 AA.
 XX AC AAB61362;
 XX DT 03-APR-2001 (first entry)
 XX DE Antibody LM609 light chain variable region protein.
 XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 XX inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI: 2001-050110/06.
 XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX PS Disclosure; Fig 2; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies

CC CC exhibiting selective binding affinity to alphavbeta₃ integrin or

CC CC their functional fragments. The antibodies or their functional

CC CC fragments can be used in the diagnosis and treatment of

CC CC alphavbeta₃-mediated diseases such as angiogenesis, inflammatory

CC CC diseases (such as psoriasis and chronic articular rheumatism),

CC CC disorders associated with inappropriate or inopportune invasion of

CC CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC CC diseases (such as macular degeneration), restenosis and

XX CC osteoporosis.

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 56; DB 22; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.0058;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11

Db 24 qasqsisnhl 34

|||||

RESULT 11

AA61364

ID AAB61364 standard; protein; 107 AA.

AC AAB61364;

XX 03-APR-2001 (first entry)

XX DE Light chain variable region of LM609.

XX KW LM609; grafted antibody; alphavbeta₃ integrin; angiogenesis;

XX KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT PT osteoporosis -

XX PS Disclosure; Fig 7; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies

CC CC exhibiting selective binding affinity to alphavbeta₃ integrin or

CC CC their functional fragments. The antibodies or their functional

CC CC fragments can be used in the diagnosis and treatment of

CC CC alphavbeta₃-mediated diseases such as angiogenesis, inflammatory

CC CC diseases (such as psoriasis and chronic articular rheumatism),

CC CC disorders associated with inappropriate or inopportune invasion of

CC CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC CC diseases (such as macular degeneration), restenosis and

XX CC osteoporosis.

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 56; DB 22; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.0058;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11

Db 24 qasqsisnhl 34

|||||

RESULT 12

AAW87456

ID AAW87456 standard; Protein; 105 AA.

XX AC AAW87456;

XX DT 15-MAR-1999 (first entry)

XX DE Jk gene product.

XX KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;

XX KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

XX KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;

XX KW angiogenesis; diabetic retinopathy; inflammation;

XX KW macular degeneration; osteoporosis; Paget's disease;

XX KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;

XX KW DL2HZREI; Jk protein.

XX OS Mus sp.

XX PN WO9840488-A1.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US04987.

XX PR 12-MAR-1997; 97US-0039609.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Johanson KO, Jonak ZL, Taylor AH;

XX DR WPI; 1999-034590/03.

XX DR N-PSDB; AAV71803.

XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for

PT PT immunotherapeutic treatment of e.g. diabetic retinopathy,

PT PT inflammatory disorders, atherosclerosis, restenosis, cancers or

PT PT osteoporosis

XX PS Example 14; Page 66; 97pp; English.

XX CC This polypeptide is encoded by a Jk synthetic gene segment (see

CC CC AAV71803). It was utilising in novel DL2HZREI humanised light chain

CC CC variable region (see AAW87456), which comprises a human REI framework

CC CC and complementarity determining regions from the anti-human alpha-v

CC CC beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12

CC CC antibodies can be used for passive immunotherapy of disorders

CC CC mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis

CC CC and angiogenic associated diseases.

XX SQ Sequence 105 AA;

Query Match 92.9%; Score 52; DB 20; Length 105;

Best Local Similarity 90.9%; Pred. No. 0.031;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11

Db 24 rasqsishlh 34
:|||||

RESULT 13

AAW87458
ID AAW87458 standard; Protein; 105 AA.

XX
AC AAW87458;

XX
DT 15-MAR-1999 (first entry)

XX
DE Humanised anti-alpha-v beta-3 MAB D12HZLCREI VL.

XX
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12HZLCREI.

XX
OS Homo sapiens.

OS Synthetic.

XX
PN WO9840488-A1.

XX
PD 17-SEP-1998.

XX
PF 12-MAR-1998; 98WO-US04987.

XX
PR 12-MAR-1997; 97US-0039609.

XX
PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
PI Johanson KO, Jonak ZL, Taylor AH;

XX
DR WPI; 1999-034590/03.

XX
DR N-PSDB; AAV71805.

XX
PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis

XX
PS Example 14; Page 68-69; 97pp; English.

XX
CC This is the amino acid sequence of the light chain variable region
CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
CC monoclonal antibody D12HZLCREI. It is based on a synthetic
CC humanised kappa chain based on a modified human REI kappa
CC framework and complementarity determining regions from the murine
CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC D12 (see AAW84094). Humanised antibodies of the invention can be used
CC for passive immunotherapy of a disorder mediated by the alpha-v
CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
CC related disorders, such as angiogenesis associated with diabetic
CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
CC disorders, macular degeneration, rheumatoid arthritis and cancer.
CC e.g. solid tumour metastasis, and diseases where bone resorption is
CC associated with pathology such as osteoporosis, hyperparathyroidism,
CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
CC produced by bone metastasis, bone loss due to immobilisation or sex
CC hormone deficiency. They can also be used for targeted drug
CC therapy, and for detection and diagnosis.

XX
SQ Sequence 105 AA;

Query Match 92.9%; Score 52; DB 20; Length 105;
Best Local Similarity 90.9%; Pred. No. 0.031;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
Db :|||||
24 rasqsishlh 34

RESULT 14

AAW84098

ID AAW84098 standard; Protein; 107 AA.

XX
AC AAW84098;

XX
DT 15-MAR-1999 (first entry)

XX
DE Humanised anti-alpha-v beta-3 MAB D12HZHC 1-0 VL.

XX
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12HZHC-10.

XX
OS Homo sapiens.

OS Synthetic.

XX
FH Key Location/Qualifiers
FT Region 24..34
FT /label= CDR1

FT Region 50..56
FT /label= CDR2

FT Region 89..97
FT /label= CDR3

XX
PN WO9840488-A1.

XX
PD 17-SEP-1998.

XX
PF 12-MAR-1998; 98WO-US04987.

XX
PR 12-MAR-1997; 97US-0039609.

XX
PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
PI Johanson KO, Jonak ZL, Taylor AH;

XX
DR WPI; 1999-034590/03.

XX
DR N-PSDB; AAV71800.

XX
PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis

XX
PS Claim 2; Page 61-62; 97pp; English.

XX
CC This is the amino acid sequence of the light chain variable region
CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
CC monoclonal antibody D12HZHC 1-0. It is based on the VL sequence
CC (see AAW84096) of human Kabat subgroup III kappa chain, with
CC complementarity determining regions (CDRs) from the murine
CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC D12 (see AAW84093). 3 Murine framework residues (1, 49 and 60)
CC are retained. The humanised light chain can be expressed in host
CC cells using nucleic acid molecules (see AAV71800) of the invention.
CC Humanised D12 VH is also provided (see AAW84097). The humanised
CC antibodies can be used for passive immunotherapy of disorders
CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
CC angiogenic-related disorders, such as angiogenesis associated
CC with diabetic retinopathy, atherosclerosis and restenosis, chronic
CC inflammatory disorders, macular degeneration, rheumatoid arthritis
CC and cancer, e.g. solid tumour metastasis, and diseases where bone
CC resorption is associated with pathology such as osteoporosis,

CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
 CC osteolytic lesions produced by bone metastasis, bone loss due to
 CC immobilisation or sex hormone deficiency. They can also be used for
 CC targeted drug therapy, and for detection and diagnosis.

SQ Sequence 107 AA;

Query Match 92.9%; Score 52; DB 20; Length 107;
 Best Local Similarity 90.9%; Pred. No. 0.032;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11
 :|||||
 Db 24 rasqsisnhlh 34

RESULT 15

AAW84094
 ID AAW84094 standard; Protein: 108 AA.

XX AC AAW84094;

XX DT 15-MAR-1999 (first entry)

XX DE Murine vitronectin alpha-v beta-3 receptor MAB VL region.

XX KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

XX OS Mus sp.

Key	Location/Qualifiers
Region	24..34
FT	/label= CDR1
FT	50..56
FT	/label= CDR2
FT	89..97
FT	/label= CDR3

XX WO9840488-A1.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US04987.

XX PR 12-MAR-1997; 97US-0039609.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Johanson KO, Jonak ZL, Taylor AH;

XX DR WPI: 1999-034590/03.

XX N-PSDB: AAV71798.

XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

XX PS Example 13; Page 59-60; 97pp; English.

XX This is the amino acid sequence of the light chain variable region
 CC (VL) of the anti-human alpha-v beta-3 vitronectin receptor murine
 CC monoclonal antibody D12, as deduced from isolated cDNA (see
 CC AAV71798). D12 VH (see AAW84093) and VL show sequence similarity to
 CC Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see
 CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see
 CC AAW84098) were constructed by combining the framework regions of the

CC human V region consensus sequences with complementarity determining
 CC regions of D12 (keeping some preferred murine framework residues).
 CC The humanised antibodies are specifically reactive with the human
 CC alpha-v beta-3 protein receptor and capable of neutralising the
 CC receptor. They can be used for passive immunotherapy of a disorder
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
 CC disorders or angiogenic-related disorders, such as angiogenesis
 CC associated with diabetic retinopathy, atherosclerosis and
 CC restenosis, chronic inflammatory disorders, macular degeneration,
 CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
 CC diseases where bone resorption is associated with pathology such as
 CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
 CC of malignancy, osteolytic lesions produced by bone metastasis, bone
 CC loss due to immobilisation or sex hormone deficiency. They can also
 CC be used for targeted drug therapy, and for detection and diagnosis.

XX SQ Sequence 108 AA;

Query Match 92.9%; Score 52; DB 20; Length 108;
 Best Local Similarity 90.9%; Pred. No. 0.032;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11

Db 24 rasqsisnhlh 34

Search completed: August 19, 2002, 06:39:14
 Job time: 1475 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:42 ; Search time 61.75 Seconds
(without alignments)
4.351 Million cell updates/sec

Title: US-09-339-922A-108

Perfect score: 56

Sequence: 1 QASQISNHLH 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	45	80.4	100	1	US-08-436-463-19	Sequence 19, Appl
2	45	80.4	103	1	US-08-436-463-21	Sequence 21, Appl
3	45	80.4	107	1	US-07-634-278-62	Sequence 62, Appl
4	45	80.4	107	1	US-07-634-278-63	Sequence 63, Appl
5	45	80.4	107	1	US-07-634-278-87	Sequence 87, Appl
6	45	80.4	107	1	US-08-477-728-62	Sequence 62, Appl
7	45	80.4	107	1	US-08-477-728-63	Sequence 63, Appl
8	45	80.4	107	1	US-08-477-728-87	Sequence 87, Appl
9	45	80.4	107	1	US-08-276-852-108	Sequence 108, App
10	45	80.4	107	1	US-08-474-040-62	Sequence 62, Appl
11	45	80.4	107	1	US-08-474-040-63	Sequence 63, Appl
12	45	80.4	107	1	US-08-474-040-87	Sequence 87, Appl
13	45	80.4	107	1	US-08-487-200-62	Sequence 62, Appl
14	45	80.4	107	1	US-08-487-200-63	Sequence 63, Appl
15	45	80.4	107	1	US-08-487-200-87	Sequence 87, Appl
16	45	80.4	107	1	US-08-899-575-108	Sequence 108, App
17	45	80.4	107	1	US-08-899-575-108	Sequence 108, App
18	45	80.4	107	4	US-08-484-537-62	Sequence 62, Appl
19	45	80.4	107	4	US-08-484-537-63	Sequence 63, Appl
20	45	80.4	107	4	US-08-484-537-87	Sequence 87, Appl
21	45	80.4	107	5	PTC-US95-08743-108	Sequence 108, App
22	45	80.4	127	1	US-07-634-278-83	Sequence 83, Appl
23	45	80.4	127	1	US-08-477-728-83	Sequence 83, Appl
24	45	80.4	127	1	US-08-474-040-83	Sequence 83, Appl
25	45	80.4	127	1	US-08-487-200-83	Sequence 83, Appl
26	45	80.4	127	1	US-08-436-463-4	Sequence 4, Appl
27	45	80.4	127	1	US-08-436-463-18	Sequence 18, Appl

28	45	80.4	127	4	US-08-484-537-83	Sequence 83, Appl
29	41	73.2	11	1	US-07-942-245-497	Sequence 497, App
30	41	73.2	31	4	US-08-525-539A-3	Sequence 3, Appli
31	41	73.2	96	2	US-08-737-560A-9	Sequence 9, Appli
32	41	73.2	107	1	US-08-436-463-20	Sequence 20, Appl
33	41	73.2	107	1	US-08-107-669D-1	Sequence 1, Appli
34	41	73.2	107	1	US-08-472-788A-1	Sequence 1, Appli
35	41	73.2	107	2	US-08-477-531B-1	Sequence 1, Appli
36	41	73.2	107	2	US-08-082-842A-1	Sequence 1, Appli
37	41	73.2	107	4	US-09-247-352-8	Sequence 8, Appli
38	41	73.2	107	4	US-09-247-352-12	Sequence 12, Appl
39	41	73.2	108	2	US-08-378-939-20	Sequence 20, Appl
40	41	73.2	108	4	US-09-247-352-1	Sequence 1, Appli
41	41	73.2	109	1	US-07-942-245-4	Sequence 4, Appli
42	41	73.2	214	4	US-09-247-352-4	Sequence 4, Appli
43	40	71.4	108	4	US-09-157-370-4	Sequence 4, Appli
44	39	69.6	76	4	US-08-851-362D-20	Sequence 20, Appl
45	39	69.6	105	4	US-08-851-362D-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-463-19

Query Match 80.4%; Score 45; DB 1; Length 100;
Best Local Similarity 81.8%; Pred. No. 0.35;

```
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 RASQISNNLH 34

RESULT 2
US-08-436-463-21
; Sequence 21, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-PELINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-463-21

Query Match 80.4%; Score 45; DB 1; Length 103;
Best Local Similarity 81.8%; Pred. No. 0.36;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 22 RASQISNNLH 32

RESULT 3
US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 RASQISNNLH 34

RESULT 4
US-07-634-278-63
; Sequence 63, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 RASQISNNLH 34

RESULT 5
US-07-634-278-64
; Sequence 64, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-634-278-63

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
DB 24 RASQISNHLH 34

RESULT 5
US-07-634-278-87
; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278

; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-634-278-87

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
DB 24 RASQISNHLH 34

RESULT 6
US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQTSNHLH 11
Db 24 RASQTSNHLH 34

RESULT 7

US-08-477-728-63
; Sequence 63, Application US/08477728
; Patent No. 5385089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQTSNHLH 11
Db 24 RASQTSNHLH 34

RESULT 8

US-08-477-728-87
; Sequence 87, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSI5NHLH 11
:|||||:|
Db 24 RASQSI5NHLH 34

RESULT 9

US-08-276-852-108
; Sequence 108, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SC1452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-276-852-108

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSI5NHLH 11
|||||
Db 22 QASQSI5NHLH 32

RESULT 10

US-08-474-040-62
; Sequence 62, Application US/08474040

; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-62

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSI5NHLH 11
:|||||:|
Db 24 RASQSI5NHLH 34

RESULT 11

US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-63

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 RASQISNHLH 34

RESULT 12
US-08-474-040-87
Sequence 87, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto

STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-87

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 RASQISNHLH 34

RESULT 13
US-08-487-200-62
Sequence 62, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-62

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNHLH 11
Db 24 RASQSISNHLH 34

RESULT 14
US-08-487-200-63
Sequence 63, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-63

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNHLH 11
Db 24 RASQSISNHLH 34

RESULT 15
US-08-487-200-87
Sequence 87, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-87

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 RASQISNHLH 34

Search completed: August 19, 2002, 06:34:42
Job time: 1203 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:07 ; Search time 78.53 Seconds
(without alignments)
13.460 Million cell updates/sec

Title: US-09-339-922a-110
Perfect score: 54
Sequence: 1 QASQSISNFLH 11
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	87.0	106	2 PL0267	Ig kappa chain V r
2	47	87.0	123	2 S35479	Ig kappa chain pre
3	44	81.5	122	2 S40370	Ig kappa chain - h
4	43	79.6	107	2 S32188	Ig kappa chain V r
5	42	77.8	96	2 G33730	Ig kappa chain V r
6	42	77.8	103	2 S19975	Ig kappa chain V r
7	41	75.9	95	2 PH0867	Ig kappa chain V r
8	41	75.9	102	2 S26346	Ig kappa chain V r
9	41	75.9	104	2 B43413	Ig kappa chain V r
10	41	75.9	107	2 B45722	anti-glycoprotein
11	41	75.9	107	2 A45722	anti-glycoprotein
12	41	75.9	138	2 A26471	Ig kappa chain pre
13	40	74.1	62	2 S42365	Ig kappa chain V r
14	40	74.1	87	2 I52592	Ig kappa chain V r
15	40	74.1	88	2 S34088	Ig kappa chain V r
16	40	74.1	88	2 S34087	Ig kappa chain V r
17	40	74.1	95	2 PH0862	Ig kappa chain V r
18	40	74.1	107	2 C45722	anti-glycoprotein
19	40	74.1	108	2 S19674	Ig kappa chain V r
20	40	74.1	110	2 S44118	Ig kappa chain V-J
21	40	74.1	117	2 S43528	Ig kappa chain V r
22	40	74.1	117	2 S42263	Ig kappa chain V r
23	40	74.1	127	2 S40367	Ig kappa chain V-J
24	40	74.1	129	1 K1HUWK	Ig kappa chain pre
25	40	74.1	129	2 S52789	Ig kappa chain V r
26	38	70.4	92	1 KVRB38	Ig kappa chain V r
27	38	70.4	106	2 PC4282	Ig kappa chain (an
28	38	70.4	162	2 T18855	hypothetical prote
29	37	68.5	103	2 S44121	Ig kappa chain V-J

30 37 68.5 117 1 K4RBF2 Ig kappa chain pre
31 37 68.5 122 2 S40314 Ig kappa chain - h
32 37 68.5 334 2 B72033 conserved hypothet
33 37 68.5 334 2 S86593 C1566 hypothetical
34 36 66.7 93 2 S38564 Ig kappa chain V r
35 36 66.7 107 2 B28044 Ig kappa chain V r
36 36 66.7 107 2 A28044 Ig kappa chain V r
37 36 66.7 107 2 D48677 Ig kappa chain V-J
38 36 66.7 107 2 B49026 Ig kappa chain (cl
39 36 66.7 107 2 S69901 Ig kappa chain (cl
40 36 66.7 107 2 S69906 Ig kappa chain V r
41 36 66.7 108 1 KVMSAR Ig kappa chain V r
42 36 66.7 108 2 C26405 Ig kappa chain V r
43 36 66.7 108 2 B30551 Ig kappa chain V r
44 36 66.7 108 2 PL0282 Ig kappa chain V r
45 36 66.7 108 2 S38862 Ig kappa chain V r

ALIGNMENTS

RESULT 1

PL0267
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0267
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J.; Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0267
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 87.0%; Score 47; DB 2; Length 106;
Best Local Similarity 81.8%; Pred. No. 0.025;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNFLH 11
Db 24 RASQSISNLYH 34
:|||||:|

RESULT 2

S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from
A:Reference number: S35479; MUID:92375706
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 123;
Best Local Similarity 81.8%; Pred. No. 0.03;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|||||:|
DB 36 RASQISNYLH 46

RESULT 3
S40370
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40370
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:9408091
A:Accession: S40370
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <KLE>
A:Cross-references: EMBL:X72480; NID:g441428; PIDN:CRA51148.1; PID:g441429
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 44; DB 2; Length 122;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|||||:|
DB 38 RASQISNYLH 48

RESULT 4
S32188
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32188
R:Izui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32188
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <IZU>
A:Cross-references: EMBL:X70090; NID:g288253; PIDN:CRA49695.1; PID:g288254
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 43; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|||||:|
DB 24 RASQISNYLH 34

RESULT 5
S40370
Ig kappa chain V region (23.32) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: G33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u
A:Reference number: A33730; MUID:89367325
A:Accession: G33730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <LAW>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 42; DB 2; Length 96;
Best Local Similarity 72.7%; Pred. No. 0.24;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|||||:|
DB 24 RASQISNYLH 34

RESULT 6
S1975
Ig kappa chain V region (M-T408) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S1975
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S1975
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <WEI>
A:Cross-references: EMBL:X65097; NID:g52296; PIDN:CRA46225.1; PID:g52297
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-85/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 42; DB 2; Length 103;
Best Local Similarity 72.7%; Pred. No. 0.26;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|||||:|
DB 19 RASQISNYLH 29

RESULT 7
PH0867
Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0867
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Grosse, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
A:Reference number: PH0862; MUID:92078875
A:Accession: PH0867
A:Molecule type: DNA
A:Residues: 1-95 <MAN>
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-95/Region: complementarity-determining 3

Query Match 75.9%; Score 41; DB 2; Length 95;
 Best Local Similarity 72.7%; Pred. No. 0.38;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNFLH 11
 Db 24 RASQISGFLH 34

RESULT 8

S26346
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26346
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26346
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-102 <STA>
 A:Cross-references: EMBL:X59211; NID:952338; PIDN:CAA41921.1; PID:91334075
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 41; DB 2; Length 102;
 Best Local Similarity 81.8%; Pred. No. 0.41;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNFLH 11
 Db 22 RASQISNNLH 32

RESULT 9

B43413
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B43413
 R:Tomyana, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
 J. Biol. Chem. 267, 18085-18092, 1992
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specif
 A:Reference number: A43413; MUID:92388177
 A:Accession: B43413
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-104 <TOM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 41; DB 2; Length 104;
 Best Local Similarity 81.8%; Pred. No. 0.42;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNFLH 11
 Db 21 RASQISNNLH 31

RESULT 10

B45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: B45722

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 41; DB 2; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.43;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNFLH 11
 Db 24 RASQISNNLH 34

RESULT 11

A45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: A45722

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 41; DB 2; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.43;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNFLH 11
 Db 24 RASQISNNLH 34

RESULT 12

A26471
 Ig kappa chain precursor V region (MAK33) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
 C:Accession: A26471
 R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987
 A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
 A:Reference number: A91572; MUID:87248058
 A:Accession: A26471
 A:Molecule type: mRNA
 A:Residues: 1-138 <BUC>

A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 75.9%; Score 41; DB 2; Length 138;
Best Local Similarity 81.8%; Pred. No. 0.57;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|||||:|
DB 44 RASQISNNLH 54

RESULT 13

S42265
Ig kappa chain V region (018) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42265
R:Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
J. Immunol. 147, 4007-4013, 1991
A:Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
A:Reference number: S42263; MUID:92043792
A:Accession: S42265

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <SCO>
A:Cross-references: EMBL:M64856
C:Genetics:

A:Introns: 19/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.1%; Score 40; DB 2; Length 62;
Best Local Similarity 72.7%; Pred. No. 0.38;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|||||:|
DB 24 QASQDISNYLN 34

RESULT 14

I52592
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I52592
R:Wagner, S.D.; Martinelli, V.; Luzzatto, L.
Blood 83, 3647-3653, 1994
A:Title: Similar patterns of V kappa gene usage but different degrees of somatic mutatio
A:Reference number: I52592; MUID:94264318
A:Accession: I52592
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-87 <RES>
A:Cross-references: GB:S71057; NID:g547053; PIDN:AAB30971.1; PID:g547054
C:Genetics:
A:Gene: IgKV
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 87;
Best Local Similarity 72.7%; Pred. No. 0.55;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|||||:|

Db 17 QASQDISNYLN 27

RESULT 15

S34088
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34088
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distrib
A:Reference number: S34076; MUID:93170387
A:Accession: S34088

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <WAG>
A:Cross-references: EMBL:X67172
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 88;
Best Local Similarity 72.7%; Pred. No. 0.56;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|||||:|
DB 17 QASQDISNYLN 27

Search completed: August 19, 2002, 06:36:07
Job time: 1288 sec

{

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:11 ; Search time 51.81 Seconds
(without alignments)
8.221 Million cell updates/sec

Title: US-09-339-922A-110
Perfect score: 54
Sequence: 1 QASQSISNLFH 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	74.1	129	1 KVIW_HUMAN	P04431 homo sapien
2	38	70.4	92	1 KV09_RABIT	P01690 oryctolagus
3	37	68.5	117	1 KV10_RABIT	P01691 oryctolagus
4	36	66.7	108	1 KV5K_MOUSE	P01644 mus musculus
5	36	66.7	108	1 KV5L_MOUSE	P01645 mus musculus
6	36	66.7	108	1 KV5M_MOUSE	P01646 mus musculus
7	36	66.7	2345	1 COA1_RAT	P11497 rattus norv
8	36	66.7	2346	1 COA1_BOVIN	Q9TIS3 bos taurus
9	36	66.7	2346	1 COA1_SHEEP	Q28559 ovis aries
10	35	64.8	108	1 KV1B_HUMAN	P01594 homo sapien
11	35	64.8	108	1 KV5U_MOUSE	P04946 mus musculus
12	35	64.8	2324	1 COAC_CHICK	P11029 gallus gall
13	35	64.8	2346	1 COAL_HUMAN	Q13085 homo sapien
14	34	63.0	108	1 KV1H_HUMAN	P01600 homo sapien
15	34	63.0	108	1 KV1P_HUMAN	P01608 homo sapien
16	34	63.0	108	1 KV5J_MOUSE	P01643 mus musculus
17	34	63.0	187	1 PABA_ECOLI	P09303 escherichia
18	34	63.0	3083	1 POLG_ZYMRV	Q89330 z genome po
19	33	61.1	108	1 KV5N_MOUSE	P01647 mus musculus
20	33	61.1	108	1 KV5O_MOUSE	P01648 mus musculus
21	33	61.1	115	1 KV3J_HUMAN	P04433 homo sapien
22	33	61.1	329	1 YDA8_SCHPO	Q10350 schizosacch
23	33	61.1	349	1 PERM_HAEIN	P43969 haemophilus
24	33	61.1	379	1 FLIP_BUCAL	P57184 buchnera ap
25	32	59.3	108	1 KV1A_HUMAN	P01593 homo sapien
26	32	59.3	109	1 KV3F_HUMAN	P01624 homo sapien
27	32	59.3	117	1 KV1J_HUMAN	P01602 homo sapien
28	32	59.3	129	1 KV3H_HUMAN	P04207 homo sapien
29	32	59.3	412	1 YL57_YEAST	Q12358 saccharomyc
30	32	59.3	459	1 NUAM_CHICK	P18939 gallus gall
31	32	59.3	485	1 Y4E_CAEEL	Q18411 caenorhabd
32	32	59.3	509	1 CPT7_BOVIN	P05185 bos taurus
33	32	59.3	523	1 C9B1_GLYEC	P93149 glycyrrhiza

ALIGNMENTS

```

RESULT 1
KVIW_HUMAN
ID      KVIW_HUMAN      STANDARD;      PRT;      129 AA.
AC      P04431;
DT      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-I region Walker precursor.
DE      Homo sapiens (Human).
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=85014148; PubMed=6091049;
RA      Klobbeck H.G., Combrinato G., Zachau H.G.;
RT      "Immunoglobulin genes of the kappa light chain type from two human
RT      lymphoid cell lines are closely related.";
RL      Nucleic Acids Res. 12:6995-7006(1984)
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed, usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; X00965; CAA25477.1; ALT_TERM.
CC      PIR; A01883; KIHUWK.
CC      HSSP; P01607; IREI.
CC      InterPro; IPR003006; Ig_MHC.
CC      InterPro; IPR003596; Ig_V.
CC      Pfam; PF00047; Ig; 1.
CC      SMART; SM00406; IGv; 1.
CC      Immunoglobulin V region; Signal.
CC      SIGNAL      1      22
CC      CHAIN      23      129      IG KAPPA CHAIN V-I REGION WALKER.
CC      DOMAIN      23      45      FRAMEWORK-1.
CC      DOMAIN      46      56      COMPLEMENTARITY-DETERMINING-1.
CC      DOMAIN      57      71      FRAMEWORK-2.
CC      DOMAIN      72      78      COMPLEMENTARITY-DETERMINING-2.
CC      DOMAIN      79      110      FRAMEWORK-3.
CC      DOMAIN      111      119      COMPLEMENTARITY-DETERMINING-3.
CC      DOMAIN      120      129      FRAMEWORK-4.
CC      DISULFID      45      110      BY SIMILARITY.
CC      NON_TER      129      129
CC      SEQUENCE      129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

```

Query Match 74.1%; Score 40; DB 1; Length 129;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11
:|||||||:

```

Db      46 RASQSISNYLN 56

RESULT 2
KV09_RABIT
ID   KV09_RABIT      STANDARD;          PRT;          92 AA.
AC   P01690;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V region 3381 (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75176905; PubMed=1094456;
RA   Margolies M.N., Cannon L.E. III, Strosberg A.D., Haber E.;
RT   "Diversity of light chain variable region sequences among rabbit
RT   antibodies elicited by the same antigens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).
CC   -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM THE SERUM OF A SINGLE RABBIT.
CC   PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
CC   PIR; A01953; KVR38.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
KW   Immunoglobulin V region.
FT   DOMAIN          1 23
FT   DOMAIN          24 34
FT   DOMAIN          35 49
FT   DOMAIN          50 56
FT   DOMAIN          57 88
FT   DOMAIN          89 >92
FT   NON_TER         92
FT   SEQUENCE        92 AA; 9730 MW; 9A36B15913CB3BEE CRC64;

Query Match      70.4%; Score 38; DB 1; Length 92;
Best Local Similarity 80.0%; Pred. No. 0.45;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QASQISNPL 10
Db      24 QASESISNWL 33

RESULT 3
KV10_RABIT
ID   KV10_RABIT      STANDARD;          PRT;          117 AA.
AC   P01691;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V region 12f2 precursor (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83273646; PubMed=6410392;
RA   Dreher K.L., Emorine L., Kindt T.J., Max E.E.;
RT   "CDNA clone encoding a complete rabbit immunoglobulin kappa light
RT   chain of b4 allotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4489-4493(1983).
CC   -1- MISCELLANEOUS: THIS CLONE WAS DERIVED FROM THE RABBIT-MOUSE
CC   HYBRIDOMA 12f2; THE CHAIN PRODUCED IS A MONOCLONAL ANTIBODY
CC   AGAINST STREPTOCOCCAL GROUP C VACCINE.
CC   -----
CC   { This SWISS-PROT entry is copyright. It is produced through a collaboration

```

```

CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; K01358; AAB59259.1; ALT_TERM.
DR   PIR; A01954; K4RBF2.
DR   HSSP; P01789; IMCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
KW   Immunoglobulin V region; Monoclonal antibody; Hybridoma; Signal.
FT   NON_TER         1 1
FT   SIGNAL          <1 6
FT   CHAIN           7 117
FT   DOMAIN          7 29
FT   DOMAIN          30 40
FT   DOMAIN          41 55
FT   DOMAIN          56 62
FT   DOMAIN          63 94
FT   DOMAIN          95 106
FT   DOMAIN          107 116
FT   DISULFID        29 86
FT   NON_TER         117 117
SQ   SEQUENCE        117 AA; 12288 MW; E24A7582389E4439 CRC64;

Query Match      68.5%; Score 37; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.95;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 QASQISNPL 10
Db      30 QASQISISTYL 39

RESULT 4
KV5K_MOUSE
ID   KV5K_MOUSE      STANDARD;          PRT;          108 AA.
AC   P01644;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region Hp R16.7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsenate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
KW   Immunoglobulin V region; Antiarsenate antibody.
FT   DOMAIN          1 23
FT   DOMAIN          24 34
FT   DOMAIN          35 49
FT   DOMAIN          50 56
FT   DOMAIN          57 88
FT   DOMAIN          89 97

```

FT DOMAIN 98 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 108;
 Best Local Similarity 63.6%; Pred. No. 1.4;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLH 11
 :||| |||:|:
 Db 24 RASQDISNYLN 34

RESULT 5
 KV5L_MOUSE STANDARD; PRT; 108 AA.
 AC P01645;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region HP 93G7.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsonate antibodies differing
 with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -I- MISCELLANEOUS; ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVMASR.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Antiarsonate antibody.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 66.7%; Score 36; DB 1; Length 108;
 Best Local Similarity 63.6%; Pred. No. 1.4;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLH 11
 :||| |||:|:
 Db 24 RASQDISNYLN 34

RESULT 6
 KV5M_MOUSE STANDARD; PRT; 108 AA.
 AC P01646;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region HP 123E6.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsonate antibodies differing
 with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -I- MISCELLANEOUS; ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVMASR.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Antiarsonate antibody.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 66.7%; Score 36; DB 1; Length 108;
 Best Local Similarity 63.6%; Pred. No. 1.4;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLH 11
 :||| |||:|:
 Db 24 RASQDISNYLN 34

RESULT 7
 COAL_RAT STANDARD; PRT; 2345 AA.
 ID COAL_RAT P11497; P97902;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetyl-CoA carboxylase 1 [EC 6.4.1.2] (ACC-alpha) [Includes: Biotin
 carboxylase (EC 6.3.4.14)].
 GN ACACA OR ACAC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88320328; PubMed=2901088;
 RA Lopez-Casillas F., Bai D.-H., Luo X., Kong I.-S., Hermodson M.A.,
 RA Kim K.-H.;
 RT "Structure of the coding sequence and primary amino acid sequence of
 acetyl-coenzyme A carboxylase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5784-5788(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89264558; PubMed=2566999;
 RA Luo X.N., Park K., Lopez-Casillas F., Kim K.-H.;
 RT "Structural features of the acetyl-CoA carboxylase gene: mechanisms
 for the generation of mRNAs with 5' end heterogeneity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4042-4046(1989).
 RN [3]
 RP SEQUENCE OF 1-33 FROM N.A.
 RX MEDLINE=89214151; PubMed=2565337;
 RA Lopez-Casillas F., Kim K.-H.;

DR PROSITE: PS00188; BIOTIN: 1.
 DR PROSITE: PS00866; CPSASE_1; 1.
 DR PROSITE: PS00867; CPSASE_2; 1.
 KW Fatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme;
 ATP-binding; Phosphorylation.
 FT NP_BIND 315 320 ATP (POTENTIAL).
 FT ACT_SITE 441 441 BY SIMILARITY.
 FT BINDING 786 786 BIOTIN (BY SIMILARITY).
 FT DOMAIN 1959 1988 COENZYME A-BINDING (BY SIMILARITY).
 FT MOD_RES 78 78 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 80 80 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1201 1201 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 2346 AA; 265301 MW; 32886C5D03EEAE0E CRC64;

Query Match 66.7%; Score 36; DB 1; Length 2346;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNFLH 11
 Db 647 SISNFLH 653

RESULT 9
 COAL_SHEEP STANDARD; PRT; 2346 AA.
 ID COAL_SHEEP STANDARD; PRT; 2346 AA.
 AC Q28559;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin
 carboxylase (EC 6.3.4.14)].
 GN ACACA OR ACAC.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FINN-DORSET; TISSUE=Adipose tissue;
 RX MEDLINE=95197015; PubMed=7890176;
 RA Barber M.C., Travers M.T.;
 RT "Cloning and characterisation of multiple acetyl-CoA carboxylase
 transcripts in ovine adipose tissue";
 RL Gene 154:271-275(1995).
 CC -!- FUNCTION: CATALYZES THE RATE-LIMITING REACTION IN THE BIOGENESIS
 OF LONG-CHAIN FATTY ACIDS. THIS PROTEIN CARRIES THREE FUNCTIONS:
 BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND
 CARBOXYLTRANSFERASE.
 CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
 + malonyl-CoA.
 CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
 = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
 CC -!- COFACTOR: BIOTIN.
 CC -!- ENZYME REGULATION: BY PHOSPHORYLATION (BY SIMILARITY).
 CC -!- PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID
 SYNTHESIS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: PARTIAL TO CARBAMOYL PHOSPHATE SYNTHETASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X80045; CAA56352.1; -.
 DR HSP: P24182; IDV1.
 DR InterPro: IPR001882; Biotin.

DR InterPro: IPR000089; Biotin_lipoyl.
 DR InterPro: IPR000901; CPSase.
 DR InterPro: IPR000022; Carboxyl_trans.
 DR Pfam: PF02785; Biotin_carb_C; 1.
 DR Pfam: PF00364; Biotin_lipoyl; 1.
 DR Pfam: PF01039; Carboxyl_trans; 1.
 DR Pfam: PF00289; CPSase_L_chain; 1.
 DR Pfam: PF02786; CPSase_L_D2; 1.
 DR PROSITE: PS00188; BIOTIN; 1.
 DR PROSITE: PS00866; CPSASE_1; 1.
 DR PROSITE: PS00867; CPSASE_2; 1.
 KW Fatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme;
 ATP-binding; Phosphorylation.
 FT NP_BIND 315 320 ATP (POTENTIAL).
 FT ACT_SITE 441 441 BY SIMILARITY.
 FT BINDING 786 786 BIOTIN (BY SIMILARITY).
 FT DOMAIN 1959 1988 COENZYME A-BINDING (BY SIMILARITY).
 FT MOD_RES 78 78 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 80 80 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1201 1201 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 2346 AA; 265249 MW; BCA010ADF6CD24EF CRC64;

Query Match 66.7%; Score 36; DB 1; Length 2346;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNFLH 11
 Db 647 SISNFLH 653

RESULT 10
 KV1B_HUMAN STANDARD; PRT; 108 AA.
 ID KV1B_HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 protein Au).";
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Feilhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 Bence-Jones protein Au";
 RT Biophys. Struct. Mech. 1:139-146(1975).
 CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 REGION OF THE KAPPA CHAIN REI.
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR: A01862; KIHU4U.
 DR HSP: P01607; IREI.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW immunoglobulin V region; Bence-Jones protein.
 DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E6F6FB9 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 108;
 Best Local Similarity 63.6%; Pred. No. 2.3;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QASQISNPLH 11
 |||||
 Db 24 QASQDISDYLN 34

RESULT 11
 KV5U_MOUSE
 ID KV5U_MOUSE STANDARD; PRT; 108 AA.
 AC P04946;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region NQ5-89.4.
 DE OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone and its early diversification";
 RL Nature 304:324(1983).
 CC -1- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; K00745; AAA38690.1; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23
 FT DOMAIN 24 34 FRAMEWORK-1.
 FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 50 56 FRAMEWORK-2.
 FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 89 97 FRAMEWORK-3.
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DDD CRC64;

Query Match 64.8%; Score 35; DB 1; Length 108;
 Best Local Similarity 70.0%; Pred. No. 2.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ASQDISNPLH 11
 |||||

Db 25 ASQDISNPLN 34

RESULT 12
 COAC_CHICK STANDARD; PRT; 2324 AA.
 ID COAC_CHICK
 AC P11029;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: Biotin
 DE carboxylase (EC 6.3.4.14)].
 GN ACAC.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=88139305; PubMed=2893793;
 RA Takai T., Yokoyama C., Wada K., Tanabe T.;
 RT "Primary structure of chicken liver acetyl-CoA carboxylase deduced
 RT from cDNA sequence";
 RL J. Biol. Chem. 263:2651-2657(1988).
 RN [2]
 RP SEQUENCE OF 493-820 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=87106011; PubMed=2879745;
 RA Takai T., Wada K., Tanabe T.;
 RT "Primary structure of the biotin-binding site of chicken liver
 RT acetyl-CoA carboxylase";
 RL FEBS Lett. 212:98-102(1987).
 CC -1- FUNCTION: CATALYZES THE RATE-LIMITING REACTION IN THE BIOGENESIS
 CC OF LONG-CHAIN FATTY ACIDS. THIS PROTEIN CARRIES THREE FUNCTIONS:
 CC BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND
 CC CARBOXYLTRANSFERASE.
 CC -1- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
 CC + malonyl-CoA.
 CC -1- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
 CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
 CC -1- COFACTOR: BIOTIN.
 CC -1- ENZYME REGULATION: BY PHOSPHORYLATION.
 CC -1- PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID
 CC SYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: PARTIAL TO CARBAMOYL PHOSPHATE SYNTHETASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J03541; AAA48701.1; -
 CC EMBL; X05019; CAA28675.1; -
 CC PIR; A27903; A27903.
 CC PIR; A29337; A29337.
 CC PIR; A29924; A29924.
 CC HSSP; P24182; 1DVL.
 DR InterPro; IPR001882; Biotin.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR000901; CPSase.
 DR InterPro; IPR000022; Carboxyl_trans.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR Pfam; PF01039; Carboxyl_trans; 1.
 DR Pfam; PF00289; CPSase_L_chain; 1.
 DR Pfam; PF02786; CPSase_L_D2; 1.
 DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS00866; CPSASE_1; 1.
 DR PROSITE; PS00867; CPSASE_2; 1.
 KW Fatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme;
 KW ATP-binding; Phosphorylation.
 FT NP_BIND 315 320 ATP (POTENTIAL).
 FT ACT_SITE 441 441 BY SIMILARITY.
 FT BINDING 786 786 BIOTIN.
 FT MOD_RES 78 78 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 80 80 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1193 1193 PHOSPHORYLATION (BY SIMILARITY).
 FT DOMAIN 1936 1965 COENZYME A-BINDING (BY SIMILARITY).
 SQ SEQUENCE 2324 AA; 262717 MW; 3F1C541F01BBBF6 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 2324;
 Best Local Similarity 85.7%; Pred. No. 73;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNFLH 11
 I:|||||
 Db 647 SVSNFLH 653

RESULT 13
 COAL_HUMAN STANDARD; PRT; 2346 AA.
 AC COAL_HUMAN
 ID Q13085;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin
 carboxylase (EC 6.3.4.14)].
 GN ACACA OR ACAC OR ACC1 OR ACCA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95249602; PubMed=7732023;
 RA Abu-Elheiga L., Jayakumar A., Baldini A., Chirala S.S., Wakil S.J.;
 RT "Human acetyl-CoA carboxylase: characterization, molecular cloning,
 and evidence for two isoforms.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:4011-4015(1995).
 CC -1- FUNCTION: CATALYZES THE RATE-LIMITING REACTION IN THE BIOGENESIS
 OF LONG-CHAIN FATTY ACIDS. THIS PROTEIN CARRIES THREE FUNCTIONS:
 BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND
 CARBOXYLTRANSFERASE.
 CC -1- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
 + malonyl-CoA.
 CC -1- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
 = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
 CC -1- COFACTOR: BIOTIN.
 CC -1- ENZYME REGULATION: BY PHOSPHORYLATION (BY SIMILARITY).
 CC -1- PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID
 SYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENTAL, SKELETAL
 MUSCLE, RENAL, PANCREATIC AND ADIPOSE TISSUES; EXPRESSED AT LOW
 LEVEL IN PULMONARY TISSUE; NOT DETECTED IN THE LIVER.
 CC -1- SIMILARITY: PARTIAL TO CARBAMOYL PHOSPHATE SYNTHETASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U19822; AAC50139.1; -;
 DR HSSP; P24182; 1DV1.

DR MIM; 200350; -;
 DR InterPro; IPR001882; Biotin.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR000901; CPSase.
 DR InterPro; IPR000022; Carboxyl_trans.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR Pfam; PF01039; Carboxyl_trans; 1.
 DR Pfam; PF00289; CPSase_L_chain; 1.
 DR Pfam; PF02786; CPSase_L_D2; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00866; CPSASE_1; 1.
 DR PROSITE; PS00867; CPSASE_2; 1.
 KW Fatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme;
 KW ATP-binding; Phosphorylation.
 FT NP_BIND 315 320 ATP (POTENTIAL).
 FT ACT_SITE 441 441 BY SIMILARITY.
 FT BINDING 786 786 BIOTIN (BY SIMILARITY).
 FT DOMAIN 1959 1988 COENZYME A-BINDING (POTENTIAL).
 FT MOD_RES 78 78 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 80 80 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1201 1201 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 2346 AA; 265038 MW; 9519190D40190D14 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 2346;
 Best Local Similarity 85.7%; Pred. No. 74;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNFLH 11
 I:|||||
 Db 647 SVSNFLH 653

RESULT 14
 KVH_HUMAN STANDARD; PRT; 108 AA.
 ID KVIH_HUMAN
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 subgroups.";
 RT Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01868; KIHUHU.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 98 107 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 108;
 Best Local Similarity 70.0%; Pred. No. 3.7;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLF 10
 DB 24 RASQSISSYL 33

RESULT 15
 KVIP_HUMAN STANDARD; PRT; 108 AA.
 AC PO1608;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=68362076; PubMed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 Cum.)";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RP REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (In) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,
 RL New York (1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01874; K1HURY.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 63.0%; Score 34; DB 1; Length 108;
 Best Local Similarity 72.7%; Pred. No. 3.7;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11
 DB 24 QASQDISIFLN 34

Search completed: August 19, 2002, 06:59:12
 Job time: 1377 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:18 ; Search time 140.4 Seconds
(without alignments)
13.554 Million cell updates/sec

Title: US-09-339-922A-110

Perfect score: 54

Sequence: 1 QASQISINFLH 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	74.1	107	4 Q9UL81	Q9ul81 homo sapien
2	38	70.4	162	5 Q17590	Q17590 caenorhabdi
3	37	68.5	334	16 Q9Z785	Q9Z785 chlamydia p
4	36	66.7	234	11 Q91WF8	Q91wf8 mus musculu
5	36	66.7	256	6 Q06980	Q06980 capra hircu
6	36	66.7	293	10 Q49020	Q49020 gossypium h
7	36	66.7	293	10 Q94JN5	Q94jn5 gossypium h
8	36	66.7	293	10 Q94JN4	Q94jn4 gossypium h
9	36	66.7	307	3 Q59680	Q59680 schizosacch
10	36	66.7	336	10 Q9LM02	Q9lm02 arabidopsis
11	36	66.7	340	2 Q9ZIT2	Q9zit2 escherichia
12	36	66.7	340	2 Q9R9D5	Q9r9d5 escherichia
13	36	66.7	340	2 Q9R9C9	Q9r9c9 escherichia
14	36	66.7	572	16 Q9KSI6	Q9ksl6 vibrio chol
15	36	66.7	573	5 Q95PR8	Q95pr8 leishmania
16	36	66.7	816	5 Q9N9P7	Q9n9p7 leishmania

17	35	64.8	107	4 Q96SA9	Q96sa9 homo sapien
18	35	64.8	108	4 Q9UL77	Q9ul77 homo sapien
19	35	64.8	108	4 Q9UL70	Q9ul70 homo sapien
20	35	64.8	267	13 Q98909	Q98909 gallus gall
21	35	64.8	375	8 Q9TLL0	Q9tll0 nephroselmi
22	35	64.8	395	10 Q9LU60	Q9lu60 arabidopsis
23	35	64.8	698	16 Q92RJ4	Q92rj4 rhizobium m
24	35	64.8	707	2 Q9FSN1	Q9fsn1 rhizobium m
25	35	64.8	1360	2 Q9RFK6	Q9rfk6 stigmatella
26	34	63.0	534	5 Q9XUR9	Q9xur9 caenorhabdi
27	34	63.0	536	16 Q99SK4	Q99sk4 staphylococ
28	34	63.0	592	4 Q9NU33	Q9nu33 homo sapien
29	34	63.0	605	3 Q74207	Q74207 candida alb
30	34	63.0	605	3 Q9UNF6	Q9unf6 candida alb
31	34	63.0	753	13 Q9DE07	Q9de07 gallus gall
32	34	63.0	800	12 Q9WA54	Q9wa54 zucchini ye
33	34	63.0	803	11 Q9DC20	Q9dc20 mus musculu
34	34	63.0	889	3 Q9USQ6	Q9usq6 schizosacch
35	34	63.0	929	5 Q18759	Q18759 caenorhabdi
36	34	63.0	996	5 Q95XN3	Q95xn3 caenorhabdi
37	34	63.0	1416	5 Q9XZ34	Q9xz34 drosophila
38	34	63.0	2553	5 Q22860	Q22860 caenorhabdi
39	34	63.0	3944	5 Q18667	Q18667 caenorhabdi
40	33	61.1	116	4 Q96PF6	Q96pf6 homo sapien
41	33	61.1	184	11 Q9CTM3	Q9ctm3 mus musculu
42	33	61.1	219	4 Q9NT75	Q9nt75 homo sapien
43	33	61.1	292	16 Q97J05	Q97j05 clostridium
44	33	61.1	312	11 Q9DIP6	Q9dip6 mus musculu
45	33	61.1	323	10 Q9AWW7	Q9aww7 oryza sativ

ALIGNMENTS

RESULT 1

Q9UL81 ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -;
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 74.1%; Score 40; DB 4; Length 107;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11

:|||||:

DB 24 RASQISISNYLN 34

```

RESULT 2
ID Q17590 PRELIMINARY; PRT; 162 AA.
AC Q17590;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE C02B4.3 PROTEIN.
GN C02B4.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z50004; CAA90292.1; -.
SQ SEQUENCE 162 AA; 19034 MW; B9731BD4E3A37B18 CRC64;

Query Match 70.4%; Score 38; DB 5; Length 162;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQTSISNFLH 11
:|:|||||
Db 107 SSEDVSNFLH 116

RESULT 3
ID Q92785 PRELIMINARY; PRT; 334 AA.
AC Q92785;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE C5566 HYPOTHETICAL PROTEIN.
GN CPN0821 OR CPJ0821 OR CPJ050.
OS Chlamydia pneumoniae (Chlamydothilla pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydothilla.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=J138;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shirai M.;
RT "Genomic sequence comparison of two unrelated isolates of chlamydia
pneumoniae from Japan and U.S.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AE001662; AAD18959.1; -.
DR EMBL; AB035931; BAA88639.1; -.
DR EMBL; AF002548; BAA99029.1; -.
DR EMBL; AE002261; AAF38823.1; -.
DR TIGR; CP1050; -.
KW Complete proteome.
SQ SEQUENCE 334 AA; 38106 MW; C4D557A9464EAEF9 CRC64;

Query Match 68.5%; Score 37; DB 16; Length 334;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQSISNFLH 11
|||:||||
Db 197 SQSLLNFLH 205

RESULT 4
Q91WF8
ID Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 25.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 66.7%; Score 36; DB 11; Length 234;
Best Local Similarity 63.6%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11
:|||||:|
Db 44 RASQDISNYLN 54

RESULT 5
Q06980
ID Q06980 PRELIMINARY; PRT; 256 AA.
AC Q06980;
DT 01-NOV-1996 (TReMBLrel. 01, Created)

```

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE ACETYL-COA CARBOXYLASE (FRAGMENT).
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY GLAND;
 RX MEDLINE=93278985; PubMed=8099321;
 RA Travers M.T., Barber M.C.;
 RT "Isolation of a goat acetyl-CoA carboxylase complementary DNA and
 RT effect of milking frequency on the expression of the acetyl-CoA
 RT carboxylase and fatty acid synthase genes in goat mammary gland.";
 RL Comp. Biochem. Physiol. 105B:123-128(1993).
 DR EMBL: Z17803; CAA79077.1; -;
 DR InterPro: IPR000901; CPSase.
 DR Pfam: PF02785; Biotin_carb_C; 1.
 DR NON_TER 1
 FT NON_TER 256 256
 SQ SEQUENCE 256 AA; 28454 MW; 3BC340D409C43B9D CRC64;

Query Match 66.7%; Score 36; DB 6; Length 256;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNFLH 11
 DB 125 SISNFLH 131

RESULT 6

ID 049020 PRELIMINARY; PRT; 293 AA.
 AC 049020;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYB-LIKE DNA-BINDING DOMAIN PROTEIN.
 GN CMY-N.
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Gossypium.
 OX NCBI_TaxID=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ACALA SJ-2; TISSUE=OVULE;
 RA Loquerio L.L., Zhang J., Wilkins T.A.;
 RT "Structure and expression of six classes of myb-domain genes in
 RT allotetraploid cotton (Gossypium hirsutum L.).";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF034133; AAC04719.1; -;
 DR HSP; P06876; IMSE.
 DR InterPro: IPR001005; Myb_DNA_bind.
 DR Pfam: PF00249; myb_DNA-binding; 2.
 DR SMART: SM00395; SANT; 2.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00334; MYB_2; 1.
 DR PROSITE: PS50090; MYB_3; 2.
 KW DNA-binding.
 SQ SEQUENCE 293 AA; 33746 MW; 06901890BD174772 CRC64;

Query Match 66.7%; Score 36; DB 10; Length 293;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 QSISNFLH 11
 DB 125 SISNFLH 131

Db 227 QSLSNYLH 234
 RESULT 7
 Q94JN5
 ID 094JN5 PRELIMINARY; PRT; 293 AA.
 AC 094JN5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYB-LIKE TRANSCRIPTION FACTOR MYB 5.
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Gossypium.
 OX NCBI_TaxID=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. LANDRACE 'PALMERI';
 RA Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;
 RT "PCR-mediated recombination in a polyploid plant.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF377316; AAK57698.1; -;
 SQ SEQUENCE 293 AA; 33557 MW; 4F8912A79659F53E CRC64;

Query Match 66.7%; Score 36; DB 10; Length 293;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 QSISNFLH 11
 DB 228 QSLSNYLH 235

RESULT 8

ID 094JN4 PRELIMINARY; PRT; 293 AA.
 AC 094JN4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYB-LIKE TRANSCRIPTION FACTOR MYB 5.
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Gossypium.
 OX NCBI_TaxID=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. LANDRACE 'PALMERI';
 RA Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;
 RT "PCR-mediated recombination in a polyploid plant.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF377317; AAK57699.1; -;
 SQ SEQUENCE 293 AA; 33407 MW; C1F1ADBA5966401A CRC64;

Query Match 66.7%; Score 36; DB 10; Length 293;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 QSISNFLH 11
 DB 228 QSLSNYLH 235

RESULT 9
 O59680 PRELIMINARY; PRT; 307 AA.
 ID O59680
 AC O59680;
 DT 01-JAN-1999 (TREMBLrel. 09, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PROBABLE CYTOCHROME C1, HEME PROTEIN PRECURSOR.
GN SPBC29A3.18.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Rajandream M.A., Barrell B.G., Volckaert G.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS THE HEME-CONTAINING COMPONENT OF THE CYTOCHROME
CC B-C1 COMPLEX, WHICH ACCEPTS ELECTRONS FROM RIESKE PROTEIN AND
CC TRANSFERS ELECTRONS TO CYTOCHROME C IN THE MITOCHONDRIAL
CC RESPIRATORY CHAIN.
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -!- SUBCELLULAR LOCATION: ANCHORED IN THE INNER MITOCHONDRIAL MEMBRANE
CC WITH ITS N-TERMINUS PROTRUDING INTO THE MITOCHONDRIAL
CC INTERMEMBRANE SPACE (BY SIMILARITY).
DR EMBL; AL022299; CAA18395.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR002326; Cyt_C1.
DR Pfam; PF02167; Cytochrome_C1; 1.
DR PRINTS; PR00603; CYTOCHROME_C1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Electron transport; Respiratory chain; Oxidative phosphorylation;
KW Heme; Mitochondrion; Transmembrane; Transit peptide.
FT TRANSIT 1 62 MITOCHDRION (BY SIMILARITY).
FT CHAIN 63 307 PROBABLE CYTOCHROME C1, HEME PROTEIN.
FT BINDING 102 102 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 105 105 HEME (COVALENT) (BY SIMILARITY).
FT METAL 106 106 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 225 225 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT TRANSMEM 273 287 ANCHORS TO THE MEMBRANE (BY SIMILARITY).
SQ SEQUENCE 307 AA; 34340 MW; FAD8B9D3A9A3C1B3 CRC64;

Query Match 66.7%; Score 36; DB 3; Length 307;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11
II:::|||||
DB 246 QAAKDVVNFH 256

RESULT 10
Q9LM02 PRELIMINARY; PRT; 336 AA.
AC Q9LM02;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE SAM:CYCLOARTENOL-C24-METHYLTRANSFERASE (24-STEROL C-METHYLTRANSFERASE)
DE (STEROL METHYLTRANSFERASE SMT1).
GN SMT1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Schaeffer A., Schaller H., Benveniste P.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98069011; PubMed=9405937;

RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
RT Sequence features of the regions of 1,044,062 bp covered by thirteen
RT physically assigned P1 clones.";
RL DNA Res. 4:291-300(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Diener A.C., Li H., Zhou W.-X., Whoriskey W.J., Nes W.D., Fink G.R.;
RT "Effects of reduced C-24 sterol alkylation on plant growth due to a
RT deficiency in sterol methyltransferase 1.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090372; AAF78847.1; -.
DR EMBL; AB006704; BAB08698.1; -.
DR EMBL; AF195648; AAG28462.1; -.
DR InterPro; IPR00051; SAM_bind.
KW Transferase; Methyltransferase.
SQ SEQUENCE 336 AA; 38268 MW; 4649BB3868DE1CE9 CRC64;

Query Match 66.7%; Score 36; DB 10; Length 336;
Best Local Similarity 70.0%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNFL 10
I:::|||||
DB 299 QGSQSVSNFL 308

RESULT 11
Q9ZIT2 PRELIMINARY; PRT; 340 AA.
ID Q9ZIT2
AC Q9ZIT2;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE WAAQ.
GN WAAQ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F653;
RX MEDLINE=99009352; PubMed=9791168;
RA Heinrichs D.E., Yethon J.A., Whitfield C.;
RT "Molecular basis for structural diversity in the core regions of the
RT lipopolysaccharides of Escherichia coli and salmonella enterica.";
RL Mol. Microbiol. 30:221-232(1998).
DR EMBL; AF019745; AAC69668.1; -.
DR InterPro; IPR002201; Glyco_transf_9.
DR Pfam; PF01075; Glyco_transf_9; 1_
SQ SEQUENCE 340 AA; 37934 MW; FF3818CF4A687D24 CRC64;

Query Match 66.7%; Score 36; DB 2; Length 340;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11
I:::|||||
DB 56 KASEKIANFFH 66

RESULT 12
Q9R9D5 PRELIMINARY; PRT; 340 AA.
ID Q9R9D5
AC Q9R9D5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE WAAQ.
GN WAAQ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F470;
RX MEDLINE=99009352; PubMed=9791168;
RA Heinrichs D.E., Yethon J.A., Whitfield C.;
RT "Molecular basis for structural diversity in the core regions of the
lipopolysaccharides of *Escherichia coli* and *salmonella enterica*.";
RL Mol. Microbiol. 30:221-232(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F470;
RX MEDLINE=98434532; PubMed=9756860;
RA Yethon J.A., Heinrichs D.E., Monteiro M.A., Perry M.B., Whitfield C.;
RT "Involvement of waaY, waaQ, and waaP in the modification of
Escherichia coli lipopolysaccharide and their role in the formation of
a stable outer membrane.";
RL J. Biol. Chem. 273:26310-26316(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=F470;
RX MEDLINE=99009057; PubMed=9792656;
RA Heinrichs D.E., Yethon J.A., Amor P.A., Whitfield C.;
RT "The assembly system for the outer core portion of R1- and R4-type
lipopolysaccharides of *Escherichia coli*. The R1 core-specific beta-
glucosyltransferase provides a novel attachment site for O-
polysaccharides.";
RL J. Biol. Chem. 273:29497-29505(1998).
DR EMBL; AF019746; AAC69679.1; -.
DR InterPro; IPR002201; Glyco_transf_9.
DR Pfam; PF01075; Glyco_transf_9; 1.
SQ SEQUENCE 340 AA; 37920 MW; FBA620791EFA61DF CRC64;

Query Match 66.7%; Score 36; DB 2; Length 340;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|: |::| |
Db 56 KASEKIANFFH 66

RESULT 13
ID Q9R9C9 PRELIMINARY; PRT; 340 AA.
AC Q9R9C9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE WAAQ.
GN WAAQ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F2513;
RX MEDLINE=99009352; PubMed=9791168;
RA Heinrichs D.E., Yethon J.A., Whitfield C.;
RT "Molecular basis for structural diversity in the core regions of the
lipopolysaccharides of *Escherichia coli* and *salmonella enterica*.";
RL Mol. Microbiol. 30:221-232(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F2513;
RX MEDLINE=99009057; PubMed=9792656;

RA Heinrichs D.E., Yethon J.A., Amor P.A., Whitfield C.;
RT "The assembly system for the outer core portion of R1- and R4-type
lipopolysaccharides of *Escherichia coli*. The R1 core-specific beta-
glucosyltransferase provides a novel attachment site for O-
polysaccharides.";
RL J. Biol. Chem. 273:29497-29505(1998).
DR EMBL; AF019747; AAC69690.1; -.
DR InterPro; IPR002201; Glyco_transf_9.
DR Pfam; PF01075; Glyco_transf_9; 1.
SQ SEQUENCE 340 AA; 37948 MW; AE76AB57B3A792E4 CRC64;

Query Match 66.7%; Score 36; DB 2; Length 340;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11
:|: |::| |
Db 56 KASEKIANFFH 66

RESULT 14
ID Q9KS16 PRELIMINARY; PRT; 572 AA.
AC Q9KS16;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SENSOR HISTIDINE KINASE/RESPONSE REGULATOR.
GN VC1445.
OS *Vibrio cholerae*.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eise J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
cholerae.";
RL Nature 406:477-483(2000).
CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
CC -!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
DR EMBL; AE004223; AAF94602.1; -.
DR HSP; P06628; 1SRR.
DR TIGR; VC1445; -.
DR InterPro; IPR003594; HATPase_c.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR004359; His_kinA.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00512; signal; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HiskA; 1.
DR SMART; SM00448; REC; 1.
KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
KW Transferase.
SQ SEQUENCE 572 AA; 64561 MW; 8769513FFC8EDED CRC64;

Query Match 66.7%; Score 36; DB 16; Length 572;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 10

Db 207 QANQSKSNFL 216
 !!:!! !!!!!

RESULT 15
 Q95PR8 PRELIMINARY; PRT; 573 AA.
 AC Q95PR8;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE POSSIBLE HYPOTHETICAL 88.2 KDA PROTEIN.
 GN P1046.14.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Aert R., Robben J., Volckaert G., Ivens A.C., Quail M.,
 RA Rajandream M.A., Barrell B.G.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RX MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome."
 RL Genome Res. 8:135-145(1998).
 DR EMBL; AL359683; CAC69084.1; -. 2573CCB7AE6476B6 CRC64;
 SQ SEQUENCE 573 AA; 62853 MW; 2573CCB7AE6476B6 CRC64;

Query Match 66.7%; Score 36; DB 5; Length 573;
 Best Local Similarity 77.8%; Pred. No. 55;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQISNFL 10
 !:!!:!!
 Db 320 ANQSLSNFL 328

Search completed: August 19, 2002, 06:58:19
 Job time: 1409 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:14 ; Search time 180.34 Seconds
(without alignments)
6.775 Million cell updates/sec

Title: US-09-339-922A-110

Perfect score: 54

Sequence: 1 QASQISINFLH 11

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

- 1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	11	22 AAB61403	Enhanced LM609 VH
2	54	100.0	13	19 AAW76031	LM609 grafted anti
3	54	100.0	13	22 AAB61389	Mutant VL CDR1 pep
4	50	92.6	259	21 AAB09775	TMV 30K movement p
5	47	87.0	11	22 AAB61402	Enhanced 6H6LH lig
6	47	87.0	13	19 AAW76011	LM609 grafted anti
7	47	87.0	13	22 AAB61369	LM609 VL CDR1 pep
8	47	87.0	107	19 AAW76006	LM609 grafted anti
9	47	87.0	107	19 AAW76002	Vitaxin antibody 1
10	47	87.0	107	19 AAW76004	LM609 antibody lig
11	47	87.0	107	22 AAG63588	A light chain vari

12	47	87.0	107	22 AAG63590	A light chain vari
13	47	87.0	107	22 AAB61360	Vitaxin light chai
14	47	87.0	107	22 AAB61362	Antibody LM609 lig
15	47	87.0	107	22 AAB61364	Light chain variab
16	43	79.6	88	21 AAY56654	Partial peptide fr
17	43	79.6	105	20 AAW87456	JK gene product.
18	43	79.6	105	20 AAW87458	Humanised anti-alp
19	43	79.6	107	20 AAW84098	Humanised anti-alp
20	43	79.6	108	20 AAW84094	Murine vitronectin
21	43	79.6	109	20 AAY06380	Murine monoclonal
22	43	79.6	111	22 AAG63629	Vitronectin alpha-
23	43	79.6	112	20 AAW84100	Amino acid sequenc
24	43	79.6	124	21 AAY56719	Amino acid sequenc
25	43	79.6	299	22 AAG63633	Amino acid sequenc
26	43	79.6	299	22 AAG63638	Amino acid sequenc
27	42	77.8	107	20 AAY30203	The variable light
28	42	77.8	107	20 AAY30205	The variable light
29	42	77.8	107	21 AAY71240	Humanised antibody
30	42	77.8	107	22 AAB80987	Murine antiCD40 re
31	42	77.8	108	17 AAW00241	EGF receptor chime
32	42	77.8	128	20 AAY30199	Light chain variab
33	42	77.8	214	20 AAY30202	Light chain sequen
34	41	75.9	107	13 AAR25729	Humanised VL regio
35	41	75.9	107	22 AAB69677	Murine CMV5 antibo
36	41	75.9	107	22 AAB69678	Humanised CMV5 ant
37	41	75.9	107	22 AAB69690	Human WOL antibody
38	41	75.9	108	12 AAR15438	Light chain variab
39	41	75.9	109	20 AAW89176	Anti-p53 monoclonal
40	41	75.9	127	15 AAR54093	Sequence of mouse
41	41	75.9	127	22 AAB69687	Murine CMV5 antibo
42	41	75.9	240	12 AAR15443	Single chain Fv fr
43	40	74.1	11	18 AAW24543	CDR #1 of rB087 l1
44	40	74.1	11	22 AAG63614	Complementarity de
45	40	74.1	75	19 AAW62818	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAB61403
ID AAB61403 standard; peptide; 11 AA.
XX AAB61403;
AC AAB61403;
DT 03-APR-2001 (first entry)
XX
XX Enhanced LM609 VH CDR1 peptide.
DE
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
XX inflammatory; cancer; retina; restenosis; osteoporosis.
XX Unidentified.
OS
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
PD
XX
XX 23-JUN-2000; 2000WO-US17454.
PF
XX
XX 24-JUN-1999; 99US-0339922.
PR
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX
XX LM609 grafted anti
PI
XX
XX TMV 30K movement p
XX
XX Enhanced 6H6LH lig
DR
XX
XX LM609 grafted anti
XX
XX LM609 VL CDR1 pep
XX
XX LM609 grafted anti
PT
XX
XX Vitaxin antibody 1
XX
XX LM609 antibody lig
XX
XX A light chain vari

Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -

PS Claim 1; Page 46; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta₃ integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX Sequence 11 AA;

SQ

Query Match 100.0%; Score 54; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00057;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11

Db 1 qasqsisnflh 11

RESULT 2

AAW76031

ID AAW76031 standard; Protein; 13 AA.

XX

AC AAW76031;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-L region CDR1 protein fragment #2.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-L region; CDR;

KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI; 1998-437472/37.

XX

DR N-PSDB; AAV49868.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta₃

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 62; Page 41; 129pp; English.

XX

AAW76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphaVbeta₃ and can be used to

CC inhibit binding of alphaVbeta₃ to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphaVbeta₃-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX Sequence 13 AA;

SQ

Query Match 100.0%; Score 54; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00068;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11

Db 1 qasqsisnflh 11

RESULT 3

AAB61389

ID AAB61389 standard; peptide; 13 AA.

XX

AC AAB61389;

XX

DT 03-APR-2001 (first entry)

XX

DE Mutant VL CDR1 peptide.

XX

KW LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX

OS Unidentified.

XX

PN WO200078815-A1.

XX

PD 28-DEC-2000.

XX

PF 23-JUN-2000; 2000WO-US17454.

XX

PR 24-JUN-1999; 99US-0339922.

XX

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX

PI Huse WD, Wu H;

XX

DR WPI; 2001-050110/06.

XX

PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta₃ integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

PS Disclosure; Page 41; 132pp; English.

XX

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta₃ integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 54; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00068;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNFLH 11
:|||||
Db 1 qasqsisnflh 11

RESULT 4

AAB09775
ID AAB09775 standard; Protein; 259 AA.

XX AC AAB09775;

XX DT 06-SEP-2000 (first entry)

XX DE TMV 30K movement protein and scFv fusion protein scFv 30-1 SEQ ID NO:29.

XX KW Molecular pathogenicide; plant disease; resistance; antibody; scFv;
KW gene construct; pathogen; toxin; fusion protein; antimicrobial;
KW deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.

XX OS Tobacco mosaic virus.

XX PN WO200023593-A2.

XX PD 27-APR-2000.

XX PF 15-OCT-1999; 99WO-EF07844.

XX PR 16-OCT-1998; 98EP-0119630.

XX PR 16-OCT-1998; 98IN-0000666.

XX PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX PI Fischer R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y;

XX PI Spiegel H, Zimmerman S, Emans N, Holzem A;

XX DR WPI; 2000-339692/29.

XX PT New fusion proteins and gene constructs for expressing agents
PT (antibodies, enzymes, vectors or molecular pathogenicides), useful for
PT protecting plants against pathogens and increasing resistance to
PT disease

XX PS Example 5; Page 149-150; 193pp; English.

XX CC The present invention describes a fusion protein (I) comprising at least
CC one binding domain specifically recognising an epitope of a plant
CC pathogen and at least one further domain comprising a protein or peptide
CC sequence which is toxic to the pathogen or detrimental to its
CC replication, transmission or life cycle. Also described is a
CC pathogenicide (II) comprising (I) and a cellular targeting sequence
CC and/or membrane localisation sequence and/or motif that leads to
CC membrane anchoring; or at least one binding domain that specifically
CC recognises a viral movement and/or replicase protein. The fusion
CC protein, pathogenicide, polynucleotide, vectors, and compositions from
CC the present invention are useful for the protection of a plant against
CC the action of a pathogen. The kit from the present invention is useful
CC for carrying out the methods and may be employed in different
CC applications, for example in the diagnostic field or as research tools.
CC The kit or its components, such as the fusion protein, pathogenicide,
CC polynucleotides, vectors or compositions are useful in plant cell and
CC plant tissue culture, in agriculture. They are extremely useful for
CC breeding new varieties of plants that display improved properties such as
CC resistance to pathogens. AA56587 to AA56702 and AAB09774 to B097820
CC represent sequences used in the exemplification of the present
CC invention.

XX SQ Sequence 259 AA;

Query Match 92.6%; Score 50; DB 21; Length 259;
Best Local Similarity 90.9%; Pred. No. 0.1;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNFLH 11
:|||||
Db 155 rasqsisnflh 165

RESULT 5

AAB61402
ID AAB61402 standard; peptide; 11 AA.

XX AC AAB61402;

XX DT 03-APR-2001 (first entry)

XX DE Enhanced 6H6LH light chain CDR1.

XX KW LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis

XX PS Claim 4; Page 46; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX SQ Sequence 11 AA;

Query Match 87.0%; Score 47; DB 22; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.013; Length 11;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSISNFLH 11

Db 1 qasqsishlh 11

RESULT 6

AAW76011
ID AAW76011 standard; Protein; 13 AA.

XX AC AAW76011;

XX DT 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-L region CDR1 protein fragment #1.
 DE XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.
 XX OS Mus sp.
 XX WO9833919-A2.
 PN XX
 XX 06-AUG-1998.
 PD XX
 XX 30-JAN-1998; 98WO-US01826.
 PF XX
 XX 30-JAN-1997; 97US-0791391.
 PR XX
 XX (IXSY-) IXSYS INC.
 PA XX
 XX Glaser SM, Huse WD;
 PI XX
 XX WPI: 1998-437472/37.
 DR XX
 DR N-PSDB; AAV49848.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure: Page 40; 129pp; English.
 XX
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the antibody.
 XX
 SQ Sequence 13 AA;
 Query Match 87.0%; Score 47; DB 19; Length 13;
 Best Local Similarity 90.9%; Pred. No. 0.015;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QASQISINFLH 11
 Db 1 gasqsisnhh 11
 RESULT 7
 AAB61369
 ID AAB61369 standard; peptide; 13 AA.
 XX AAB61369;
 XX
 XX 03-APR-2001 (first entry)
 DT XX
 DE LM609 VL CDR1 peptide.
 XX
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.

XX WO200078815-A1.
 PN XX
 XX 28-DEC-2000.
 PD XX
 XX 23-JUN-2000; 2000WO-US17454.
 PF XX
 XX 24-JUN-1999; 99US-0339922.
 PR XX
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA XX
 XX Huse WD, Wu H;
 PI XX
 XX WPI: 2001-050110/06.
 DR XX
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 PT
 XX Disclosure: Page 39; 132pp; English.
 PS
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 13 AA;
 Query Match 87.0%; Score 47; DB 22; Length 13;
 Best Local Similarity 90.9%; Pred. No. 0.015;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QASQISINFLH 11
 Db 1 gasqsisnhh 11
 RESULT 8
 AAW76006
 ID AAW76006 standard; Protein; 107 AA.
 XX
 XX AAW76006;
 AC
 XX 02-NOV-1998 (first entry)
 DT XX
 XX LM609 grafted antibody light chain variable region protein fragment.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 KW
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 49
 FT /label= Arg, Met
 XX
 XX WO9833919-A2.
 PN
 XX 06-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US01826.
 PF

```

XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI: 1998-437472/37.
XX N-PSDB; AAV49843.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX Claim 19; Fig 7; 129pp; English.
XX This sequence represents a LM609 grafted antibody variable light chain
XX region. LM609 and the antibody vitaxin bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
XX and thus block integrin-mediated signal transduction. This is useful in
XX the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity
XX more than 90 times greater than that of parent the parent antibody.
XX Sequence 107 AA;

Query Match 87.0%; Score 47; DB 19; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11
DB 24 gasqsisnhlh 34

RESULT 9
AAW76002
ID AAW76002 standard; Protein; 107 AA.
XX AC AAW76002;
XX DT 02-NOV-1998 (first entry)
XX DE Vitaxin antibody light chain variable region protein fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX WPI: 1998-437472/37.
XX N-PSDB; AAV49821.

```

```

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX Claim 1; Fig 1b; 129pp; English.
XX This sequence represents the vitaxin antibody variable light chain
XX region. Vitaxin and the antibody LM609 bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
XX ligand and thus block integrin-mediated signal transduction. This is
XX useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
XX disease, specifically angiogenesis and restenosis (but also e.g.
XX (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
XX cancer, psoriasis, rheumatoid arthritis, macular degeneration,
XX osteoporosis etc.). The antibodies contain non-murine framework regions
XX so are suitable for use in humans. Enhanced types of LM609 have affinity
XX more than 90 times greater than that of parent the parent antibody.
XX Sequence 107 AA;

Query Match 87.0%; Score 47; DB 19; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11
DB 24 gasqsisnhlh 34

RESULT 10
AAW76004
ID AAW76004 standard; Protein; 107 AA.
XX AC AAW76004;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 antibody light chain variable region protein fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX WPI: 1998-437472/37.
XX N-PSDB; AAW76004.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX Claim 46; Fig 2b; 129pp; English.
XX This sequence represents the LM609 antibody variable light chain region.

```

CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 107 AA;

Query Match 87.0%; Score 47; DB 19; Length 107;
 Best Local Similarity 90.9%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11
 ||||| ||
 Db 24 qasqsishh 34

RESULT 11
 AAG63588
 ID AAG63588 standard; Protein; 107 AA.
 XX
 AC AAG63588;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE A light chain variable region of LM609 grafted antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX Synthetic.
 OS Mus sp.

XX Key Location/Qualifiers
 FT Misc-difference 49 /note= "unspecified residue encoded by MKK"
 FT

XX US2001011125-A1.

XX 02-AUG-2001.

XX 30-JAN-1997; 97US-0790540.

XX 30-JAN-1997; 97US-0790540.

XX (HUSE/) HUSE W D.

XX Huse WD;

XX WPI: 2001-496171/54.

XX N-PSDB; AAH74624.

XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -

XX Claim 1; Fig 1B; 25pp; English.

XX The present sequence represents the light chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain

CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX
 SQ Sequence 107 AA;

Query Match 87.0%; Score 47; DB 22; Length 107;
 Best Local Similarity 90.9%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11
 ||||| ||
 Db 24 qasqsishh 34

RESULT 12
 AAG63590
 ID AAG63590 standard; Protein; 107 AA.
 XX
 AC AAG63590;

XX 15-OCT-2001 (first entry)

XX A light chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.
 XX Synthetic.
 OS Mus sp.

XX US2001011125-A1.

XX 02-AUG-2001.

XX 30-JAN-1997; 97US-0790540.

XX 30-JAN-1997; 97US-0790540.

XX (HUSE/) HUSE W D.

XX Huse WD;

XX WPI: 2001-496171/54.

XX N-PSDB; AAH74626.

XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -

XX Disclosure; Fig 2B; 25pp; English.

XX The present sequence represents the light chain variable region of the
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.
 CC The specification describes a LM609 grafted antibody which has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis

CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX Sequence 107 AA;

Query Match 87.0%; Score 47; DB 22; Length 107;

Best Local Similarity 90.9%; Pred. No. 0.15;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQTSNPLH 11
 Db 24 qasqsishlh 34
 ||||| ||

RESULT 13

AAB61360

ID AAB61360 standard; protein; 107 AA.

XX

AC AAB61360;

XX 03-APR-2001 (first entry)

XX Vitaxin light chain variable region protein.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;

XX inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 107 AA;

XX Query Match 87.0%; Score 47; DB 22; Length 107;

Best Local Similarity 90.9%; Pred. No. 0.15;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQTSNPLH 11
 Db 24 qasqsishlh 34
 ||||| ||

RESULT 15

AAB61364

ID AAB61364 standard; protein; 107 AA.

XX

AC AAB61364;

XX Sequence 107 AA;

XX Query Match 87.0%; Score 47; DB 22; Length 107;

Best Local Similarity 90.9%; Pred. No. 0.15;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQTSNPLH 11
 Db 24 qasqsishlh 34
 ||||| ||

RESULT 14

AAB61362

ID AAB61362 standard; protein; 107 AA.

XX

AC AAB61362;

XX 03-APR-2001 (first entry)

XX Antibody LM609 light chain variable region protein.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;

XX inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 107 AA;

XX Query Match 87.0%; Score 47; DB 22; Length 107;

Best Local Similarity 90.9%; Pred. No. 0.15;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DT 03-APR-2001 (first entry)
 XX
 DE Light chain variable region of LM609.
 XX
 KW LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;
 KW inflammatory; cancer; retins; restenosis; osteoporosis.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta₃ integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Fig 7; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 107 AA;

Query Match 87.0%; Score 47; DB 22; Length 107;
 Best Local Similarity 90.9%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNPLH 11
 |||||
 Db 24 gasqsisnlh 34

Search completed: August 19, 2002, 06:39:14
 Job time: 1475 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:42 ; Search time 61.75 Seconds
(without alignments)
4.351 Million cell updates/sec

Title: US-09-339-922A-110
Perfect score: 54
Sequence: 1 QASQISNPLH 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	77.8	96	2	US-08-737-560A-9
2	42	77.8	107	4	US-09-247-352-8
3	42	77.8	107	4	US-09-247-352-12
4	42	77.8	108	2	US-08-378-939-20
5	42	77.8	108	4	US-09-247-352-1
6	42	77.8	214	4	US-09-247-352-4
7	41	75.9	100	1	US-08-436-463-19
8	41	75.9	103	1	US-08-436-463-21
9	41	75.9	107	1	US-07-634-278-62
10	41	75.9	107	1	US-07-634-278-63
11	41	75.9	107	1	US-07-634-278-87
12	41	75.9	107	1	US-08-477-728-62
13	41	75.9	107	1	US-08-477-728-63
14	41	75.9	107	1	US-08-477-728-87
15	41	75.9	107	1	US-08-474-040-62
16	41	75.9	107	1	US-08-474-040-63
17	41	75.9	107	1	US-08-474-040-87
18	41	75.9	107	1	US-08-487-200-62
19	41	75.9	107	1	US-08-487-200-63
20	41	75.9	107	1	US-08-487-200-87
21	41	75.9	107	4	US-08-484-537-62
22	41	75.9	107	4	US-08-484-537-63
23	41	75.9	107	4	US-08-484-537-87
24	41	75.9	108	4	US-09-157-370-4
25	41	75.9	127	1	US-07-634-278-83
26	41	75.9	127	1	US-08-477-728-83
27	41	75.9	127	1	US-08-474-040-83

28	41	75.9	127	1	US-08-487-200-83	Sequence 83, Appl
29	41	75.9	127	1	US-08-436-463-4	Sequence 4, Appl
30	41	75.9	127	1	US-08-436-463-18	Sequence 18, Appl
31	41	75.9	127	4	US-08-484-537-83	Sequence 83, Appl
32	40	74.1	76	4	US-08-851-362D-20	Sequence 20, Appl
33	40	74.1	105	4	US-08-851-362D-28	Sequence 28, Appl
34	40	74.1	105	4	US-08-851-362D-34	Sequence 34, Appl
35	40	74.1	105	4	US-08-851-362D-38	Sequence 38, Appl
36	40	74.1	107	2	US-08-652-558-36	Sequence 36, Appl
37	40	74.1	107	2	US-08-378-939-14	Sequence 14, Appl
38	40	74.1	107	4	US-09-240-274-173	Sequence 173, App
39	40	74.1	108	1	US-08-276-852-102	Sequence 102, App
40	40	74.1	108	1	US-08-899-575-102	Sequence 102, App
41	40	74.1	108	1	US-08-899-575-102	Sequence 102, App
42	40	74.1	108	2	US-08-378-939-30	Sequence 30, Appl
43	40	74.1	108	4	US-09-025-769B-14	Sequence 14, Appl
44	40	74.1	108	5	PCT-US95-08743-102	Sequence 102, App
45	39	72.2	56	1	US-08-162-102C-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-08-737-560A-9
; Sequence 9, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuill
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuill
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; CITY: Keanak-gu
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

OTHER INFORMATION: VK23.32'CL
US-08-737-560A-9

Query Match 77.8%; Score 42; DB 2; Length 96;
Best Local Similarity 72.7%; Pred. No. 0.46;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11
Db 24 RASQSISDYLH 34

RESULT 2

US-09-247-352-8
; Sequence 8, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffery D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Human and Mouse
US-09-247-352-8

Query Match 77.8%; Score 42; DB 4; Length 107;
Best Local Similarity 72.7%; Pred. No. 0.46;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11
Db 24 RASQSISDYLH 34

RESULT 3

US-09-247-352-12
; Sequence 12, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffery D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Human and Mouse
US-09-247-352-12

Query Match 77.8%; Score 42; DB 4; Length 107;
Best Local Similarity 72.7%; Pred. No. 0.46;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11
Db 24 RASQSISDYLH 34

RESULT 4

US-08-378-939-20
; Sequence 20, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-20

Query Match 77.8%; Score 42; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 0.46;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11
Db 24 QASQSLSNLYN 34

RESULT 5

US-09-247-352-1
; Sequence 1, Application US/09247352
; Patent No. 6312693

; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-463-21

Query Match 75.9%; Score 41; DB 1; Length 103;
Best Local Similarity 81.8%; Pred. No. 0.68;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNPLH 11
:||||| ||
Db 22 RASQISNNLH 32

RESULT 9
US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600

; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-634-278-62

Query Match 75.9%; Score 41; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNPLH 11
:||||| ||
Db 24 RASQISNNLH 34

RESULT 10
US-07-634-278-63
; Sequence 63, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 75.9%; Score 41; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 1 QASQISINFLH 11
:|||||||
DB 24 RASQISINLH 34

RESULT 11

US-07-634-278-87
; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLEI, Nicholas F.
; APPLICANT: COELLINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 75.9%; Score 41; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 1 QASQISINFLH 11
:|||||||
DB 24 RASQISINLH 34

RESULT 12

US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 75.9%; Score 41; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 1 QASQISINFLH 11

```

: APPLICANT: QUEEN, Cary L.
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,728
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/634,278
: FILING DATE: 19-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/590,274
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/310,252
: FILING DATE: 13-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/290,975
: FILING DATE: 28-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-002600
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 87:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 107 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-477-728-87

Query Match 75.9%; Score 41; DB 1; Length:
Best Local Similarity 81.8%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 1; Index

Qy 1 QASQISNLFH 11
:|||||||
Db 24 RASQISNNLH 34

RESULT 15
US-08-474-040-62
: Sequence 62, Application US/08474040
: Patent No. 5693761
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas P.
: APPLICANT: COELINGH, Kathleen L.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-62

Query Match 75.9%; Score 41; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSSISNLFH 11
Db 24 RASQSSISNLFH 34

Search completed: August 19, 2002, 06:34:43
Job time: 1204 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:07 ; Search time 78.53 Seconds
(without alignments)
8.565 Million cell updates/sec

Title: US-09-339-922A-112

Perfect score: 33

Sequence: 1 YRSQIS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	90.9	629	2 T31626	hypothetical prote
2	29	87.9	406	2 B96982	probable membrane
3	29	87.9	409	2 T29517	hypothetical prote
4	29	87.9	944	2 F90600	exonuclease ABC s
5	28	84.8	191	2 T43737	heat shock protein
6	28	84.8	191	2 AB1259	heat shock protein
7	28	84.8	191	2 AF1621	heat shock protein
8	28	84.8	206	2 T47433	hypothetical prote
9	28	84.8	250	2 G83283	precorrin-2 methyl
10	28	84.8	345	2 AB1813	hypothetical prote
11	28	84.8	368	1 HLBECH	membrane glycoprot
12	28	84.8	2028	2 T08025	DNA-directed RNA p
13	27	81.8	69	2 PH1080	Ig light chain V r
14	27	81.8	96	2 G33730	Ig kappa chain V r
15	27	81.8	104	2 B43413	Ig kappa chain V r
16	27	81.8	106	2 PL0267	Ig kappa chain V r
17	27	81.8	107	2 B45722	anti-glycoprotein
18	27	81.8	107	2 C45722	anti-glycoprotein
19	27	81.8	107	2 A45722	Ig kappa chain pre
20	27	81.8	115	2 S10146	Ig kappa chain pre
21	27	81.8	138	2 A26471	Ig kappa chain pre
22	27	81.8	144	2 S34150	Ig mu chain - axol
23	27	81.8	291	2 A81662	UDP-3-O-(3-hydroxy
24	27	81.8	367	2 T24298	hypothetical prote
25	27	81.8	423	2 E97165	flagellar hook pro
26	27	81.8	438	2 G64513	hypothetical prote
27	27	81.8	490	2 T43149	probable beta-fruc
28	27	81.8	493	2 T01495	hypothetical prote
29	27	81.8	504	2 I53868	alpha-internexin -

ALIGNMENTS

RESULT 1

T31626

hypothetical protein Y57A10A.d - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000

C:Accession: T31626

R:Smyle, R.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z21048

A:Accession: T31626

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-629 <WIL>

A:Cross-references: EMBL:AL117195; PIDN:CAB55009.1; CESP:Y57A10A.d

A:Experimental source: clone Y57A10A

C:Genetics:

A:Gene: CESP:Y57A10A.d

A:Introns: 51/2; 89/2; 183/2; 221/2; 284/2; 318/2; 399/2; 611/1

C:Superfamily: Caenorhabditis elegans hypothetical protein Y57A10A.d

Query Match 90.9%; Score 30; DB 2; Length 629;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7

Db 466 YRNQIS 472

RESULT 2

B96982

probable membrane protein [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: B96982

R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.;

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B96982

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-406 <KUR>

A:Cross-references: GB:AB001437; PIDN:AAK78645.1; PID:gl5023544; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0668

Query Match 87.9%; Score 29; DB 2; Length 406;

Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7

Db 193 YRSQSI 199

RESULT 3

T29517

hypothetical protein T25F10.3 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29517

R:Pauley, A.; Gattung, S.

submitted to the EMBL Data Library, July 1996

A:Description: The sequence of *C. elegans* cosmid T25F10.

A:Reference number: Z20634

A:Accession: T29517

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-409 <PAU>

A:Cross-references: EMBL:U64856; PIDN:AAB04985.1; GSPDB:GN00023; CESP:T25F10.3

A:Experimental source: strain Bristol N2; clone T25F10

C:Genetics:

A:Gene: CESP:T25F10.3

A:Map position: 5

A:Introns: 86/3; 112/1; 233/3; 268/3; 291/1; 348/2

Query Match

Best Local Similarity 87.9%; Score 29; DB 2; Length 409;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 6

Db 133 YRSQSI 138

RESULT 4

F90600

excinuclease ABC subunit a [imported] - *Mycoplasma pulmonis* (strain UAB CTIP)

C:Species: *Mycoplasma pulmonis*

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

C:Accession: F90600

R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulmonis*

A:Reference number: A95512; MUID:21267165; PMID:11353084

A:Accession: F90600

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-944 <KUR>

A:Cross-references: GB:A445566; PID:gl4090125; PIDN:CAC13883.1; GSPDB:GN00153

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPu_7100

C:Superfamily: excinuclease ABC chain A; ATP-binding cassette homology

Query Match

Best Local Similarity 87.9%; Score 29; DB 2; Length 944;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 7

Db 784 YRSQSI 790

RESULT 5

T43737

heat shock-protein grpE [imported] - *Listeria monocytogenes*

C:Species: *Listeria monocytogenes*
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T43737

R:Hanawa, T.; Kai, M.; Kamiya, S.; Yamamoto, T.

submitted to the EMBL Data Library, February 1999

A:Description: Cloning, sequencing, and transcriptional analysis of the dnaK heat shock

A:Reference number: Z22656

A:Accession: T43737

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-191 <HAN>

A:Cross-references: EMBL:AB023064; PIDN:BAA82788.1

A:Experimental source: strain 10403S

C:Genetics:

A:Note: grpE

C:Superfamily: heat shock protein grpE

C:Keywords: stress-induced protein

Query Match

Best Local Similarity 84.8%; Score 28; DB 2; Length 191;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 7

Db 84 YRSQSLA 90

RESULT 6

AB1259

heat shock protein GrpE [Imported] - *Listeria monocytogenes* (strain EGD-e)

C:Species: *Listeria monocytogenes*

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AB1259

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl

.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A:Title: Comparative genomics of *Listeria species*.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AB1259

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-191 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAC99552.1; PID:gl16410903; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: grpE

C:Superfamily: heat shock protein grpE

Query Match

Best Local Similarity 84.8%; Score 28; DB 2; Length 191;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 7

Db 84 YRSQSLA 90

RESULT 7

AF1621

heat shock protein GrpE [Imported] - *Listeria innocua* (strain Clip11262)

C:Species: *Listeria innocua*

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AF1621

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;

OK, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AF1621
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96742.1; PID:g16413984; GSPDB:GN00178
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: grpE
C:Superfamily: heat shock protein grpE

Query Match 84.8%; Score 28; DB 2; Length 191;
Best Local Similarity 71.4%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSTS 7

Db 84 YRSQSLA 90

RESULT 8

T47433
hypothetical protein T22K7.110 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T47433

R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K. submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24459

A:Accession: T47433

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-206 <RIE>

A:Cross-references: EMBL:AL138641

A:Experimental source: cultivar Columbia; BAC clone T22K7

C:Genetics:

A:Map position: 3

A:Note: T22K7.110

Query Match 84.8%; Score 28; DB 2; Length 206;

Best Local Similarity 71.4%; Pred. No. 26;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSTS 7

Db 107 YRSRSVS 113

RESULT 9

g83283
precorin-2 methyltransferase Cobi PA2904 [imported] - Pseudomonas aeruginosa (strain PA

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G83283

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bro

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337

A:Accession: G83283

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-250 <STO>

A:Cross-references: GB:AE004716; GB:AE004091; NID:g9948986; PIDN:AAG06292.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: cobi; PA2904

Query Match 84.8%; Score 28; DB 2; Length 250;

Best Local Similarity 71.4%; Pred. No. 32;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSIS 7

Db 154 YRQSLS 160

RESULT 10

AB1813

hypothetical protein al10050 [imported] - *Anabaena* sp. (strain PCC 7120)

C:Species: *Anabaena* sp.

A:Note: *Anabaena* sp. (strain PCC 7120) is a synonym of *Nostoc* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002

C:Accession: AB1813

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriku

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AB1813

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-345 <KUR>

A:Cross-references: GB:BA000019; PIDN:BAW7574.1; PID:g17135028; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: al10050

Query Match 84.8%; Score 28; DB 2; Length 345;

Best Local Similarity 85.7%; Pred. No. 45;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRSQSIS 7

Db 178 YRSNSIS 184

RESULT 11

HLBECM

membrane glycoprotein H301 alpha chain precursor - human cytomegalovirus

A:Alternate names: class I histocompatibility antigen homolog; UL18 glycoprotein prec

C:Species: human cytomegalovirus, human herpesvirus 5

A:Note: host *Homo sapiens* (man)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999

C:Accession: S09781; S00661

R:Chee, W.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T

M.; Barrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovi

A:Reference number: S09749; MUID:90269039

A:Accession: S09781

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-368 <CHE>

A:Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35417.1; PID:g59623

A:Experimental source: strain Ad169

A:Note: possible protein-coding frames are given

A:Note: the DNA sequence was submitted to EMBL, December 1989

R:Beck, S.; Barrell, B.G.

Nature 331, 269-272, 1988

A:Title: Human cytomegalovirus encodes a glycoprotein homologous to MHC class-I anti

A:Reference number: S00661; MUID:88094735

A:Accession: S00661

A:Molecule type: DNA

A:Residues: 1-368 <BEC>

A:Cross-references: EMBL:Y00293; NID:g59456; PIDN:CAA68399.1; PID:g59457

C:Genetics:

A:Gene: H301

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C;Keywords: glycoprotein; heterodimer; transmembrane protein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-368/Product: membrane glycoprotein H301 alpha chain #status predicted <MAT>

F;321-349/Domain: transmembrane #status predicted <TM>

F;56-66,95,123,127,150,167,177,193,240,282,291/Binding site: carbohydrate (Asn) (covalent)

Query Match 84.8%; Score 28; DB 1; Length 368;

Best Local Similarity 83.3%; Pred. No. 48;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 6

Db 110 YRSQSV 115

RESULT 12

T08025 DNA-directed RNA polymerase beta' chain homolog - Chlamydomonas reinhardtii chloroplast

N;Alternate names: rpoC2 protein

C;Species: chloroplast Chlamydomonas reinhardtii

C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999

C;Accession: T08025

R;Nucleo. S.: Purton, S.

submitted to the EMBL Data Library, May 1996

A;Description: The chloroplast rpoC2 gene of Chlamydomonas reinhardtii.

A;Reference number: Z16298

A;Accession: T08025

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2028 <NUO>

A;Cross-references: EMBL:U57326; NID:g1354831; PIDN:AAB01997.1; PID:g1354832

C;Genetics:

A;Gene: rpoC2

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 84.8%; Score 28; DB 2; Length 2028;

Best Local Similarity 71.4%; Pred. No. 2.8e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7

Db 1734 YRSQSVS 1740

RESULT 13

PH1080

Ig light chain V region (clone 165.60) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C;Accession: PH1080

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A;Reference number: PH0971; MUID:92381444

A;Accession: PH1080

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-69 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

Query Match 81.8%; Score 27; DB 2; Length 69;

Best Local Similarity 85.7%; Pred. No. 15;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7

Db 21 YRSQSIS 27

RESULT 14

G33730

Ig kappa chain V region (23.32) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000

C;Accession: G33730

R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u

A;Reference number: A33730; MUID:89367325

A;Accession: G33730

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-96 <LAW>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 27; DB 2; Length 96;

Best Local Similarity 85.7%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7

Db 50 YASQSIS 56

RESULT 15

B43413

Ig kappa chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C;Accession: B43413

R;Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.;

J. Biol. Chem. 267, 18085-18092, 1992

A;Title: A molecular model of RGD ligands. Antibody D gene segments that direct speci

A;Reference number: A43413; MUID:92388177

A;Accession: B43413

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-104 <TOM>

A;Note: sequence extracted from NCBI backbone (NCBIP:112818)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;13-87/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 27; DB 2; Length 104;

Best Local Similarity 85.7%; Pred. No. 23;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7

Db 47 YASQSIS 53

Search completed: August 19, 2002, 06:36:09

Job time: 1290 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:12 ; Search time 51.81 Seconds
(without alignments)
5.231 Million cell updates/sec

Title: US-09-339-922A-112
Perfect score: 33
Sequence: 1 YRSQIS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	84.8	191	GRPE_LISIN	Q92bn7 listeria in
2	28	84.8	191	GRPE_LISIN	Q9s5a5 listeria mo
3	28	84.8	368	VGH3_HCMVA	P08560 human cytom
4	27	81.8	208	TRAL_RHISN	P55394 rhizobium s
5	27	81.8	286	LPXC_CHLMU	Q9pjk9 chlamydia m
6	27	81.8	438	Y232_METJA	Q60289 methanococc
7	27	81.8	499	AINX_HUMAN	Q16352 homo sapien
8	27	81.8	504	AINX_MOUSE	P46650 mus musculu
9	27	81.8	505	AINX_RAT	P23565 rattus norv
10	27	81.8	581	INVL_SCHPO	O59852 schizosacch
11	27	81.8	3097	CADN_DROME	O15943 drosophila
12	26	78.8	186	GRPE_BACSU	P15874 bacillus su
13	26	78.8	494	VE2_HPV12	P36782 human papil
14	26	78.8	542	CBPY_CANAL	P30574 candida alb
15	26	78.8	1080	NRK1_YEAST	P38692 saccharomyc
16	26	78.8	1093	SWR4_YEAST	P25302 saccharomyc
17	26	78.8	1807	TSC2_HUMAN	P49815 homo sapien
18	26	78.8	1809	TSC2_RAT	P49816 rattus norv
19	26	78.8	1814	TSC2_MOUSE	O61037 mus musculu
20	25	75.8	216	YH21_HAEIN	O05086 haemophilus
21	25	75.8	222	Y364_MYCLE	O69601 mycobacteri
22	25	75.8	264	MOV2_CGMVW	P19522 cucumber gr
23	25	75.8	330	GRP2_HUMAN	O75791 h grb2-rela
24	25	75.8	351	COLF_ARATH	O9fh88 arabidopsis
25	25	75.8	410	ODBA_PSEPU	P09060 pseudomonas
26	25	75.8	418	HEM1_SALTY	P13581 salmonella
27	25	75.8	451	YPVB_METTF	P29578 methanobact
28	25	75.8	507	SEPA_STAEF	P43148 staphylococ
29	25	75.8	525	ACUB_NEUCR	P15937 neurospora
30	25	75.8	532	P72_MYCWM	P55801 mycoplasma
31	25	75.8	555	VGLF_PTILHC	P12605 human parai
32	25	75.8	951	SFR8_HUMAN	Q12872 homo sapien
33	25	75.8	1081	ULS2_HSVB	P28962 equine herp

34	25	75.8	1089	Y553_HUMAN	Q9ukj3 homo sapien
35	25	75.8	1283	PEX1_HUMAN	O43933 homo sapien
36	25	75.8	1316	RPOC_MYCLE	P30761 mycobacteri
37	25	75.8	1316	RPOC_MYCTU	P47769 mycobacteri
38	25	75.8	1369	YAZG_SCHPO	Q09706 schizosacch
39	25	75.8	1403	YGN1_YEAST	P53127 saccharomyc
40	25	75.8	1447	DCC_HUMAN	P43146 homo sapien
41	25	75.8	1481	RPOD_ODOSI	P49468 odontella s
42	25	75.8	1572	BAI2_HUMAN	O60241 homo sapien
43	25	75.8	1629	ATS9_HUMAN	Q9p2n4 homo sapien
44	25	75.8	2517	NCR2_HUMAN	Q9Y618 h nuclear r
45	24	72.7	38	TRPD_SERMA	P12321 serratia ma

ALIGNMENTS

RESULT 1					
GRPE_LISIN					
ID GRPE_LISIN	STANDARD;	PRT;	191 AA.		
AC	Q92BN7;				
DT	01-MAR-2002 (Rel. 41, Created)				
DT	01-MAR-2002 (Rel. 41, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	GrpE protein (HSP-70 cofactor).				
GN	GRPE OR LIN1511.				
OS	Listeria innocua.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;				
OC	Bacillus/Staphylococcus group; Listeria.				
OX	NCBI_TaxID=1642;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Clp 11262 / Serovar 6a;				
RX	MEDLINE=21537279; PubMed=11679669;				
RA	Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,				
RA	Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,				
RA	Charbit A., Chetouani F., Couve E., de Daruvar A., Deloux P.,				
RA	Dommann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,				
RA	Entian K.-D., Fathi H., Garcia-del Portillo F., Garrido P.,				
RA	Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,				
RA	Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,				
RA	Madueno E., Maitouram A., Mata Vicente J., Ng E., Nedjari H.,				
RA	Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,				
RA	Rommel B., Rose M., Schlueter T., Simoes N., Tierrez A.,				
RA	Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;				
RL	Science 294:849-852(2001).				
CC	- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF				
CC	DNAK HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECYCLE				
CC	MORE EFFICIENTLY (BY SIMILARITY).				
CC	- SIMILARITY: BELONGS TO THE GRPE FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AL596168; CAC96742.1; -				
DR	Listlist; LIN01511; -				
DR	PROSITE; PS01071; GRPE; 1.				
KW	Chaperone; Heat shock; Complete proteome.				
SQ	SEQUENCE 191 AA; 21952 MW; 853F11392E126981 CRC64;				

Query Match 84.8%; Score 28; DB 1; Length 191;
Best Local Similarity 71.4%; Pred. No. 8;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7
|||||:

Db 84 YRSQSLA 90

RESULT 2

GRPE_LISMO STANDARD; PRT; 191 AA.

AC Q955A5;

DT 16-OCT-2001 (Rel. 40, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE GrpE protein (HSP-70 cofactor).

GN GRPE OR LM01474.

OS Listeria monocytogenes.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Listeria.

OX NCBI_TaxID=1639;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=104035;

RX MEDLINE=20163771; PubMed=10701836;

RA Hanawa T., Kai M., Kamiya S., Yamamoto T.;

RT "Cloning, sequencing, and transcriptional analysis of the dnaK heat

RT shock operon of Listeria monocytogenes.;"

RL Cell Stress Chaperones 5:21-29(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=EGD-e / Serovar 1/2a;

RX MEDLINE=21537279; PubMed=11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

RA Jones L.-M., Maertens U., Krest J., Kuhn M., Kunz F., Kurapkat G.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

RA Varquez-Boland J.-A., Voss H., Wenling J., Cossart P.;

RT "Comparative genomics of Listeria species.;"

RL Science 294:849-852(2001).

CC -!- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF

CC DNAK. HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECYCLE

CC MORE EFFICIENTLY (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE GRPE FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; AB023064; BAA82788.1; -.

CC DR EMBL; AL591979; CAC9552.1; -.

CC DR ListinList; LM001474; -.

CC DR HSSP; P09372; 1DKG.

CC DR InterPro; IPR000740; GrpE.

CC DR Pfam; PF01025; GrpE; 1.

CC DR PRINTS; PR00773; GRPEPROTEIN.

CC DR PROSITE; PS01071; GRPE; 1.

CC DR Chaperone; Heat shock; Complete proteome.

CC KW Chaperone; Heat shock; Complete proteome.

CC SEQUENCE 191 AA; 21918 MW; D93CFA0EB86CF0C8 CRC64;

Query Match 84.8%; Score 28; DB 1; Length 191;

Best Local Similarity 71.4%; Pred. No. 8;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSLA 7

|||||:

Db 84 YRSQSLA 90

RESULT 3

VGH3_HCMVA STANDARD; PRT; 368 AA.

AC P08560;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 01-FEB-1991 (Rel. 17, Last annotation update)

DE Glycoprotein H301 precursor.

GN H301 OR ULI18.

OS Human cytomegalovirus (strain AD169).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Betaherpesvirinae; Cytomegalovirus.

OX NCBI_TaxID=10360;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88094735; PubMed=2827039;

RA Beck S., Barrell B.G.;

RT "Human cytomegalovirus encodes a glycoprotein homologous to MHC

RT class-I antigens.;"

RL Nature 331:269-272(1988).

RN [2]

RP COMPLETE GENOME.

RX MEDLINE=90269039; PubMed=2161319;

RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,

RA Horsnell T., Hutchison C.A. III, Kourzides T., Martignetti J.A.,

RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;

RT "Analysis of the protein-coding content of the sequence of human

RT cytomegalovirus strain AD169.;"

RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).

CC -!- FUNCTION: THIS PROTEIN IS PROBABLY RESPONSIBLE FOR BINDING TO

CC BETA-2-MICROGLOBULIN.

CC -!- SIMILARITY: SPRONG TO THE MHC CLASS-I ANTIGENS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; X17403; CAA35417.1; -.

CC DR EMBL; Y00293; CAA68399.1; -.

CC DR PIR; S09781; HLBECH.

CC DR PIR; S00661; S00661.

CC DR InterPro; IPR003006; Ig_MHC.

CC DR InterPro; IPR003600; Ig_Like.

CC DR InterPro; IPR001039; MHC_I.

CC DR ProDom; PD000050; MHC_I; 1.

CC DR SMART; SM00410; IG_Like; 1.

CC DR PROSITE; PS00290; IG_MHC; 1.

CC KW Glycoprotein; MHC I; Transmembrane; Signal.

CC FT SIGNAL 1 18 POTENTIAL.

CC FT CHAIN 19 368 GLYCOPROTEIN H301.

CC FT DOMAIN 19 114 ALPHA-1 LIKE.

CC FT DOMAIN 115 208 ALPHA-2 LIKE.

CC FT DOMAIN 209 303 ALPHA-3 LIKE.

CC FT TRANSMEM 321 342 POTENTIAL.

CC FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

SQ SEQUENCE 368 AA; 41735 MW; 48AE7EFB4DCCB4E CRC64;

Query Match 84.8%; Score 28; DB 1; Length 368;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 6
| | | | |
Db 110 YRSQSV 115

RESULT 4
TRAI_RHSIN STANDARD; PRT; 208 AA.
ID TRAI_RHSIN
AC P55394;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable autoinducer synthesis protein trai.
GN TRAI OR Y4CL.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.; basis of symbiosis between Rhizobium and legumes.";
RT Nature 387:394-401(1997).
RL -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF OHHL (N-(3-OXOOCTANOYL)-L-
CC HOMOSERINE LACTONE), AN AUTOINDUCER MOLECULE WHICH BINDS TO TRAI
CC AND THUS ACTS IN THE CONTROL OF CONJUGAL TRANSFER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AUTOINDUCER SYNTHETASE FAMILY.
CC STRONGEST, TO A.TUMEFACIENS TI PLASMID TRAI.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE000068; AAB92427.1; -
CC InterPro: IPR001690; Autoinducers_synth.
CC Pfam: PF00765; Autoind_synth; 1.
CC PRINTS: PR01549; AUTOINDCRSYN.
CC ProDom: PD002752; Autoinducers_synth; 1.
CC PROSITE: PS00949; AUTOINDUCERS_SYNTH; 1.
KW Quorum sensing; Autoinducer synthesis; Conjugation; Plasmid.
SQ SEQUENCE 208 AA; 22826 MW; DF2F053C7A20D28E CRC64;

Query Match 81.8%; Score 27; DB 1; Length 208;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7
| | | | |
Db 196 YRSQIS 202

RESULT 5
LPXC_CHLMU STANDARD; PRT; 286 AA.
ID LPXC_CHLMU
AC Q9PJK9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
```

```

DE UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
DE (EC 3.5.1.-) (UDP-3-O-acyl-GlcNAc deacetylase).
GN LPXC OR TC0820.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Winn M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RL pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF LIPID A, A
CC PHOSPHORYLATED GLYCOLIPID THAT ANCHORS THE LIPOPOLYSACCHARIDE TO
CC THE OUTER MEMBRANE OF THE CELL (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: UDP-3-O-(3-HYDROXYTETRADECANOYL)-N-
CC ACETYLGLUCOSAMINE + H(2)O = UDP-3-O-(3-HYDROXYTETRADECANOYL)-
CC GLUCOSAMINE + ACETATE
CC -1- PATHWAY: LIPID A BIOSYNTHESIS; SECOND STEP.
CC -1- SIMILARITY: BELONGS TO THE LPXC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE002347; AAF39622.1; ALT_INIT.
CC TIGR: TC0820; -
CC Hydrolyase; Lipid A biosynthesis; Lipid synthesis; Complete proteome.
SQ SEQUENCE 286 AA; 31149 MW; ICF81B900979D2A1 CRC64;

Query Match 81.8%; Score 27; DB 1; Length 286;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7
| | | | |
Db 171 YRSQVIS 177

RESULT 6
YZ32_METJA STANDARD; PRT; 438 AA.
ID YZ32_METJA
AC Q60289;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJEC132.
GN MJEC132.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
```

RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL Jannaschii.";
RL Science 273:1058-1073(1996).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L77118; AAC37101.1; -;
DR TIGR; MJEC32; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 438 AA; 50925 MW; DC8FB11505F5DEE3 CRC64;

Query Match 81.8%; Score 27; DB 1; Length 438;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7
Db |||||
359 YRSTSI 365

RESULT 7
AINX_HUMAN
ID AINX_HUMAN STANDARD; PRT; 499 AA.
AC Q16352; Q9BRC5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-interneixin (Alpha-Inx) (66 kDa neurofilament protein)
DE (Neurofilament-66) (NF-66).
GN INA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95287809; PubMed=7769995;
RA Chan S.-O., Chiu F.-C.;
RT "Cloning and developmental expression of human 66 kd neurofilament
RL protein.";
RL Brain Res. Mol. Brain Res. 29:177-184(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CLASS-IV NEURONAL INTERMEDIATE FILAMENT THAT IS ABLE TO
CC SELF-ASSEMBLE. IT IS INVOLVED IN THE MORPHOGENESIS OF NEURONS. IT
CC MAY FORM AN INDEPENDENT STRUCTURAL NETWORK WITHOUT THE INVOLVEMENT
CC OF OTHER NEUROFILAMENTS OR IT MAY COOPERATE WITH NF-L TO FORM THE
CC FILAMENTOUS BACKBONE TO WHICH NF-M AND NF-H ATTACH TO FORM THE
CC CROSS-BRIDGES.
CC -!- TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN ADULT CNS.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN BRAIN AS EARLY AS THE 16TH OF
CC GESTATION, AND INCREASED RAPIDLY AND REACHED A STEADY STATE LEVEL
CC BY THE 18TH WEEK OF GESTATION.
CC -!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S78296; AAB34482.1; -;
DR EMBL; BC006359; AAB06359.1; -;
DR MIM; 605338; -;
DR InterPro: IPR001664; IF.
DR Pfam: PF00038; filament; 1.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Coiled coil; Neurone.
FT DOMAIN 1 87
FT DOMAIN 88 408
FT DOMAIN 409 499
FT DOMAIN 499 499
FT DOMAIN 88 129
FT DOMAIN 130 142
FT DOMAIN 143 238
FT DOMAIN 239 262
FT DOMAIN 263 408
FT DOMAIN 449 454
FT CONFLICT 37 41
FT CONFLICT 67 67
FT CONFLICT 92 92
FT CONFLICT 128 132
FT CONFLICT 141 141
FT CONFLICT 147 152
FT CONFLICT 191 198
FT CONFLICT 244 244
FT CONFLICT 263 301
FT CONFLICT 301 311
FT CONFLICT 310 311
FT CONFLICT 318 318
SQ SEQUENCE 499 AA; 55390 MW; 4C972764E9E8D3E CRC64;

Query Match 81.8%; Score 27; DB 1; Length 499;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSIS 7
Db |||||
38 FRSQSLS 44

RESULT 8
AINX_MOUSE
ID AINX_MOUSE STANDARD; PRT; 504 AA.
AC P46660; O61958;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-interneixin (Alpha-Inx) (66 kDa neurofilament protein)
DE (Neurofilament-66) (NF-66).
GN INA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=Spleen;
RX MEDLINE=95047490; PubMed=7959004;
RA Chien C.-L., Liem R.K.H.;
RT "Characterization of the mouse gene encoding the neuronal
RL intermediate filament protein alpha-interneixin.";
RL Gene 149:289-292(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96322433; PubMed=8734438;
RA Chan S.-O., Chiu F.-C.;
RT "The 66-kDa neurofilament protein (NF-66): sequence analysis and
RL evolution.";
RL Neurochem. Res. 21:449-455(1996).

OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98204792; PubMed=9535817;
 RA Tanaka N., Ohuchi N., Mukai Y., Ozaka Y., Ohtani Y., Tabuchi M.,
 RA Bhuviyan M.S., Fukui H., Harashima S., Takegawa K.;
 RT "Isolation and characterization of an invertase and its repressor
 genes from Schizosaccharomycetes pombe.";
 RL Biochem. Biophys. Res. Commun. 245:246-253(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Rajandream M.A., Barrell B.G., Volckaert G.;
 RN Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE OF 88-581 FROM N.A.
 RC STRAIN=PR745;
 RX MEDLINE=98162722; PubMed=9501991;
 RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
 RT "Identification of open reading frames in Schizosaccharomycetes pombe
 cDNAs.";
 RL DNA Res. 4:363-369(1997).
 RN [4]
 RP CARBOHYDRATES.
 RX MEDLINE=90253381; PubMed=2187435;
 RA Moreno S., Sanchez Y., Rodriguez L.;
 RT "Purification and characterization of the invertase from
 Schizosaccharomycetes pombe.";
 RL Biochem. J. 267:697-702(1990).
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-
 fructofuranoside residues in beta-D-fructofuranosides.
 CC -!- PTM: THE CARBOHYDRATE CONTENT OF THIS PROTEIN IS 67%. THIS IS
 COMPOSED OF EQUI MOLAR AMOUNTS OF MANNOSE AND GALACTOSE. THERE IS
 ALSO A SMALL AMOUNT OF GLUCOSAMINE PRESENT.
 CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB011433; BAA25684.1; -;
 DR EMBL; AL049644; CAB41057.1; -;
 DR EMBL; D89242; BAA13903.1; -;
 DR InterPro; IPR001362; Glyco_hydro_32.
 DR Pfam; PF00251; Glyco_hydro_32; 1.
 DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 581
 FT ACT_SITE 97 97
 FT BY SIMILARITY.
 FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 425 425 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (PROBABLE).

FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CONFLICT 186 189 MISSING (IN REF. 3).
 FT CONFLICT 190 190 H -> Y (IN REF. 3).
 FT CONFLICT 195 195 A -> P (IN REF. 3).
 FT CONFLICT 198 198 Q -> L (IN REF. 3).
 FT CONFLICT 205 205 D -> N (IN REF. 3).
 FT CONFLICT 243 243 I -> M (IN REF. 3).
 FT CONFLICT 246 246 M -> L (IN REF. 3).
 FT CONFLICT 256 256 S -> P (IN REF. 3).
 SQ SEQUENCE 581 AA; 64407 MW; 70206A6CD1F27EC4 CRC64;
 Query Match 81.8%; Score 27; DB 1; Length 581;
 Best Local Similarity 85.7%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YRSQIS 7
 DB 474 YRLQIS 480
 RESULT 11
 CADN_DROME
 ID CADN_DROME STANDARD; PRG; 3097 AA.
 AC O15943; Q9VJB7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Neural-cadherin precursor (Cadherin-N protein) (DN-cadherin).
 GN CADN OR CG7100.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridia; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head, and Embryo;
 RX MEDLINE=97388431; PubMed=9247265;
 RA Iwai Y., Hirano S., Steward R., Takeichi M., Uemura T.;
 RT "Axon patterning requires DN-cadherin, a novel neuronal adhesion
 receptor, in the Drosophila embryonic CNS.";
 RL Neuron 19:77-89(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrlaskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [3]
RP INTERACTION WITH ARM
RX MEDLINE=98298928; PubMed=9635189;
RA Loureiro J., Peifer M.;
RT "Roles of Armadillo, a Drosophila catenin, during central nervous
RT system development.";
RL Curr. Biol. 8:622-632(1998).
CC -1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
CC THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
CC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
CC SORTING OF HETEROGENEOUS CELL TYPES. MAY ASSOCIATE WITH ARM NEURAL
CC ISOFORM AND PARTICIPATE IN THE TRANSMISSION OF DEVELOPMENTAL
CC INFORMATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, THE PROTEIN FIRST APPEARS IN
CC THE MESODERM AT STAGE 9 AND IS PRESENT IN THE MYOBLASTS AND MUSCLE
CC FIBERS BY STAGE 12 AND STAGE 14, RESPECTIVELY. AT STAGE 12 THE
CC PROTEIN IS ALSO LOCATED IN THE AXONS OF THE ENTIRE CNS, BUT NOT IN
CC THE GLIAL CELLS. IN THIRD INSTAR LARVAE PROTEIN IS EXPRESSED IN
CC THE CNS NEUROPILE, PHOTORECEPTOR AXONS AND PRECURSORS OF ADULT
CC MUSCLES.
CC -1- SIMILARITY: CONTAINS 16 CADHERIN DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB002397; BAA22151.1; -;
CC EMBL; AE003656; AAF53635.1; -;
CC HSP; P00740; IIXA.
CC Flybase; FBgn0015609; CadN.
CC InterPro; IPR002126; Cadherin.
CC InterPro; IPR000233; Cadherin_C_term.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR000742; EGF_2
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001791; Laminin_G.
CC Pfam; PF00028; cadherin; 14.
CC Pfam; PF01049; Cadherin_C_term; 1.
CC Pfam; PF00008; EGF; 3.
CC Pfam; PF00054; laminin_G; 2.
CC PRINTS; PR00205; CADHERIN.
CC SMART; SM00112; CA; 16.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00001; EGF_like; 3.
CC SMART; SM00282; LamG; 2.
CC PROSITE; PS00232; CADHERIN_1; 9.
CC PROSITE; PS00468; CADHERIN_2; 16.
CC PROSITE; PS00022; EGF_1; 3.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS00025; LAM_G_DOMAIN; 2.
CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW Signal; EGF-like domain.
FT SIGNAL 1 36 POTENTIAL.
FT PROPEP 37 7

FT CHAIN ? 3097 ?
FT DOMAIN 1454 ?
FT TRANSMEM 1475
FT DOMAIN 1476 3097
FT DOMAIN 181 305
FT DOMAIN 430 543
FT DOMAIN 554 651
FT DOMAIN 660 756
FT DOMAIN 766 858
FT DOMAIN 867 968
FT DOMAIN 978 1078
FT DOMAIN 1087 1183
FT DOMAIN 1193 1299
FT DOMAIN 1307 1414
FT DOMAIN 1423 1514
FT DOMAIN 1523 1630
FT DOMAIN 1639 1742
FT DOMAIN 1749 1861
FT DOMAIN 1870 1966
FT DOMAIN 1974 2085
FT DOMAIN 2346 2377
FT DOMAIN 2379 2585
FT DOMAIN 2592 2627
FT DOMAIN 2631 2822
FT DOMAIN 2869 2902
FT DISULFID 2346 2357
FT DISULFID 2351 2366
FT DISULFID 2368 2377
FT DISULFID 2592 2607
FT DISULFID 2601 2616
FT DISULFID 2618 2627
FT DISULFID 2869 2880
FT DISULFID 2874 2891
FT DISULFID 2893 2902
FT CARBOHYD 97 97
FT CARBOHYD 150 150
FT CARBOHYD 325 325
FT CARBOHYD 426 426
FT CARBOHYD 930 930
FT CARBOHYD 1266 1266
FT VARIANT 1425 1425
FT CONFLICT 1342 1342
FT CONFLICT 2786 2786
FT CONFLICT 3097 AA; 347201 MW; 082242F28D9B5CC3 CRC64;
SQ SEQUENCE 3097 AA; 347201 MW; 082242F28D9B5CC3 CRC64;
Query Match 81.8%; Score 27; DB 1; Length 3097;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YRSOSIS 7
DB 2204 YRTQSMS 2210
||:||||
RESULT 12
GRPE_BACSU STANDARD; PRT; 186 AA.
ID GRPE_BACSU
AC P15874;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GRPE protein (HSP-70 cofactor).
GN GRPE.
OS *Bacillus subtilis*.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC *Bacillus/Staphylococcus* group; *Bacillus*.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / MB11;
RX MEDLINE=90206795; PubMed=2108432;

RA Wetzstein M., Schumann W.;
RT "Nucleotide sequence of a Bacillus subtilis gene homologous to the
RL grpE gene of E. coli located immediately upstream of the dnaK gene."; Nucleic Acids Res. 18:1289-1289(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168 / MB11;
RX MEDLINE-92250426; PubMed-1339421;
RA Wetzstein M., Voelker U., Dedio J., Loebau S., Zuber U.,
RA Schiesswohl M., Herget C., Hecker M., Schumann W.;
RT "Cloning, sequencing, and molecular analysis of the dnaK locus from
RL Bacillus subtilis."; J. Bacteriol. 174:3300-3310(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-168 / JH642;
RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,
RA Sato T., Takeuchi M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-10.
RC STRAIN-1558;
RX MEDLINE-94282319; PubMed-8012595;
RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,
RA Schmid R., Mach H., Hecker M.;
RT "Analysis of the induction of general stress proteins of Bacillus
RL subtilis."; Microbiology 140:741-752(1994).
CC -!- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF
CC DNAK. HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECYCLE
CC MORE EFFICIENTLY (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE GRPE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X51477; CAA35841.1; -;
DR EMBL; M84964; AAA22527.1; -;
DR EMBL; D84432; BAA12463.1; -;
DR EMBL; Z99117; CAB14490.1; -;
DR PIR; S08418; S08418.
DR PIR; S27504; S27504.
DR HSP; P09372; 1DKG.
DR Subtilisin; BG10663; grpe.
DR InterPro; IPR000740; Grpe.
DR Pfam; PF01025; Grpe; 1.
DR PRINTS; PR00773; GRPEPROTEIN.
DR PROSITE; PS01071; GRPE; 1.
KW Chaperone; Heat shock; Complete proteome.
FT INIT_MET 0 0
FT VARIANT 1 1 S -> H (IN STRAIN IS58).
FT VARIANT 4 4 K -> T (IN STRAIN IS58).
SQ SEQUENCE 186 AA; 21552 MW; A06216843F3C5FD7 CRC64;

Query Match 78.8%; Score 26; DB 1; Length 186;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YRSQSI 6
Db |||||:1
79 YRSQNI 84

RESULT 13
VE2_HPVI2
ID VE2_HPVI2 STANDARD; PRT; 494 AA.
AC P36782;

DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Regulatory protein E2.
GN E2.
OS Human papillomavirus type 12.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10604;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94265501; PubMed-8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types."; Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACNNNNNGT-3') PRESENT
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC -!- SUBUNIT: BINDS DNA AS A DIMER.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X74466; CAA52499.1; -;
DR PIR; S36541; S36541.
DR HSP; P17383; 1DHM.
DR InterPro; IPR001866; E2_N.
DR InterPro; IPR000427; Early2_C.
DR Pfam; PF00511; E2_C; 1.
DR Pfam; PF00508; E2_N; 1.
DR ProDom; PD000672; Early2_C; 1.
DR ProDom; PD000678; E2_N; 1.
KW Early protein; Transcription regulation; Activator; DNA-binding;
KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ SEQUENCE 494 AA; 56039 MW; 3C20AAF3560C10EE CRC64;

Query Match 78.8%; Score 26; DB 1; Length 494;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YRSQSI 7
Db |||||:1
266 YRSQNS 272

RESULT 14
CBPY_CANAL STANDARD; PRT; 542 AA.
AC P30574;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Carboxypeptidase Y precursor (EC 3.4.16.5) (Carboxypeptidase YSCY).
GN CPY1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93051356; PubMed-1427093;

RA Mukhtar M., Logan D.A., Kaufer N.F.;
 RT "the carboxypeptidase Y-encoding gene from Candida albicans and its
 RL transcription during yeast-to-hyphae conversion.";
 CC Gene 121:173-177(1992).
 CC -1- FUNCTION: INVOLVED IN DEGRADATION OF SMALL PEPTIDES.
 CC -1- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a
 CC broad specificity.
 CC -1- SUBCELLULAR LOCATION: LYSOSOME-LIKE VACUOLES.
 CC -1- INDUCTION: TRANSIENTLY DOWN-REGULATED DURING THE EARLY EVENTS OF
 CC YEAST TO HYPAE CONVERSION.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10; ALSO KNOWN AS THE
 CC SERINE CARBOXYPEPTIDASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M95182; AAA34326.2; -;
 DR PIR; JC1380; JC1380.
 DR HSSP; P00729; 1CPY.
 DR MEROPS; S10.001; -;
 DR InterPro; IPR0003379; Est_lip_thioest_actsite.
 DR Pfam; PF00450; serine_carbpept.
 DR PRINTS; PR00724; CRBOXYPTASEC.
 DR PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
 DR PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
 DR Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
 FT SIGNAL 1 21
 FT PROPEP 1 21
 FT CHAIN 128 542
 FT ACT_SITE 269 269
 FT ACT_SITE 461 461
 FT ACT_SITE 518 518
 FT BINDING 464 464
 FT BINDING 519 519
 FT BINDING 182 421
 FT DISULFID 316 330
 FT DISULFID 340 363
 FT DISULFID 347 356
 FT DISULFID 385 391
 FT CARBOHYD 213 213
 FT CARBOHYD 291 291
 FT SEQUENCE 542 AA; 61044 MW; 7FA6B9F82F9D44AF CRC64;

Query Match 78.8%; Score 26; DB 1; Length 542;
 Best Local Similarity 71.4%; Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSVS 7
 | | | | |
 DB 229 YSSQSVS 235

RESULT 15
 NRK1_YEAST
 ID NRK1_YEAST STANDARD; PRT; 1080 AA.
 AC P38692;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase NRK1 (EC 2.7.1.37) (N-rich kinase 1).
 GN NRK1 OR KIC1 OR YHR102W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=DC-5;
 RA Fukami Y.;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
 RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
 RA Latrelle P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
 RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT VIII.";
 RL Science 265:2077-2082(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D29980; BAA06250.1; -;
 DR EMBL; U00059; AAB88860.1; -;
 DR PIR; S48944; S48944.
 DR HSSP; P24941; 1AQ1.
 DR SGD; S0001144; KIC1.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 23 276
 FT NP_BIND 29 37
 FT BINDING 52 52
 FT ACT_SITE 144 144
 FT SEQUENCE 1080 AA; 117061 MW; 9989EAF315EE0B94 CRC64;

Query Match 78.8%; Score 26; DB 1; Length 1080;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RSQSVS 7
 | | | | |
 DB 900 RSQSVS 905

Search completed: August 19, 2002, 06:59:14
 Job time: 1379 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:19 ; Search time 140.4 Seconds
(without alignments)
8.625 Million cell updates/sec

Title: US-09-339-922A-112
Perfect score: 33
Sequence: 1 YRSQIS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	30	90.9	362	2	Q9S162	Q9S162 erysipelo
2	30	90.9	362	2	Q9S161	Q9S161 erysipelo
3	30	90.9	362	2	Q9S160	Q9S160 erysipelo
4	30	90.9	606	2	O66380	O66380 erysipelo
5	30	90.9	626	2	Q9WXB8	Q9WXB8 erysipelo
6	30	90.9	629	5	Q9NA88	Q9NA88 caenorhabdi
7	29	87.9	406	16	Q97L94	Q97L94 clostridium
8	29	87.9	409	5	Q23046	Q23046 caenorhabdi
9	29	87.9	944	16	Q98PL2	Q98PL2 mycoplasma
10	28	84.8	191	16	Q92BN7	Q92BN7 listeria in
11	28	84.8	206	10	Q9M282	Q9M282 arabidopsis
12	28	84.8	250	16	Q9HZU3	Q9HZU3 pseudomonas
13	28	84.8	316	5	Q9V3Y4	Q9V3Y4 drosophila
14	28	84.8	414	13	Q90299	Q90299 xenopus lae
15	28	84.8	501	11	Q9D0C4	Q9D0C4 mus musculus
16	28	84.8	2028	8	Q32064	Q32064 chlamydomon

17	27	81.8	223	10	Q9LIJ9	Q9LIJ9 arabidopsis
18	27	81.8	367	5	Q22069	Q22069 caenorhabdi
19	27	81.8	384	2	O68157	O68157 treponema h
20	27	81.8	386	2	O30572	O30572 treponema h
21	27	81.8	389	2	O68156	O68156 treponema h
22	27	81.8	423	16	Q97H59	Q97H59 clostridium
23	27	81.8	493	10	O64609	O64609 arabidopsis
24	27	81.8	499	4	Q9BRC5	Q9BRC5 homo sapien
25	27	81.8	521	5	Q9VZX9	Q9VZX9 drosophila
26	27	81.8	543	10	Q9AY90	Q9AY90 oryza sativ
27	27	81.8	608	10	Q9FG35	Q9FG35 arabidopsis
28	27	81.8	644	16	Q92KK6	Q92KK6 rhizobium m
29	27	81.8	806	16	O34433	O34433 bacillus su
30	27	81.8	846	10	Q9LP09	Q9LP09 arabidopsis
31	27	81.8	1206	10	Q9FW39	Q9FW39 oryza sativ
32	27	81.8	1743	5	Q966V0	Q966V0 drosophila
33	27	81.8	2785	11	Q99MV3	Q99MV3 mus musculu
34	26	78.8	190	2	Q9LAE8	Q9LAE8 rhizobium l
35	26	78.8	199	4	Q96131	Q96131 homo sapien
36	26	78.8	207	10	Q9FNH5	Q9FNH5 arabidopsis
37	26	78.8	209	10	Q9SRN0	Q9SRN0 arabidopsis
38	26	78.8	217	4	Q9ULQ9	Q9ULQ9 homo sapien
39	26	78.8	237	11	Q9R0G3	Q9R0G3 marmota mar
40	26	78.8	255	16	O25494	O25494 helicobacte
41	26	78.8	255	16	Q9ZL30	Q9ZL30 helicobacte
42	26	78.8	290	10	Q943V4	Q943V4 oryza sativ
43	26	78.8	306	12	Q9DHW1	Q9DHW1 watermelon
44	26	78.8	306	12	Q9QIR9	Q9QIR9 watermelon
45	26	78.8	306	12	Q9QIR2	Q9QIR2 watermelon

ALIGNMENTS

RESULT 1					
Q9S162	1				
ID	Q9S162	PRELIMINARY;	PRT;	362	AA.
AC	Q9S162;				
DT	01-MAY-2000 (Tremblrel. 13, Created)				
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)				
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)				
DE	SPAA PROTEIN (FRAGMENT).				
GN	SPAA.				
OS	Erysipelothrix rhusiopathiae.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;				
CC	Erysipelothrix group; Erysipelothrix.				
OX	NCBI_TaxID=1648;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=KOGANEI;				
RX	MEDLINE=99386823; PubMed=10456877;				
RA	Imada Y., Goji N., Ishikawa H., Kishima M., Sekizaki T.;				
RT	"Truncated surface protective antigen (SpaA) of Erysipelothrix				
RT	rhusiopathiae serotype la elicits protection against challenge with				
RT	serotypes la and 2b in pigs."				
RL	Infect. Immun. 67:4376-4382(1999).				
DR	EMBL; AB024082; BAA84453.1; -				
FT	NON_TER 1				
FT	NON_TER 362				
SQ	SEQUENCE 362 AA; 42371 MW; 9F406ADA1619C5B7 CRC64;				

Query Match 90.9%; Score 30; DB 2; Length 362;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7
||:||||
Db 298 YRAQIS 304

RESULT 2
Q9S161

ID Q9S161 PRELIMINARY; PRT; 362 AA.
 AC Q9S161;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE SPAA PROTEIN (FRAGMENT).
 GN SPAA.
 OS Erysipelothrix rhusiopathiae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Erysipelothrix group; Erysipelothrix.
 OX NCBI_TaxID=1648;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC19414;
 RX MEDLINE=99386823; PubMed=10456877;
 RA Imada Y., Goji N., Ishikawa H., Kishima M., Sekizaki T.;
 RT "Truncated surface protective antigen (SpaA) of Erysipelothrix
 rhusiopathiae serotype la elicits protection against challenge with
 serotypes la and 2b in pigs."
 RL Infect. Immun. 67:4376-4382(1999).
 DR EMBL; AB024083; BAA84454.1; -.
 FT NON_TER 1 362
 FT NON_TER 362 362
 SQ SEQUENCE 362 AA; 42259 MW; F355931EEA3C206A CRC64;

Query Match 90.9%; Score 30; DB 2; Length 362;
 Best Local Similarity 85.7%; Pred. No. 33;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7
 ||:||||
 Db 298 YRAQIS 304

RESULT 3

ID Q9S160 PRELIMINARY; PRT; 362 AA.
 AC Q9S160;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE SPAA PROTEIN (FRAGMENT).
 GN SPAA.
 OS Erysipelothrix rhusiopathiae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Erysipelothrix group; Erysipelothrix.
 OX NCBI_TaxID=1648;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SE-9;
 RX MEDLINE=99386823; PubMed=10456877;
 RA Imada Y., Goji N., Ishikawa H., Kishima M., Sekizaki T.;
 RT "Truncated surface protective antigen (SpaA) of Erysipelothrix
 rhusiopathiae serotype la elicits protection against challenge with
 serotypes la and 2b in pigs."
 RL Infect. Immun. 67:4376-4382(1999).
 DR EMBL; AB024084; BAA84455.1; -.
 FT NON_TER 1 362
 FT NON_TER 362 362
 SQ SEQUENCE 362 AA; 42394 MW; 67C3ADA494FEE753 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 362;
 Best Local Similarity 85.7%; Pred. No. 33;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7
 ||:||||
 Db 298 YRAQIS 304

RESULT 4

O66380 PRELIMINARY; PRT; 606 AA.
 AC O66380;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE SPAA.
 GN SPAA.
 OS Erysipelothrix rhusiopathiae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Erysipelothrix group; Erysipelothrix.
 OX NCBI_TaxID=1648;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAMA-96;
 RA Makino S., Yamamoto K., Murakami S., Shirahata T., Uemura K.,
 RA Sawada T., Wakamoto H., Morita Y.;
 RT "Properties of Repeat Domain Found in A Novel Protective Antigen,
 RT SpaA, of Erysipelothrix rhusiopathiae."
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB012763; BAA28613.1; -.
 DR InterPro; IPR002479; CW_binding.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF01473; CW_binding_1; 7.
 DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 SQ SEQUENCE 606 AA; 69960 MW; 4E9D0A9EB536D0B3 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 606;
 Best Local Similarity 85.7%; Pred. No. 57;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7
 ||:||||
 Db 381 YRAQIS 387

RESULT 5

ID Q9WXB8 PRELIMINARY; PRT; 626 AA.
 AC Q9WXB8;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE PROTECTIVE ANTIGEN SPAA.1.
 GN SPAA.
 OS Erysipelothrix rhusiopathiae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Erysipelothrix group; Erysipelothrix.
 OX NCBI_TaxID=1648;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUJISAWA;
 RX MEDLINE=99184982; PubMed=10084998;
 RA Shimoji Y., Mori Y., Fischetti V.A.;
 RT "Immunological characterization of a protective antigen of
 Erysipelothrix rhusiopathiae: Identification of the region responsible
 for protective immunity."
 RL Infect. Immun. 67:1646-1651(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUJISAWA;
 RX MEDLINE=99386823; PubMed=10456877;
 RA Imada Y., Goji N., Ishikawa H., Kishima M., Sekizaki T.;
 RT "Truncated surface protective antigen (SpaA) of Erysipelothrix
 rhusiopathiae serotype la elicits protection against challenge with
 serotypes la and 2b in pigs."
 RL Infect. Immun. 67:4376-4382(1999).
 DR EMBL; AB017447; BAA76540.1; -.
 DR EMBL; AB019124; BAA84452.1; -.
 DR InterPro; IPR002479; CW_binding.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF01473; CW_binding_1; 8.

DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SQ SEQUENCE 626 AA; 72276 MW; FB50BDB8CC1D9066 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 626;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7
||:||||
Db 381 YRAQSIS 387

RESULT 6

Q9NA88 PRELIMINARY; PRT; 629 AA.
AC Q9NA88;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Y57A10A.4 PROTEIN.
GN Y57A10A.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Smye R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL117195; CAB55009.1; --
SQ SEQUENCE 629 AA; 71450 MW; 7A068C2062048121 CRC64;

Query Match 90.9%; Score 30; DB 5; Length 629;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7
||:||||
Db 466 YRNQIS 472

RESULT 7

Q97L94 PRELIMINARY; PRT; 406 AA.
AC Q97L94;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE PREDICTED MEMBRANE PROTEIN.
GN CAC0668.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R.L., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838 (2001).
DR EMBL; AE007582; AAK78645.1; --
KW Complete proteome.
SQ SEQUENCE 406 AA; 47239 MW; D020D1BAEFB707C8 CRC64;

Query Match 87.9%; Score 29; DB 16; Length 406;
Best Local Similarity 85.7%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7
|||||
Db 193 YRSQDIS 199

RESULT 8

Q23046 PRELIMINARY; PRT; 409 AA.
ID Q23046;
AC Q23046;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T25F10.3 PROTEIN.
GN T25F10.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Pauley, A., Gattung S.;
RT "The sequence of C. elegans cosmid T25F10.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64856; AAB04985.1; --
DR InterPro; IPR000561; EGF-like.
DR SMART; SM00181; EGF; 2.
DR PROSITE; PS00022; EGF_1; UNKNOWN_3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 409 AA; 45218 MW; F4F0BC370F09BED7 CRC64;

Query Match 87.9%; Score 29; DB 5; Length 409;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 6
|||||
Db 133 YRSQSI 138

```

RESULT 9
Q98PL2
ID Q98PL2 PRELIMINARY; PRT; 944 AA.
AC Q98PL2;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE EXCNUCLEASE ABC SUBUNIT A.
GN MYPU_7100.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Molllicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chabaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis."
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445565; CAC13883.1; -.
DR MypuList; MYPU_7100; -.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00005; ABC_tran; 2.
DR SMART; SM00382; AAA; 2.
KW Complete proteome.
SQ SEQUENCE 944 AA; 105297 MW; 5E52AC2B5F9E507 CRC64;

```

```

Query Match 87.9%; Score 29; DB 16; Length 944;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YRSQIS 7
|||:|
DB 784 YRSKIS 790

```

```

RESULT 10
Q92BN7
ID Q92BN7 PRELIMINARY; PRT; 191 AA.
AC Q92BN7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEAT SHOCK PROTEIN GRPE.
GN GRPE OR LIN1511.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant J., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species."
RL Science 294:849-852(2001).
DR EMBL; AL596168; CAC96742.1; -.

```

```

DR ListList; LIN01511; -.
KW Complete proteome.
SQ SEQUENCE 191 AA; 21952 MW; 853F11392E126981 CRC64;

Query Match 84.8%; Score 28; DB 16; Length 191;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7
|||:|
DB 84 YRSQSLA 90

RESULT 11
Q9M282
ID Q9M282 PRELIMINARY; PRT; 206 AA.
AC Q9M282;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 22.7 KDA PROTEIN.
GN T22K7_110.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138641; CAB86921.1; -.
KW Hypothetical protein.
SQ SEQUENCE 206 AA; 22651 MW; E5651312ABDE614B CRC64;

```

```

Query Match 84.8%; Score 28; DB 10; Length 206;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YRSQIS 7
|||:|
DB 107 YRSKVS 113

```

```

RESULT 12
Q9HZU3
ID Q9HZU3 PRELIMINARY; PRT; 250 AA.
AC Q9HZU3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE PRECORRN-2 METHYLTRANSFERASE COBI.
GN COBI OR PA2904.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

```

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 opportunistic pathogen.";
 RL Nature 406:959-964 (2000).
 DR EMBL; AF004716; AAG06292.1; -;
 DR InterPro; IPR001993; Corrin_porph_mthyltrnf.
 DR Pfam; PF00590; TP_methylase; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
 KW Transferase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 250 AA; 27274 MW; 3AC4B437C77F477E CRC64;

Query Match 84.8%; Score 28; DB 16; Length 250;
 Best Local Similarity 71.4%; Pred. No. 70;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7
 ||:||||
 Db 154 YRNQSL 160

RESULT 13

Q9V3Y4
 ID Q9V3Y4 PRELIMINARY; PRT; 316 AA.
 AC Q9V3Y4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MTCH PROTEIN (LD43650P).
 GN MTCH OR CG6851.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
 RA Fosler C., Gabrielista C.C., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.N., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jang J.S., Hahn Y., Park C., Chung J.H.;
 RT "Identification of an evolutionary conserved mitochondrial carrier
 family from various organisms.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y, CN BW SP;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunco J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003467; AAF47342.1; -;
 DR EMBL; AF176011; AAD52649.1; -;
 DR EMBL; AY051973; AAK93397.1; -;
 DR FlyBase; FBgn0027786; Mtch.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 1.
 SQ SEQUENCE 316 AA; 35011 MW; 4545D305A57A9991 CRC64;

Query Match 84.8%; Score 28; DB 5; Length 316;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7
 :||||||
 Db 292 WRSQIS 298

RESULT 14

Q90Z99
 ID Q90Z99 PRELIMINARY; PRT; 414 AA.
 AC Q90Z99;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PDCD9.
 GN PDCD9.
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; *Xenopus*.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carrodegas J.A., Bogenhagen D.F.;
 RT "The *Xenopus* homolog of chicken pro-apoptotic protein p52 and human
 PDCD9 is a mitochondrial protein.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF317657; AAK66969.1; -;
 SQ SEQUENCE 414 AA; 47229 MW; 45BB1A4C9EDFCA86 CRC64;

Query Match 84.8%; Score 28; DB 13; Length 414;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRSQIS 7
 ||||:|
 Db 150 WRSQEV 156

RESULT 15

Q9D0C4

ID O9DOC4 PRELIMINARY; PRT; 501 AA.
AC O9DOC4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 2610027018RIK PROTEIN (RIKEN CDNA 2610027018 GENE).
GN 2610027018RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK011576; BAB2710.1; -;
DR EMBL; BC012521; AAH12521.1; -;
DR MGD; MGI:1923607; 2610027018Rik.
DR InterPro; IPR003402; Met_10.
DR Pfam; PF02475; Met_10; 1.
SQ SEQUENCE 501 AA; 56794 MW; 55816182B08766C0 CRC64;

Query Match 84.8%; Score 28; DB 11; Length 501;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YRSQSIS 7
||:|:|:
Db 467 YRNQSL 473

Search completed: August 19, 2002, 06:58:22
Job time: 1412 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:14 ; Search time 180.34 Seconds
(without alignments)
4.311 Million cell updates/sec

Title: US-09-339-922A-112

Perfect score: 33

Sequence: 1 YRSQSTIS 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

- 1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	7	22 AAB61404	Enhanced 6H6LH lig
2	33	100.0	11	19 AAW76012	LM609 grafted anti
3	33	100.0	11	22 AAB61370	LM609 VL CDR2 pept
4	33	100.0	107	19 AAW76006	LM609 grafted anti
5	33	100.0	107	19 AAW76002	Vitaxin antibody 1
6	33	100.0	107	19 AAW76004	LM609 antibody lig
7	33	100.0	107	22 AAG63588	A light chain vari
8	33	100.0	107	22 AAG63590	A light chain vari
9	33	100.0	107	22 AAB61360	Vitaxin light chai
10	33	100.0	107	22 AAB61362	Antibody LM609 lig
11	33	100.0	107	22 AAB61364	Light chain variab

12	30	90.9	402	21	AAB14800	Erysipelothrix rhu
13	30	90.9	606	20	AAV43219	E. rhusiopathiae s
14	30	90.9	626	21	AAV95782	Erysipelothrix rhu
15	28	84.8	316	22	ABB62737	Drosophila melanog
16	28	84.8	368	10	AAV90471	Human cytomegalovi
17	27	81.8	11	19	AAW76032	LM609 grafted anti
18	27	81.8	11	22	AAB61390	Mutant VL CDR2 pep
19	27	81.8	44	22	AAW87562	Human immune/haema
20	27	81.8	64	22	AAW95618	Human reproductive
21	27	81.8	88	21	AAV56653	Partial peptide fr
22	27	81.8	102	22	AAW77337	Human bone marrow
23	27	81.8	105	20	AAW87456	JK gene product.
24	27	81.8	105	20	AAW87458	Humanised anti-alp
25	27	81.8	107	13	AAW25729	Humanised VL regio
26	27	81.8	107	14	AAW38601	HYH light chain.
27	27	81.8	107	19	AAW58482	Murine HyH antibod
28	27	81.8	107	20	AAW84098	Humanised anti-alp
29	27	81.8	107	21	AAV71238	Humanised antibody
30	27	81.8	107	21	AAV71240	Humanised antibody
31	27	81.8	107	21	AAV71472	Mouse monoclonal a
32	27	81.8	107	22	AAB69677	Murine CMV5 antio
33	27	81.8	107	22	AAB69678	Humanised CMV5 ant
34	27	81.8	107	22	AAB69690	Human Wol antibody
35	27	81.8	108	17	AAW04333	Light chain of mon
36	27	81.8	108	20	AAW84094	Murine vitronectin
37	27	81.8	109	15	AAW52033	Light chain variab
38	27	81.8	109	20	AAV06380	Murine monoclonal
39	27	81.8	112	20	AAW84100	Vitronectin alpha-
40	27	81.8	114	22	AAW98665	Murine protein #2.
41	27	81.8	127	15	AAW54093	Sequence of mouse
42	27	81.8	127	22	AAW69687	Murine CMV5 antio
43	27	81.8	128	21	AAV56718	Amino acid sequenc
44	27	81.8	259	21	AAW09775	TMV 30K movement p
45	27	81.8	274	21	AAG24104	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAB61404

ID AAB61404 standard; peptide; 7 AA.

AC AAB61404;

DT 03-APR-2001 (first entry)

XX

DE Enhanced 6H6LH light chain CDR2.

XX

KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX

OS Unidentified.

XX

PN WO200078815-A1.

XX

PD 28-DEC-2000.

XX

PF 23-JUN-2000; 2000WO-US17454.

XX

PR 24-JUN-1999; 99US-0339922.

XX

(MOLE-) APPLIED MOLECULAR EVOLUTION.

XX

PI Huse WD, Wu H;

XX

DR WPI; 2001-050110/06.

XX

Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -

PS Claim 4; Page 46; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta₃ integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta₃-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 33; DB 22; Length 7;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7

Db 1 yrsqsis 7

RESULT 2

AAW76012

ID AAW76012 standard; Protein; 11 AA.

XX AC AAW76012;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-L region CDR2 protein fragment #1.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

XX KW macular degeneration; osteoporosis; primer; V-L region; CDR;

XX KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAV49849.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta₃

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX PS Disclosure; Page 40; 129pp; English.

XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta₃ and can be used to

CC inhibit binding of alphavbeta₃ to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta₃-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 33; DB 19; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7

Db 5 yrsqsis 11

RESULT 3

AA61370

ID AAB61370 standard; peptide; 11 AA.

XX AC AAB61370;

XX DT 03-APR-2001 (first entry)

XX DE LM609 VL CDR2 peptide.

XX KW LM609; grafted antibody; alphavbeta₃ integrin; angiogenesis;

XX KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX PS Disclosure; Page 39; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta₃ integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta₃-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 33; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 YRSQSTS 7
Db 5 YRSQSTS 11

RESULT 4
AAW76006
ID AAW76006 standard; Protein; 107 AA.
XX
AC AAW76006;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody light chain variable region protein fragment.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; AAV49843.
XX
Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
XX
Claim 19; Fig 7; 129pp; English.
XX
This sequence represents a LM609 grafted antibody variable light chain
region. LM609 and the antibody vitaxin bind selectively to integrin
alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
and thus block integrin-mediated signal transduction. This is useful in
the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
specifically angiogenesis and restenosis (but also e.g. (non-)immune
inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
etc.). The antibodies contain non-murine framework regions so are
suitable for use in humans. Enhanced types of LM609 have affinity more
than 90 times greater than that of parent the parent antibody.
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 33; DB 19; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSTS 7
Db 50 YRSQSTS 56

RESULT 6
AAW76004
ID AAW76004 standard; Protein; 107 AA.
XX
AC AAW76004;
XX
DT 02-NOV-1998 (first entry)
XX

```

DE LM609 antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAW76004.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 46; Fig 2b; 129pp; English.

XX This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 107 AA;

Query Match 100.0%; Score 33; DB 19; Length 107;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSIS 7

Db | | | | | | | |

50 yrsqsis 56

RESULT 7

AAG63588
 ID AAG63588 standard; Protein; 107 AA.

XX AAG63588;

XX 15-OCT-2001 (first entry)

XX A light chain variable region of LM609 grafted antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.

XX Synthetic.

OS Mus sp.

XX Key Location/Qualifiers

FT Misc-difference 49 /note= "unspecified residue encoded by MKK"

XX US2001011125-A1.

XX 02-AUG-2001.

XX 30-JAN-1997; 97US-0790540.

XX 30-JAN-1997; 97US-0790540.

XX (HUSE/) HUSE W D.

XX Huse WD;

XX WPI; 2001-496171/54.

XX N-PSDB; AAH74624.

XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer

XX Claim 1; Fig 1B; 25pp; English.

XX The present sequence represents the light chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX Sequence 107 AA;

Query Match 100.0%; Score 33; DB 22; Length 107;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSIS 7

Db | | | | | | | |

50 yrsqsis 56

RESULT 8

AAG63590

ID AAG63590 standard; Protein; 107 AA.

XX AAG63590;

XX 15-OCT-2001 (first entry)

XX A light chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer.

XX Mus sp.

XX PN US2001011125-A1.
 XX PD 02-AUG-2001.
 XX PF 30-JAN-1997; 97US-0790540.
 XX PR 30-JAN-1997; 97US-0790540.
 XX PA (HUSE/) HUSE W D.
 XX PI Huse WD;
 XX DR WPI: 2001-496171/54.
 XX DR N-PSDB; AAH74626.
 XX PT New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX PS Disclosure; Fig 2B; 25pp; English.
 XX CC The present sequence represents the light chain variable region of the
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.
 CC The specification describes a LM609 grafted antibody which has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.
 XX SQ Sequence 107 AA;

 Query Match 100.0%; Score 33; DB 22; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YRSQSQS 7
 Db 50 yrsqsqs 56

 RESULT 9
 AAB61360
 ID AAB61360 standard; protein; 107 AA.
 XX AC AAB61360;
 XX DT 03-APR-2001 (first entry)
 XX DE Vitaxin light chain variable region protein.
 XX KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 23-JUN-2000; 2000WO-US17454.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI: 2001-050110/06.
 XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI: 2001-050110/06.
 XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX PS Disclosure; Fig 1; 132pp; English.
 XX CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX SQ Sequence 107 AA;

 Query Match 100.0%; Score 33; DB 22; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YRSQSQS 7
 Db 50 yrsqsqs 56

 RESULT 10
 AAB61362
 ID AAB61362 standard; protein; 107 AA.
 XX AC AAB61362;
 XX DT 03-APR-2001 (first entry)
 XX DE Antibody LM609 light chain variable region protein.
 XX KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX OS Unidentified.
 XX PN WO200078815-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-US17454.
 XX PR 24-JUN-1999; 99US-0339922.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PI Huse WD, Wu H;
 XX DR WPI: 2001-050110/06.
 XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

XX Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta₃ integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

XX osteoporosis.

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 33; DB 22; Length 107;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7

Db 50 yrsqsis 56

|||||

RESULT 11

AAB61364

ID AAB61364 standard; protein; 107 AA.

XX AAB61364;

AC AAB61364;

XX 03-APR-2001 (first entry)

DT DT

DE Light chain variable region of LM609.

XX

XX LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

KW

XX Unidentified.

OS

XX WO200078815-A1.

PN

XX 28-DEC-2000.

PD

XX 23-JUN-2000; 2000WO-US17454.

PF

XX 24-JUN-1999; 99US-0339922.

PR

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA

XX Huse WD, Wu H;

PI

XX WPI; 2001-050110/06.

DR

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

XX Disclosure; Fig 7; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta₃ integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 33; DB 22; Length 107;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7

Db 50 yrsqsis 56

|||||

RESULT 12

AAB14800

ID AAB14800 standard; Protein; 402 AA.

XX AAB14800;

AC AAB14800;

XX 11-DEC-2000 (first entry)

DT DT

DE Erysipelothrix rhusiopathiae protective polypeptide antigen fragment.

XX

XX Protective polypeptide antigen; PPA; Fujisawa strain; swine erysipelas;

KW recombinant production; Immunogenic; subunit vaccine;

KW transmucous administration.

KW

XX Erysipelothrix rhusiopathiae.

OS

XX JP3072345-B1.

PN

XX 31-JUL-2000.

PD

XX 31-MAR-1999; 99JP-0094004.

PF

XX 31-MAR-1999; 99JP-0094004.

PR

XX (NORQ) NORINSUSANSHO KACHIKU EISEI SHIKENJOCHO.

PA (HGET) HIGETA SHOYU KK.

PA (FUJI-) FUJITA GAKUEN.

XX

XX WPI; 2000-551432/51.

DR

DR N-PSDB; AAA72313, AAA72317, AAA72318.

XX

XX Novel recombinant protective polypeptide antigen useful as a vaccine

PT for protecting livestock against Erysipelothrix rhusiopathiae

PT infection -

PT

XX Claim 1; Page 14-15; 23pp; Japanese.

PS

XX This sequence represents a 46.5 kD immunogenic fragment of the

CC protective polypeptide antigen (PPA) of the bacterium Erysipelothrix

CC rhusiopathiae. This bacterium infects livestock, particularly pigs

CC (swine erysipelas), and is also able to cause disease in humans. The

CC recombinantly produced PPA fragment may be used as a subunit vaccine for

CC stimulating an immune response in animals against Erysipelothrix

CC rhusiopathiae. As the vaccine can be produced recombinantly, it can be

CC produced on a large scale. The vaccine is suitable for transmucous

CC administration.

XX

XX SQ Sequence 402 AA;

Query Match 90.9%; Score 30; DB 21; Length 402;

Best Local Similarity 85.7%; Pred. No. 80;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7

Db 352 yrsqsis 358

|||||

```

RESULT 13
AAAY43219
ID AAY43219 standard; Protein; 606 AA.
XX AC
XX AAY43219;
XX DT
XX 13-JAN-2000 (first entry)
XX DE E. rhusiopathiae surface layer protein sequence.
XX KW Surface layer protein; Immunological detection; antigen; pig erysipelas;
XX genetic detection.
XX OS Erysipelothrix rhusiopathiae.
XX PN JP11262391-A.
XX PD 28-SEP-1999.
XX PF 17-MAR-1998; 98JP-0067258.
XX PR 17-MAR-1998; 98JP-0067258.
XX PA (CHCC ) CHISSO CORP.
XX WPI; 1999-603802/52.
XX DR N-PSDB; AA231581.
XX PT New surface layer protein of Erysipelothrix rhusiopathiae - useful for
XX detecting antibody against E. rhusiopathiae
XX PS Claim 1; Page 8-11; 14pp; Japanese.
XX CC This sequence is the Erysipelothrix rhusiopathiae surface layer
XX protein of the invention. The surface layer protein can be used as an
XX antigen in a method for the immunological detection of E. rhusiopathiae.
XX It can also be used as an antigen; (1) in a method for the immunological
XX detection of an antibody against E. rhusiopathiae; and (2) in a method
XX for the immunological detection of pig erysipelas. The DNA sequence can
XX be used in a method for the genetic detection of E. rhusiopathiae or pig
XX erysipelas. The methods are simple and rapid.
XX SQ Sequence 606 AA;

```

```

Query Match 90.9%; Score 30; DB 20; Length 606;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YRSQSIS 7
||:||||
Db 381 yraqsis 387

```

```

RESULT 14
AAAY95782
ID AAY95782 standard; Protein; 626 AA.
XX AC
XX AAY95782;
XX DT 07-NOV-2000 (first entry)
XX DE Erysipelothrix rhusiopathiae erysipelas protective antigen.
XX KW Erysipelas protective antigen; Epa; SpaA.1; vaccine; infection;
XX immuno-protective epitope.
XX OS Erysipelothrix rhusiopathiae.
XX FH
XX Key Location/Qualifiers
XX Peptide 1..29
XX Protein 30..626

```

```

FT Region /label= Mature_protein
FT 50...55 /note= "LPXTGX motif"
FT Peptide 448..467
FT /label= Repeat_R1
FT Peptide 468..487
FT /label= Repeat_R2
FT Peptide 488..507
FT /label= Repeat_R3
FT Peptide 508..527
FT /label= Repeat_R4
FT Peptide 528..547
FT /label= Repeat_R5
FT Peptide 548..567
FT /label= Repeat_R6
FT Peptide 568..587
FT /label= Repeat_R7
FT Peptide 588..607
FT /label= Repeat_R8
FT Peptide 608..626
FT /label= Repeat_R9

```

WO200047744-A1.

17-AUG-2000.

10-FEB-2000; 2000WO-US03789.

10-FEB-1999; 99US-0119389.

(UYRQ) UNIV ROCKEFELLER.

Fischetti VA, Shimoji Y;

WPI; 2000-524541/47.

N-PSDB; AAA50205.

Vaccines for protecting turkeys and pigs against Erysipelothrix
rhusiopathiae infections comprising a polypeptide sequence from the
N-terminal region of an erysipelas protective antigen -

Claim 2; Fig 2; 61pp; English.

The present sequence is that of the erysipelas protective antigen
(Epa or SpaA.1) of Erysipelothrix rhusiopathiae strain Fujisawa, as
deduced from an isolate Epa gene (see AAA50205). E. rhusiopathiae is
the causative agent of erysipelas in animals and erysipeloid in
humans. Epa shows structural and sequence similarities to
pneumococcal surface protein A (PspA) and other choline binding
proteins of Streptococcus pneumoniae. Its C-terminal region
consists of a series of conserved 20-amino acid repeats (R1-R9).
The N-terminal portion of the Epa protein, especially a polypeptide
comprising residues 12-195 of the present sequence, was identified
as a vaccine antigen, protecting mice and pigs from a lethal
challenge with E. rhusiopathiae. Vaccines containing immunogenic
polypeptides of E. rhusiopathiae, where the immunogenic polypeptide
comprises an immuno-protective epitope from the N-terminal region
of Epa, especially residues 30-447, 30-195 or 30-100 of the present
sequence, are claimed. A claimed method for protecting an animal,
especially a turkey or pig, from infection by E. rhusiopathiae
involves administering the vaccine, or an expression vector
comprising a nucleic acid encoding the N-terminal portion or
full-length Epa. A claimed method for detecting the presence of
protective antibodies to E. rhusiopathiae involves detecting
binding of antibodies in a biological sample with a polypeptide
comprising an immunoprotective epitope of Epa.

Sequence 626 AA;

Query Match 90.9%; Score 30; DB 21; Length 626;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 YRSQSI 7
      11:||||
Db      381 yrsqsis 387

RESULT 15
ABB62737
ID      ABB62737 standard; Protein; 316 AA.
XX
AC      ABB62737;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Drosophila melanogaster polypeptide SEQ ID NO 15003.
XX
KW      Drosophila; developmental biology; cell signalling; insecticide;
KW      pharmaceutical.
XX
OS      Drosophila melanogaster.
XX
PN      WO200171042-A2.
XX
PD      27-SEP-2001.
XX
PF      23-MAR-2001; 2001WO-US09231.
XX
PR      23-MAR-2000; 2000US-191637P.
PR      11-JUL-2000; 2000US-0614150.
XX
PA      (PEKE ) PE CORP NY.
XX
PI      Venter JC, Adams M, Li PWD, Myers EW;
XX
DR      WPI; 2001-656860/75.
DR      N-PSDB; ABL06840.
XX
PT      New isolated nucleic acid detection reagent for detecting 1000 or more
PT      genes from Drosophila and for elucidating cell signalling and cell-cell
PT      interactions -
XX
PS      Disclosure; SEQ ID NO 15003; 21pp + Sequence Listing; English.
XX
CC      The invention relates to an isolated nucleic acid detection reagent
CC      capable of detecting 1000 or more genes from Drosophila. The invention is
CC      useful in developmental biology and in elucidating cell signalling and
CC      cell-cell interactions in higher eukaryotes for the development of
CC      insecticides, therapeutics and pharmaceutical drugs. The invention
CC      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC      sequences (ABL01840-ABL16175) and the encoded proteins
CC      (ABB57737-ABB72072).
CC      The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ      Sequence 316 AA;

Query Match      84.8%; Score 28; DB 22; Length 316;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YRSQSI 7
      11:||||
Db      292 wrsqsis 298

```

Search completed: August 19, 2002, 06:39:15
Job time: 1476 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:43 ; Search time 61.75 Seconds
(without alignments)
2.769 Million cell updates/sec

Title: US-09-339-922A-112

Perfect score: 33

Sequence: 1 YRSQIS 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents,AA:*

- 1: /cgn2.6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2.6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2.6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2.6/ptodata/2/iaa/PCUTUS_COMB.pep.*
- 6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	81.8	33	4	US-08-525-539A-12
2	27	81.8	96	2	US-08-737-560A-9
3	27	81.8	100	1	US-08-436-463-19
4	27	81.8	103	1	US-08-436-463-21
5	27	81.8	107	1	US-07-634-278-62
6	27	81.8	107	1	US-07-634-278-63
7	27	81.8	107	1	US-07-634-278-87
8	27	81.8	107	1	US-08-477-728-62
9	27	81.8	107	1	US-08-477-728-63
10	27	81.8	107	1	US-08-477-728-87
11	27	81.8	107	1	US-08-474-040-62
12	27	81.8	107	1	US-08-474-040-63
13	27	81.8	107	1	US-08-474-040-87
14	27	81.8	107	1	US-08-487-200-62
15	27	81.8	107	1	US-08-487-200-63
16	27	81.8	107	1	US-08-487-200-87
17	27	81.8	107	1	US-08-436-463-20
18	27	81.8	107	1	US-08-107-669D-1
19	27	81.8	107	1	US-08-472-788A-1
20	27	81.8	107	2	US-08-477-531B-1
21	27	81.8	107	2	US-08-082-842A-1
22	27	81.8	107	4	US-08-484-537-62
23	27	81.8	107	4	US-08-484-537-63
24	27	81.8	107	4	US-08-484-537-87
25	27	81.8	108	2	US-08-737-560A-11
26	27	81.8	109	1	US-07-942-245-4
27	27	81.8	127	1	US-07-634-278-83

28	27	81.8	127	1	US-08-477-728-83	Sequence 83, Appl
29	27	81.8	127	1	US-08-474-040-83	Sequence 83, Appl
30	27	81.8	127	1	US-08-487-200-83	Sequence 83, Appl
31	27	81.8	127	1	US-08-436-463-4	Sequence 4, Appl
32	27	81.8	127	1	US-08-436-463-18	Sequence 18, Appl
33	27	81.8	127	4	US-08-484-537-83	Sequence 83, Appl
34	27	81.8	581	4	US-09-331-581-2	Sequence 2, Appl
35	26	78.8	909	4	US-09-425-383-2	Sequence 2, Appl
36	26	78.8	1784	4	US-09-040-738-2	Sequence 2, Appl
37	26	78.8	1784	4	US-08-652-426A-2	Sequence 2, Appl
38	25	75.8	325	4	US-09-041-886-33	Sequence 33, Appl
39	25	75.8	330	2	US-08-815-176-1	Sequence 1, Appl
40	25	75.8	409	1	US-08-403-545-2	Sequence 2, Appl
41	25	75.8	409	4	US-08-404-381-2	Sequence 2, Appl
42	25	75.8	1004	4	US-08-916-352-2	Sequence 2, Appl
43	25	75.8	1052	2	US-08-852-806-2	Sequence 2, Appl
44	25	75.8	1052	3	US-09-163-669-2	Sequence 2, Appl
45	25	75.8	1137	1	US-08-369-043-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-08-525-539A-12
; Sequence 12, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A-12

Query Match 81.8%; Score 27; DB 4; Length 33;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YRSQIS 7

```

Db      1 YRSQSIG 7
      1 | | | | |
RESULT 2
US-08-737-560A-9
; Sequence 9, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuul
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuul
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: VK23.32'CL
US-08-737-560A-9

Query Match      81.8%; Score 27; DB 2; Length 96;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YRSQSIG 7
      1 | | | | |
Db      50 YASQSIG 56

RESULT 3
US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Query Match      81.8%; Score 27; DB 1; Length 100;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YRSQSIG 7
      1 | | | | |
Db      50 YASQSIG 56

RESULT 4
US-08-436-463-21
; Sequence 21, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436.463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-21

Query Match 81.8%; Score 27; DB 1; Length 103;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7
Db 48 YASQIS 54

RESULT 5
US-07-634-278-62
Sequence 62, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-62

Query Match 81.8%; Score 27; DB 1; Length 107;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7
Db 50 YASQIS 56

RESULT 6
US-07-634-278-63
Sequence 63, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 81.8%; Score 27; DB 1; Length 107;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7
| | | | |
Db 50 YASQSIS 56

RESULT 7
US-07-634-278-87

; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990

; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 81.8%; Score 27; DB 1; Length 107;

Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7
| | | | |
Db 50 YASQSIS 56

RESULT 8

US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 81.8%; Score 27; DB 1; Length 107;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7
| | | | |
Db 50 YASQSIS 56

RESULT 9

US-08-477-728-63
 ; Sequence 63, Application US/08477728
 ; Patent No. 5585089
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,728
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/634,278
 ; FILING DATE: 19-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 63:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-477-728-63

Query Match 81.8%; Score 27; DB 1; Length 107;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7
 DB 50 YASQIS 56

RESULT 10
 US-08-477-728-87
 ; Sequence 87, Application US/08477728
 ; Patent No. 5585089
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,728
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/634,278
 ; FILING DATE: 19-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 87:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-477-728-87

Query Match 81.8%; Score 27; DB 1; Length 107;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7
 DB 50 YASQIS 56

RESULT 11
 US-08-474-040-62
 ; Sequence 62, Application US/08474040
 ; Patent No. 5693761
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US

```

; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-62

```

```

Query Match      81.8%; Score 27; DB 1; Length 107;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 YRSQIS 7
Db 50 YASQIS 56

```

```

RESULT 12
US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-63

```

```

Query Match      81.8%; Score 27; DB 1; Length 107;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 YRSQIS 7
Db 50 YASQIS 56

```

```

RESULT 13
US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274

```

; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-87

Query Match 81.8%; Score 27; DB 1; Length 107;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7
| | | | |
Db 50 YASQSIS 56

RESULT 14
US-08-487-200-62
; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:

; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-62

Query Match 81.8%; Score 27; DB 1; Length 107;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7
| | | | |
Db 50 YASQSIS 56

RESULT 15
US-08-487-200-63
; Sequence 63, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-63

Query Match 81.8%; Score 27; DB 1; Length 107;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7
| | | | |
Db 50 YASQIS 56

Search completed: August 19, 2002, 06:34:43
Job time: 1204 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 08:06:25 ; Search time 2408.76 seconds
(without alignments)
260.630 Million cell updates/sec

Title: US-09-339-922A-33
Perfect score: 30
Sequence: 1 ggattcaccttcagtagcatgacatgtct 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pt.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	30	100.0	30	6	AX060812	Sequence
2	30	100.0	84	6	AX060789	Sequence
3	30	100.0	351	6	AX060780	Sequence
4	28.4	94.7	132	6	BD004402	Amellorat
5	28.4	94.7	132	6	BD004458	Therapeut
6	28.4	94.7	132	6	BD004519	Therapeut
7	28.4	94.7	132	6	BD008352	Inhibitin
8	28.4	94.7	132	6	E23322	Antibody ag
9	28.4	94.7	132	6	E27091	Remedy for
10	28.4	94.7	282	10	MMHIGVL	X58652 Mouse reari
11	28.4	94.7	411	6	BD004423	Amellorat
12	28.4	94.7	411	6	BD004479	Therapeut
13	28.4	94.7	411	6	BD004540	Therapeut
14	28.4	94.7	411	6	BD008373	Inhibitin
15	28.4	94.7	411	6	E23343	Antibody ag
16	28.4	94.7	411	6	E27112	Remedy for
17	27	90.0	330	9	AF103085	Homo sapi
18	27	90.0	338	9	AF103296	Homo sapi
19	27	90.0	381	9	HS389190	Homo sapi
20	26.8	89.3	30	6	AX060828	Sequence
21	26.8	89.3	30	6	AX164020	Sequence
22	26.8	89.3	114	10	MMIGM9	V00824 Mouse mRNA
23	26.8	89.3	226	10	MMU04232	Mus muscu
24	26.8	89.3	237	10	AF023238	Mus muscu
25	26.8	89.3	249	10	AF023235	Mus muscu
26	26.8	89.3	251	10	AF290966	Mus muscu
27	26.8	89.3	258	10	MM718312	Mus muscu
28	26.8	89.3	261	10	MM718310	Mus muscu
29	26.8	89.3	261	10	MM718314	Mus muscu
30	26.8	89.3	261	10	MM718339	Mus muscu
31	26.8	89.3	262	10	AF318409	Mus muscu
32	26.8	89.3	263	10	AF318461	Mus muscu
33	26.8	89.3	263	10	AF318463	Mus muscu
34	26.8	89.3	264	10	MMU04228	Mus muscu
35	26.8	89.3	265	10	AF318466	Mus muscu
36	26.8	89.3	269	10	AF318408	Mus muscu
37	26.8	89.3	269	10	MMU04230	Mus muscu
38	26.8	89.3	269	10	MMU04231	Mus muscu
39	26.8	89.3	270	10	AF318453	Mus muscu
40	26.8	89.3	270	10	AF318484	Mus muscu
41	26.8	89.3	272	10	AF318419	Mus muscu
42	26.8	89.3	273	10	AF318451	Mus muscu
43	26.8	89.3	273	10	AF318456	Mus muscu
44	26.8	89.3	274	10	AF318481	Mus muscu
45	26.8	89.3	275	10	AF318407	Mus muscu

ALIGNMENTS

RESULT	1	AX060812	30 bp	DNA	linear	PAT 22-JAN-2001
AX060812	Sequence 33 from Patent WO0078815.					
LOCUS	AX060812	GI:12406190				
DEFINITION	Sequence 33 from Patent WO0078815.					
ACCESSION	AX060812					
VERSION	AX060812.1					
KEYWORDS	house mouse.					
SOURCE	Mus musculus					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1 (bases 1 to 30)					
AUTHORS	Huse,W.D. and Wu,H.					
TITLE	Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use					
JOURNAL	Patent: WO 0078815-A 33 28-DEC-2000;					
FEATURES	Applied Molecular Evolution (US) Location/Qualifiers					
source	1..30					
	/organism="Mus musculus"					
	/db_xref="taxon:10090"					
CDS	<1..>30					
	/note="unnamed protein product"					

/codon_start=1
 /protein_id="CAC24892.1"
 /db_xref="GI:12406191"
 /translation="GFTFSSYDMS"
 7 a 7 c 6 g 10 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 30; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
 |||
 Db 1 GGATTCACCTTCAGTAGCTATGACATGTCT 30

RESULT 2
 AX060789/c AX060789 84 bp DNA linear PAT 22-JAN-2001
 LOCUS
 DEFINITION Sequence 10 from Patent WO0078815.
 ACCESSION AX060789
 VERSION AX060789.1 GI:12406169
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 AUTHORS Huse,W.D. and Wu,H.
 TITLE Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
 JOURNAL Patent: WO 0078815-A 10 28-DEC-2000;
 Applied Molecular Evolution (US)
 FEATURES
 source 1..84
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

BASE COUNT 22 a 27 c 20 g 15 t
 ORIGIN

Query Match 100.0%; Score 30; DB 6; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
 |||
 Db 78 GGATTCACCTTCAGTAGCTATGACATGTCT 49

RESULT 3
 AX060780 AX060780 351 bp DNA linear PAT 22-JAN-2001
 LOCUS
 DEFINITION Sequence 1 from Patent WO0078815.
 ACCESSION AX060780
 VERSION AX060780.1 GI:12406160
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 AUTHORS Huse,W.D. and Wu,H.
 TITLE Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
 JOURNAL Patent: WO 0078815-A 1 28-DEC-2000;
 Applied Molecular Evolution (US)
 FEATURES
 source 1..351
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 <1..>351
 /note="grafted antibody variable region"

CDS

/codon_start=1
 /transl_table=11
 /protein_id="CAC24888.1"
 /db_xref="GI:12406161"
 /translation="OVQLVESGGVVQGRSLRLSCAASGFTFSSYDMSWVRQAPGKG
 LEWAKVSSGGSTYYLDIVQGRFTISRDNSKNTLYLQNSLRADETAYVYCARHNYG
 SFAYWGQGTIVTVSS"

BASE COUNT 80 a 82 c 104 g 85 t
 ORIGIN

Query Match 100.0%; Score 30; DB 6; Length 351;
 Best Local Similarity 100.0%; Pred. No. 0.005; 0; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Mismatches 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
 |||
 Db 76 GGATTCACCTTCAGTAGCTATGACATGTCT 105

RESULT 4
 BD004402/c BD004402 132 bp DNA linear PAT 31-JAN-2002
 LOCUS
 DEFINITION Ameliorative agent for low vasopressin concentration.
 ACCESSION BD004402
 VERSION BD004402.1 GI:18632363
 KEYWORDS JP 03074312-T/25.
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 AUTHORS Ogata,E., Onuma,E., Tsunenari,T., Saito,H. and Azuma,Y.
 TITLE Ameliorative agent for low vasopressin concentration
 JOURNAL Patent: JP 03074312-T 25 12-JAN-2001;
 CHUGAI PHARM CO LTD,ETSURO OGATA,ETSURO ONUMA,TOSHIKI TSUNENARI,
 HIDEKI SAITO,YUMIKO AZUMA

COMMENT OS Artificial Sequence
 PN JP 03074312-T/25
 PD 12-JAN-2001
 PF 03-JUL-2000 JP 2000004413
 PR 02-JUL-1999 JP 99P 189322
 PI ETSURO OGATA,ETSURO ONUMA,TOSHIKI TSUNENARI,HIDEKI SAITO, PI
 YUMIKO AZUMA
 PC A61K45/00,A61K39/395
 CC key Location/Qualifiers
 FH key Location/Qualifiers
 FT source 1..132 /organism='Artificial Sequence'.
 FT source 1..132 /organism="synthetic construct"
 /db_xref="taxon:32630"

BASE COUNT 31 a 45 c 34 g 22 t
 ORIGIN

Query Match 94.7%; Score 28.4; DB 6; Length 132;
 Best Local Similarity 96.7%; Pred No. 0.027; 1; Indels 0; Gaps 0;
 Matches 29; Conservative 0; Mismatches 1;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
 |||
 Db 92 GGATTCACCTTCAGTAGCTATGACATGTCT 63

RESULT 5
 BD004458/c BD004458 132 bp DNA linear PAT 31-JAN-2002
 LOCUS
 DEFINITION Therapeutic agent for diseases caused with PTH or PTHrP.
 ACCESSION BD004458
 VERSION BD004458.1 GI:18632419
 KEYWORDS JP 03074341-T/25.
 SOURCE synthetic construct.

ORGANISM synthetic construct
artificial sequence.
1 (bases 1 to 132)
REFERENCE Ogata,E., Sato,K., Onuma,E., Tsunenari,T., Saito,H. and Azuma,Y.
AUTHORS Therapeutic agent for diseases caused with PTH or PTHrP
TITLE Patent: JP 03074341-T 25 12-JAN-2001;
JOURNAL CHUGAI PHARM CO LTD,ETSURO OGATA,KO SATO,ETSURO ONUMA, OSHIYAKI
TSUNENARI, HIDEKI SAITO,YUMIKO AZUMA
COMMENT OS Artificial Sequence
PN JP 03074341-T/25
PD 12-JAN-2001
PF 03-JUL-2000 JP 2000004414
PR 02-JUL-1999 JP 99P 189793
PI ETSURO OGATA,KO SATO,ETSURO ONUMA,TOSHIYAKI TSUNENARI, PI
HIDEKI SAITO,
PI YUMIKO AZUMA
PC A61K45/00,A61K39/395,A61P3/14,A61P29/00,A61P37/02 CC
FH Key Location/Qualifiers
FT source 1..132
/Organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..132
/organism="synthetic construct"
/db_xref="taxon:32630" 22 t
BASE COUNT 31 a 45 c 34 g 22 t
ORIGIN
Query Match 94.7%; Score 28.4; DB 6; Length 132;
Best Local Similarity 96.7%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ggattccaccttcagtagctatgacatgtct 30
|||||
Db 92 GGATTCACCTTCAGTAGCTATGGCATGCT 63
RESULT 6
BD004519/c
LOCUS 132 bp DNA linear PAT 31-JAN-2002
DEFINITION Therapeutic agent for treating drug-resistant hypercalcemia.
ACCESSION BD004519
VERSION BD004519.1 GI:18632480
KEYWORDS JP 03074428-T/25.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 132)
AUTHORS Saito,H., Tsunenari,T. and Onuma,E.
TITLE Therapeutic agent for treating drug-resistant hypercalcemia
JOURNAL Patent: JP 03074428-T 25 19-JAN-2001;
CHUGAI PHARM CO LTD,HIDEKI SAITO,TOSHIYAKI TSUNENARI,ETSURO ONUMA
COMMENT OS Artificial Sequence
PN JP 03074428-T/25
PD 19-JAN-2001
PF 06-JUL-2000 JP 2000004523
PR 06-JUL-1999 JP 99P 192270
PI HIDEKI SAITO,TOSHIYAKI TSUNENARI,ETSURO ONUMA
PC A61K45/00,A61K39/395,A61P3/14,A61P5/18
CC
FH Key Location/Qualifiers
FT source 1..132
/Organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..132
/organism="synthetic construct"
/db_xref="taxon:32630" 22 t
BASE COUNT 31 a 45 c 34 g 22 t
ORIGIN
Query Match 94.7%; Score 28.4; DB 6; Length 132;
Best Local Similarity 96.7%; Pred. No. 0.027;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ggattccaccttcagtagctatgacatgtct 30
|||||
Db 92 GGATTCACCTTCAGTAGCTATGGCATGCT 63
RESULT 7
BD008352/c
LOCUS 132 bp DNA linear PAT 31-JAN-2002
DEFINITION Inhibiting agent for tissue degradation.
ACCESSION BD008352
VERSION BD008352.1 GI:18636725
KEYWORDS JP 03075669-T/25.
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 132)
AUTHORS Saito,H., Tsunenari,T., Onuma,E. and Sato,K.
TITLE Inhibiting agent for tissue degradation
JOURNAL Patent: JP 03075669-T 25 27-FEB-2001;
CHUGAI PHARMACEUTICAL CO LTD,HIDEKI SAITO,TOSHIYAKI TSUNENARI, TSURO
ONUMA, KO SATO
COMMENT OS Artificial Sequence
PN JP 03075669-T/25
PD 27-FEB-2001
PF 30-AUG-2000 JP 2000005886
PR 28-FEB-2000 JP 00P 052414
PI HIDEKI SAITO,TOSHIYAKI TSUNENARI,ETSURO ONUMA,KO SATO PC
A61K45/00,A61K39/395,A61P9/02,A61P17/02,A61P21/04,A61P35/00 CC
FH Key Location/Qualifiers
FT source 1..132
/Organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..132
/organism="synthetic construct"
/db_xref="taxon:32630" 22 t
BASE COUNT 31 a 45 c 34 g 22 t
ORIGIN
Query Match 94.7%; Score 28.4; DB 6; Length 132;
Best Local Similarity 96.7%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ggattccaccttcagtagctatgacatgtct 30
|||||
Db 92 GGATTCACCTTCAGTAGCTATGGCATGCT 63
RESULT 8
E23322/c
LOCUS 132 bp DNA linear PAT 07-FEB-2001
DEFINITION Antibody against human parathormone related peptide.
ACCESSION E23322
VERSION E23322.1 GI:13024346
KEYWORDS JP 1999092500-A/25.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 132)
AUTHORS Isoo,S.Y.W.W. and Yabuta.
TITLE Antibody against human parathormone related peptide
JOURNAL Patent: JP 1999092500-A 25 06-APR-1999;
CHUGAI PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 1999092500-A/25
PD 06-APR-1999
PF 24-SEP-1997 JP 1997258739
PR
PI ISAO SATO,YUJI WAKAHARA,NAOHIRO YABUTA
PC C07K16/46,A61K39/395,C07H21/04,C07K16/18,C07K16/26,C12N1/21,
C12N5/10,


```

PF 03-JUL-2000 JP 2000004413
PR 02-JUL-1999 JP 99P 189322
PI ETSURO OGATA, ETSURO ONUMA, TOSHIAKI TSUNENARI, HIDEKI SAITO, PI
  YUMIKO AZUMA
PC A61K45/00, A61K39/395
CC Key Location/Qualifiers
FH CDS (1)..(411)
FT mat_peptide (58)..(411).
FT Location/Qualifiers
FEATURES
  source
    1. .411
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
BASE COUNT      82 a 98 c 128 g 103 t
ORIGIN
Query Match      94.7%; Score 28.4; DB 6; Length 411;
Best Local Similarity 96.7%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggtacccttcagtagctatgacatgtct 30
|||||
Db 133 GGATTCACCTTCAGTAGCTATGGCATGTCT 162

RESULT 12
BD004479
LOCUS      411 bp DNA linear PAT 31-JAN-2002
DEFINITION Therapeutic agent for diseases caused with PTH or PTHrP.
ACCESSION BD004479
VERSION    1 GI:18632440
KEYWORDS   JP 03074341-T/46.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 411)
AUTHORS    Ogata, E., Sato, K., Onuma, E., Tsunenari, T., Saito, H. and Azuma, Y.
TITLE      Therapeutic agent for diseases caused with PTH or PTHrP
JOURNAL    Patent: JP 03074341-T 46 12-JAN-2001;
            CHUGAI PHARM CO LTD, ETSURO OGATA, KO SATO, ETSURO ONUMA, OSHIAKI
            TSUNENARI, HIDEKI SAITO, YUMIKO AZUMA
COMMENT    OS Homo sapiens (human)
            PN JP 03074341-T/46
            PD 12-JAN-2001
            PF 03-JUL-2000 JP 2000004414
            PR 02-JUL-1999 JP 99P 189793
            PI ETSURO OGATA, KO SATO, ETSURO ONUMA, TOSHIAKI TSUNENARI, PI
            HIDEKI SAITO,
            YUMIKO AZUMA
            PC A61K45/00, A61K39/395, A61P3/14, A61P29/00, A61P37/02 CC
            FH Key Location/Qualifiers
            FT CDS (1)..(411)
            FT mat_peptide (58)..(411).
FEATURES
  source
    1. .411
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
BASE COUNT      82 a 98 c 128 g 103 t
ORIGIN
Query Match      94.7%; Score 28.4; DB 6; Length 411;
Best Local Similarity 96.7%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggtacccttcagtagctatgacatgtct 30
|||||
Db 133 GGATTCACCTTCAGTAGCTATGGCATGTCT 162

RESULT 13

```

```

BD004540
LOCUS      411 bp DNA linear PAT 31-JAN-2002
DEFINITION Therapeutic agent for treating drug-resistant hypercalcaemia.
ACCESSION BD004540
VERSION    1 GI:18632501
KEYWORDS   JP 03074428-T/46.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 411)
AUTHORS    Saito, H., Tsunenari, T. and Onuma, E.
TITLE      Therapeutic agent for treating drug-resistant hypercalcaemia
JOURNAL    Patent: JP 03074428-T 46 19-JAN-2001;
            CHUGAI PHARM CO LTD, HIDEKI SAITO, TOSHIAKI TSUNENARI, ETSURO ONUMA
            OS Homo sapiens (human)
            PN JP 03074428-T/46
            PD 19-JAN-2001
            PF 06-JUL-2000 JP 2000004523
            PR 06-JUL-1999 JP 99P 192270
            PI HIDEKI SAITO, TOSHIAKI TSUNENARI, ETSURO ONUMA
            PC A61K45/00, A61K39/395, A61P3/14, A61P5/18
            CC Key Location/Qualifiers
            FH CDS (1)..(411)
            FT mat_peptide (58)..(411).
            FT Location/Qualifiers
FEATURES
  source
    1. .411
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
BASE COUNT      82 a 98 c 128 g 103 t
ORIGIN
Query Match      94.7%; Score 28.4; DB 6; Length 411;
Best Local Similarity 96.7%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
|||||
Db 133 GGATTCACCTTCAGTAGCTATGGCATGTCT 162

RESULT 14
BD008373
LOCUS      411 bp DNA linear PAT 31-JAN-2002
DEFINITION Inhibiting agent for tissue degradation.
ACCESSION BD008373
VERSION    1 GI:18636746
KEYWORDS   JP 03075669-T/46.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 411)
AUTHORS    Saito, H., Tsunenari, T., Onuma, E. and Sato, K.
TITLE      Inhibiting agent for tissue degradation
JOURNAL    Patent: JP 03075669-T 46 27-FEB-2001;
            CHUGAI PHARMACEUTICAL CO LTD, HIDEKI SAITO, TOSHIAKI TSUNENARI, TSURO
            ONUMA, KO SATO
            OS Homo sapiens (human)
            PN JP 03075669-T/46
            PD 27-FEB-2001
            PR 30-AUG-2000 JP 2000005886
            PI 28-FEB-2000 JP 00P 052414
            PI HIDEKI SAITO, TOSHIAKI TSUNENARI, ETSURO ONUMA, KO SATO, PC
            A61K45/00, A61K39/395, A61P7/02, A61P21/04, A61P35/00 CC
            FH Key Location/Qualifiers
            FT CDS (1)..(411)
            FT mat_peptide (58)..(411).
            FT Location/Qualifiers
FEATURES
  source
    1. .411
      /organism="Homo sapiens"

```

BASE COUNT 82 a 98 c 128 g 103 t
ORIGIN /db_xref="taxon:9606"

Query Match 94.7%; Score 28.4; DB 6; Length 411;
Best Local Similarity 96.7%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagcatgacatgtct 30
|||||
Db 133 GGATTCACCTTCAGTAGCATGCGATGCT 162

RESULT 15
E23343 411 bp DNA linear PAT 07-FEB-2001
LOCUS Antibody against human parathormone related peptide.
DEFINITION E23343
ACCESSION E23343
VERSION E23343.1 GI:13024367
KEYWORDS JP 1999092500-A/46.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 411)
AUTHORS Isao, S.Y.W.W. and Yabuta.
TITLE Antibody against human parathormone related peptide
JOURNAL Patent: JP 1999092500-A 46 06-APR-1999;
CHUGAI PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 1999092500-A/46
PD 06-APR-1999
PF 24-SEP-1997 JP 1997258739
PR

PI ISAO SATO, YUJI WAKAHARA, NAOHIRO YABUTA
PC C07K16/46, A61K39/395, C07H21/04, C07K16/26, C12N1/21,
C12N5/10,
PC C12N15/02, C12N15/09, C12P21/08//A61K38/00, (C12N1/21, C12R1:19),
PC (C12N5/10, C12R1:91), (C12P21/08, C12R1:91), C12N5/00, C12N15/00,
PC C12N15/00,
PC A61K37/02, (C12N5/00, C12R1:91)
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. .411
FT Location/Qualifiers
1. .411
/organism="Unidentified".
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 82 a 98 c 128 g 103 t
ORIGIN

Query Match 94.7%; Score 28.4; DB 6; Length 411;
Best Local Similarity 96.7%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagcatgacatgtct 30
|||||
Db 133 GGATTCACCTTCAGTAGCATGCGATGCT 162

Search completed: August 21, 2002, 10:48:56
Job time: 9751 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 07:20:37 ; Search time 6260.2 Seconds
(without alignments)
64.680 Million cell updates/sec

Title: US-09-339-922A-33
Perfect score: 30
Sequence: 1 gattacacattcagtagcatgacatgtct 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.4	94.7	662	10	BF163874
2	28.4	94.7	908	10	BF161883
3	28.4	94.7	913	10	BF162056
4	26.8	89.3	342	9	BB869694
5	26.8	89.3	469	9	AI645111
6	26.8	89.3	823	9	AA170256
7	26.8	89.3	877	10	BF144493
8	26.8	89.3	1559	10	BF138708
9	25.4	84.7	217	10	BF757190
10	25.4	84.7	239	10	BF756793
11	25.4	84.7	253	10	BF870873
12	25.4	84.7	319	10	BE827456
13	25.4	84.7	419	10	H73816
14	25.4	84.7	436	9	AW402311
15	25.4	84.7	452	10	BI017414
16	25.4	84.7	456	10	BG503730
17	25.4	84.7	678	10	BG340648

18	25.4	84.7	698	10	BG757450
19	25.4	84.7	788	10	BG342203
20	25.4	84.7	802	10	BG756245
21	25.4	84.7	846	10	BG755572
22	25.4	84.7	870	10	BG759649
23	25.4	84.7	886	10	BF664039
24	25.4	84.7	964	10	BF663281
25	25.4	84.7	991	10	BF974524
26	25.4	84.7	1010	10	BF663436
27	25.2	84.0	224	9	AW215069
28	25.2	84.0	294	12	AZ601940
29	25.2	84.0	404	10	BF452207
30	25.2	84.0	415	9	AW215320
31	25.2	84.0	434	10	BG145342
32	25.2	84.0	650	10	BF579001
33	25.2	84.0	679	10	BE370602
34	25.2	84.0	689	10	BF579926
35	25.2	84.0	774	10	BF581450
36	25.2	84.0	837	10	BG966355
37	24.8	82.7	338	9	BB868286
38	24.2	80.7	445	9	AW408316
39	23.8	79.3	167	10	BE819773
40	23.8	79.3	248	9	BE009159
41	23.8	79.3	323	9	AW405249
42	23.8	79.3	361	9	AW403412
43	23.8	79.3	383	12	AQ098610
44	23.8	79.3	390	9	AW631411
45	23.8	79.3	401	10	BI677261

ALIGNMENTS

RESULT 1
LOCUS BF163874
DEFINITION 601772386F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3991460 5', mRNA linear EST 30-OCT-2000
ACCESSION BF163874
VERSION BF163874.1 GI:11044152
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 662)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLMS204 row: 1 column: 21
High quality sequence stop: 658.
Location/Qualifiers
1. .662
/organism="Mus musculus"
/strain="C57BL/6J (f1)"
/db_xref="taxon:10090"
/clone="IMAGE:3991460"
/tissue_type="NCI_CGAP_Lu29"
Stem cell origin."
/lab_host="DH10B"
/note="Organ: lung; Vector: pcMV-SPORT6; Site:1: SaliI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator

BASE COUNT 155 a 166 c 183 g 157 t 1 others
ORIGIN providing samples: Gilbert Smith, NIH

Query Match 94.7%; Score 28.4; DB 10; Length 662;
Best Local Similarity 96.7%; Pred. No. 0.16;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
||||| ||||||| ||||||| ||||||| |||||||

Db 198 GGATTCACCTTCAGTAGCTATGACATGTCT 227

RESULT 2

BF161883
LOCUS 601766819F1 NCI_CGAP_Lu29 908 bp mRNA linear EST 30-OCT-2000
DEFINITION Mus musculus cDNA clone IMAGE:3982828 5',
mRNA sequence.

ACCESSION BF161883

VERSION BF161883

KEYWORDS BF161883.1 GI:11042078

SOURCE EST.

ORGANISM house mouse.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS 1 (bases 1 to 908)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabps-femail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM9182 row: e column: 05

High quality sequence stop: 662.

Location/Qualifiers

1..908

/organism="Mus musculus"

/strain="CZECH II (feral)"

/db_xref="taxon:10090"

/clone="IMAGE:3982828"

/clone_lib="NCI_CGAP_Lu29"

/tissue_type="spontaneous tumor, metastatic to mammary."

Stem cell origin."

/lab_host="DH10B"

/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: Sali;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH

214 a 228 c 253 g 213 t

BASE COUNT

ORIGIN

Query Match 94.7%; Score 28.4; DB 10; Length 908;
Best Local Similarity 96.7%; Pred. No. 0.18;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
||||| ||||||| ||||||| ||||||| |||||||

Db 195 GGATTCACCTTCAGTAGCTATGACATGTCT 224

RESULT 3

BF162056
LOCUS 60176814F1 NCI_CGAP_Lu29 913 bp mRNA linear EST 30-OCT-2000
DEFINITION Mus musculus cDNA clone IMAGE:3987986 5',
mRNA sequence.

ACCESSION BF162056
VERSION BF162056.1
KEYWORDS GI:11042257
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS 1 (bases 1 to 913)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabps-femail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM9195 row: 1 column: 03

High quality sequence stop: 581.

Location/Qualifiers

1..913

/organism="Mus musculus"

/strain="CZECH II (feral)"

/db_xref="taxon:10090"

/clone="IMAGE:3987986"

/clone_lib="NCI_CGAP_Lu29"

/tissue_type="spontaneous tumor, metastatic to mammary."

Stem cell origin."

/lab_host="DH10B"

/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: Sali;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH

218 a 248 c 260 g 187 t

BASE COUNT

ORIGIN

Query Match 94.7%; Score 28.4; DB 10; Length 913;

Best Local Similarity 96.7%; Pred. No. 0.18;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
||||| ||||||| ||||||| ||||||| |||||||

Db 202 GGATTCACCTTCAGTAGCTATGACATGTCT 231

RESULT 4

BB869694

LOCUS BB869694

DEFINITION lymph node Mus musculus cDNA clone G630015C08 5', mRNA sequence.

ACCESSION BB869694

VERSION BB869694.1

KEYWORDS GI:17115904

SOURCE EST.

ORGANISM house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 342)

AUTHORS Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii

, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,

Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,

Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa

, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,

Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.

2001)

JOURNAL Unpublished (2001)

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gs.c.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,K., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
 S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
 Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
 Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES	Location/Qualifiers
source	1. .342
	/organism="Mus musculus"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="G630015C08"
	/clone_lib="RIKEN full-length enriched, adult male
	accessory axillary lymph node"
	/sex="male"
	/tissue_type="accessory axillary lymph node"
	/dev_stage="adult"
BASE COUNT	73 a 83 c 98 g 88 t
ORIGIN	
Query Match	89.3%; Score 26.8; DB 9; Length 342;
Best Local Similarity	93.3%; Pred. No. 0.58;
Matches	28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1 ggattccaccttcagtagctatgacatgtct 30
Db	215 GGATTTCATTTCAGTAGCTATGGCATGTCT 244
RESULT	5
LOCUS	AI645111
DEFINITION	ms87g10.y1 Soares mouse 3NbWS Mus musculus cDNA clone IMAGE:618594 5' similar to gb:XI414584 IG HEAVY CHAIN PRECURSOR V-III REGION (HUMAN); gb:U23089 Mus musculus CB17 SCID immunoglobulin heavy chain v region mRNA, (MOUSE);, mRNA sequence.
ACCESSION	AI645111
VERSION	AI645111.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 469)
AUTHORS	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepec,M., Theising,B., Allen,M., Bowers,Y., Person B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:379418

Putative full length read

vector to vector length is 867

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 492.

FEATURES

Location/Qualifiers

1..823

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone_lib="IMAGE:618594"

/clone_lib="Soares mouse 3NbMS"

/sex="male"

/tissue_type="Spleen"

/dev_stage="4 weeks"

/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCGAAGTGGAGCGCGCGCTGTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."

BASE COUNT 200 a 208 c 202 g 213 t

ORIGIN

Query Match 89.3%; Score 26.8; DB 9; Length 823;

Best Local Similarity 93.3%; Pred. No. 0.78;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcacccttcagctagctatgacatgtct 30

||||| ||||| ||||| ||||| ||||| |||||

Db 193 GGATTCACCTTCAGTAGCTATGCCATGTCT 222

RESULT 7

BF144493

LOCUS

DEFINITION 601790133F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4020753 5',

EST.

ACCESSION BF144493.1 GI:10983533

VERSION

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 877)

NIH-MGC http://mgc.nci.nih.gov/;

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CNA Library Preparation: Life Technologies, Inc.

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9275 row: a column: 10

High quality sequence stop: 644.

FEATURES

source

Location/Qualifiers

1..877

/organism="Mus musculus"

/strain="CZECH II"

/db_xref="taxon:10090"

/clone_lib="IMAGE:4020753"

/clone_lib="NCI_CGAP_Lu30"

/tissue_type="tumor, metastatic to mammary"

/lab_host="DH10B"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.

Investigator providing samples: Gilbert Smith, NIH

BASE COUNT 198 a 233 c 254 g 192 t

ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 877;

Best Local Similarity 93.3%; Pred. No. 0.8;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcacccttcagctagctatgacatgtct 30

||||| ||||| ||||| ||||| ||||| |||||

Db 170 GGATTCACCTTCAGTAGCTATGCCATGTCT 199

RESULT 8

BF138708

LOCUS

DEFINITION 601781893F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009847 5',

EST.

ACCESSION BF138708.1 GI:10977748

VERSION

KEYWORDS

SOURCE

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 1559)

NIH-MGC http://mgc.nci.nih.gov/;

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CNA Library Preparation: Life Technologies, Inc.

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9246 row: j column: 24

High quality sequence stop: 562.

FEATURES

source

Location/Qualifiers

1..1559

/organism="Mus musculus"

/strain="CZECH II"

/db_xref="taxon:10090"

/clone_lib="IMAGE:4009847"

/clone_lib="NCI_CGAP_Lu30"

/tissue_type="tumor, metastatic to mammary"

/lab_host="DH10B"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.

Investigator providing samples: Gilbert Smith, NIH

BASE COUNT 482 a 376 c 432 g 268 t

ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 1559;

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL0&t2=ILO-ET0152-301000-501-b05at3-2000-10-30&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 253.

FEATURES

Location/Qualifiers
 1..253
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ET0152"
 /dev_stage="Adult"
 /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 62 a 81 c 64 g 46 t
 ORIGIN

Query Match 84.7%; Score 25.4; DB 10; Length 253;
 Best Local Similarity 96.3%; Pred. No. 2;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
 |||||
 Db 60 GGATTCACCTTCAGTAGCTATGCATG 34

RESULT 12

BE827456
 LOCUS BE827456 319 bp mRNA linear EST 22-SEP-2000
 DEFINITION CM2-ET0016-310500-206-d09 ET0016 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE827456
 VERSION BE827456.1 GI:10259821
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 319)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2-ET0016-310500-206-d09&t3=2000-05-31&t4=1>)
 Seq primer: puc 18 forward

High quality sequence start: 7
 High quality sequence stop: 319.
 Location/Qualifiers
 1..319
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ET0016"
 /dev_stage="Adult"

/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 71 a 74 c 98 g 76 t
 ORIGIN

Query Match 84.7%; Score 25.4; DB 10; Length 319;
 Best Local Similarity 96.3%; Pred. No. 2.1;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
 |||||
 Db 113 GGATTCACCTTCAGTAGCTATGCATG 139

RESULT 13

H73816
 LOCUS H73816 419 bp mRNA linear EST 31-OCT-1995
 DEFINITION YS1B01.r1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
 (IMAGE:214441 5' similar to gb:M62726 IG HEAVY CHAIN V-III REGION
 (HUMAN));, mRNA sequence.

ACCESSION H73816
 VERSION H73816.1 GI:1046750

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 419)
 Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
 Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
 M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
 B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
 Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
 Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

97044478

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewartson.wustl.edu
 Insert Size: 2006
 High quality sequence stops: 261
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 2006 Std Error: 0.00
 Seq primer: M13p1

High quality sequence stop: 261.
 Location/Qualifiers
 1..419

FEATURES source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Soares fetal liver spleen lNFLS"
 /dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
 with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
 1st strand cDNA was primed with a Pac I - oligo(dT) primer
 [5' - AACTGGAAGAATTAATAAGATCTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."
 91 a 100 c 116 g 102 t 10 others

Query Match 84.7%; Score 25.4; DB 10; Length 419;

Best Local Similarity 96.3%; Pred. No. 2.3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgcacatg 27

|||||

Db 62 GGATTCACCTTCAGTAGCTATGGCATG 88

RESULT 14

AW402311

LOCUS 436 bp mRNA linear EST 16-FEB-2000

DEFINITION UI-HF-BK0-asj-h-04-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone

IMAGE:3054175 5', mRNA sequence.

ACCESSION AW402311

VERSION AW402311.1 GI:6920997

KEYWORDS EST.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 436)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

FEATURES

source

1..436

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:3054175"

/clone_lib="NIH_MGC_36"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(0.5-1.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

89 a 109 c 136 g 102 t

BASE COUNT

ORIGIN

Query Match 84.7%; Score 25.4; DB 9; Length 436;

Best Local Similarity 96.3%; Pred. No. 2.4;

Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgcacatg 27

|||||

Db 146 GGATTCACCTTCAGTAGCTATGGCATG 172

RESULT 15

BI017414

LOCUS 452 bp mRNA linear

DEFINITION PM3-ET0272-020401-007-d05 ET0272 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI017414

VERSION BI017414.1 GI:14421485

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 452)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-ET0272-

020401-007-d05&t3=2001-04-02&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 14

High quality sequence stop: 398.

FEATURES

source

1..452

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="ET0272"

/dev_stage="Adult"

/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 103 a 103 c 134 g 112 t

ORIGIN

Query Match 84.7%; Score 25.4; DB 10; Length 452;

Best Local Similarity 96.3%; Pred. No. 2.4;

Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgcacatg 27

|||||

Db 203 GGATTCACCTTCAGTAGCTATGGCATG 229

Search completed: August 21, 2002, 09:55:34

Job time: 9297 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 07:21:02 ; Search time 754.01 seconds
(without alignments)
68.311 Million cell updates/sec

Title: US-09-339-922A-33
Perfect score: 30
Sequence: 1 ggattcaaccttcagtagctatgacatgtct 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

```

1: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	19	AAV49844
2	30	100.0	30	22	AAV28200
C 3	30	100.0	84	19	AAV49825
C 4	30	100.0	84	22	AAH74628
C 5	30	100.0	84	22	AAE28180
C 6	30	100.0	351	19	AAV49820
7	30	100.0	351	22	AAH74623
8	30	100.0	351	22	AAV28175
C 9	28.4	94.7	132	19	AAV24268

C 10	28.4	94.7	132	20	AAV49844
C 11	28.4	94.7	132	21	AAV58893
C 12	28.4	94.7	132	22	AAH75086
C 13	28.4	94.7	132	22	AAH74265
C 14	28.4	94.7	132	22	AAH76624
C 15	28.4	94.7	132	22	AAV69109
C 16	28.4	94.7	132	22	AAV69165
C 17	28.4	94.7	132	22	AAV69221
18	28.4	94.7	411	19	AAV24243
19	28.4	94.7	411	20	AAV49844
20	28.4	94.7	411	21	AAV58914
21	28.4	94.7	411	22	AAH75115
22	28.4	94.7	411	22	AAH74285
23	28.4	94.7	411	22	AAH76645
24	28.4	94.7	411	22	AAV69130
25	28.4	94.7	411	22	AAV69186
26	28.4	94.7	411	22	AAV69242
27	26.8	89.3	30	19	AAV49852
28	26.8	89.3	30	22	AAV51879
29	26.8	89.3	30	22	AAV28208
30	26.8	89.3	306	13	AAQ20302
31	26.8	89.3	324	13	AAQ20303
32	26.8	89.3	348	17	AAV49448
33	26.8	89.3	351	19	AAV49822
34	26.8	89.3	351	22	AAH74625
35	26.8	89.3	351	22	AAV28177
36	26.8	89.3	354	15	AAQ44842
37	26.8	89.3	354	19	AAV11906
38	26.8	89.3	357	16	AAV51438
39	26.8	89.3	372	22	AAH27516
40	26.8	89.3	374	22	AAV11885
41	26.8	89.3	411	19	AAV24232
42	26.8	89.3	411	20	AAV49844
43	26.8	89.3	411	21	AAV58913
44	26.8	89.3	411	22	AAH75106
45	26.8	89.3	411	22	AAH74284

ALIGNMENTS

RESULT 1

AAV49844
ID AAV49844 standard; DNA; 30 BP.

AC AAV49844;

XX AAV49844;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR1 DNA fragment #1.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region; ss.

OS Mus sp.

XX WO9833919-A2.

PN 06-AUG-1998.

PD 30-JAN-1998;

XX 98WO-US01826.

XX 30-JAN-1997;

XX 97US-0791391.

XX (IXSV-) IXSYS INC.

PA Glaser SM, Huse WD;

PI WPI; 1998-437472/37.

XX

DR

DR P-PSDB; AAW76007.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Disclosure; Page 40; 129pp; English.

XX

CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal

CC antibody LM609 heavy and light chain variable region. LM609 and the

CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used

CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX

SQ Sequence 30 BP; 7 A; 7 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 30; DB 19; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00042;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaccctcagtagctatgacatgtct 30

Db 1 ggattcaccctcagtagctatgacatgtct 30

RESULT 2

AAV28200

ID AAV28200 standard; DNA; 30 BP.

XX

AC AAV28200;

XX

DT 03-APR-2001 (first entry)

XX

DE DNA encoding LM609 VH CDR1 peptide.

XX

KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX

OS Unidentified.

XX

PN WO200078815-A1.

XX

PD 28-DEC-2000.

XX

PF 23-JUN-2000; 2000WO-US17454.

XX

PR 24-JUN-1999; 99US-0339922.

XX

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX

PI Huse WD, Wu H;

XX

XX WPI; 2001-050110/06.

XX

PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

PS Claim 16; Page 40; 132pp; English.

XX

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 30 BP; 7 A; 7 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00042;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaccctcagtagctatgacatgtct 30

Db 1 ggattcaccctcagtagctatgacatgtct 30

RESULT 3

AAV49825/c

ID AAV49825 standard; DNA; 84 BP.

XX

AC AAV49825;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody variable region oligonucleotide #2.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; ss.

XX

OS Synthetic.

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

XX WPI; 1998-437472/37.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Example 2; Page 65; 129pp; English.

XX

CC AAV49824-V49833 are oligonucleotides used in the construction of grafted

CC LM609 monoclonal antibody heavy and light chain variable regions. LM609

CC and the antibody vitaxin bind selectively to integrin alphavbeta3 and

CC can be used to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX SQ Sequence 84 BP; 22 A; 27 C; 20 G; 15 T; 0 other;

Query Match 100.0%; Score 30; DB 19; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaaccttcagtagctatgacatgtct 30
| | | | | | | | | | | | | | | | | | | | | |
Db 78 GGATTCACCTTCAGTAGCTATGACATGTCT 49

RESULT 4
AAH74628/c
ID AAH74628 standard; DNA; 84 BP.

XX AC AAH74628;
XX DT 15-OCT-2001 (first entry)

DE PCR primer for heavy chain variable region of LM609 antibody.

XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
XX KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
XX KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
XX KW cancer; PCR primer; ss.

XX OS Mus sp.
XX PN US2001011125-A1.

XX PD 02-AUG-2001.

XX PF 30-JAN-1997; 97US-0790540.

XX PR 30-JAN-1997; 97US-0790540.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX DR WPI; 2001-496171/54.

XX PT New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer -

XX PS Example 2; Page 16; 25pp; English.

XX CC PCR primers AAH74627-31 were used to amplify DNA encoding fragments
CC of the heavy chain variable region of the monoclonal antibody LM609.
CC LM609 is a murine antibody which specifically recognises the integrin
CC alphavbeta3, and inhibits its functional activity. The specification
CC describes a LM609 grafted antibody which has the complementarity
CC determining regions (CDRs) substituted into a non-murine framework.
CC Nucleic acids encoding LM609 grafted heavy and light chain polypeptides
CC and fragments are useful in diagnostic and therapeutic purposes, such
CC as in the production of LM609 grafted antibodies and fragments having
CC binding specificity and inhibitory activity against the integrin
CC alphavbeta3. The antibody can be used for the diagnosis or treatment
CC of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic
CC articular rheumatism, psoriasis, disorders associated with inappropriate
CC or inopportune invasion of vessels such as diabetic retinopathy,
CC neovascular glaucoma and capillary proliferation in atherosclerotic
CC plaques, or cancers), and to inhibit binding activity of alphavbeta3
CC that are necessary for progression of an alphavbeta3-mediated disease.

XX SQ Sequence 84 BP; 22 A; 27 C; 20 G; 15 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 84;

Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaaccttcagtagctatgacatgtct 30
| | | | | | | | | | | | | | | | | | | | | |
Db 78 GGATTCACCTTCAGTAGCTATGACATGTCT 49

RESULT 5
AAF28180/c
ID AAF28180 standard; DNA; 84 BP.

XX AC AAF28180;

XX DT 03-APR-2001 (first entry)

XX DE Oligonucleotide #2.

XX KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -

XX PS Example 2; Page 67; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX SQ Sequence 84 BP; 22 A; 27 C; 20 G; 15 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaaccttcagtagctatgacatgtct 30
| | | | | | | | | | | | | | | | | | | | | |
Db 78 GGATTCACCTTCAGTAGCTATGACATGTCT 49

RESULT 6
AAV49820
ID AAV49820 standard; DNA; 351 BP.

XX AC AAV49820;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

OS Unidentified.

XX WO200078815-A1.

PN 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

PI WPI; 2001-050110/06.

DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of osteoporosis -

XX Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphavbeta3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and osteoporosis.

XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 351;

Best Local Similarity 100.0%; Pred. No. 0.00063;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30

|||||
Db 76 ggattcaccttcagtagctatgacatgtct 105

RESULT 9

AAV24268/c

ID AAV24268 standard; DNA; 132 BP.

XX AAV24268;

XX 03-SEP-1998 (first entry)

XX Chimeric antibody against hPTRP human H chain PCR primer MBC1HGP2.

XX Chimeric; antibody; human parathormone related peptide; hPTRP; mouse; L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR; hypophosphemia; pathogen; vitamin D resistance; V region; C region; humanised; PCR primer ss.

XX Synthetic.

XX Homo sapiens.

XX WO9813388-A1.

XX 02-APR-1998.

XX 24-SEP-1997; 97WO-JP03382.

XX

PR 24-JUL-1997; 97JP-0214168.

PR 26-SEP-1996; 96JP-0255196.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Sato K, Wakahara Y, Yabuta N;

PI WPI; 1998-230640/20.

DR New chimeric antibodies against human parathormone related

PT peptide(s) - useful for, e.g. treatment of hypercalcaemia and other disorders caused by malignant neoplasm(s)

XX Example 3; Page 104; 182pp; Japanese.

XX New antibodies have been developed which are specific for human parathormone related peptides (hPTRP). The antibodies comprise chimeric L and/or H chains, where the C region is of human and L region of mouse, CC origin. The present sequence represents a PCR primer used in an example of the present invention. Host cells, transformed with vectors containing DNA encoding antibodies of the invention, can be used to produce the antibodies. The antibodies may be used to treat hypercalcaemia, especially that due to a malignancy, e.g. cancers of CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver, CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They CC pathogens or to vitamin D resistance.

XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;

Query Match 94.7%; Score 28.4; DB 19; Length 132;

Best Local Similarity 96.7%; Pred. No. 0.0028;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30

|||||
Db 92 GGATTCACCTTCAGTAGCTATGGCATGTCT 63

RESULT 10

AAAX00112/c

ID AAAX00112 standard; DNA; 132 BP.

XX AAAX00112;

XX 14-APR-1999 (first entry)

XX Human antibody PCR antisense primer MBC1HGP2.

XX Human; parathyroid hormone related protein; PTHrP; cachexia; cancer; inhibitor; humanised; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9851329-A1.

XX 19-NOV-1998.

XX 13-MAY-1998; 98WO-JP02116.

XX 18-JUL-1997; 97JP-0194445.

XX 15-MAY-1997; 97JP-0125505.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Ishii K, Sato K, Tunenari T;

XX WPI; 1999-070101/06.

XX Inhibitors of binding of parathyroid hormone related peptide to its receptor - useful for, e.g. treatment of cachexia arising from

PT cancer or other diseases
 PS Example 4; Page 65; 125pp; Japanese.
 XX

CC The present invention describes compositions for the treatment of
 CC cachexia containing a substance which inhibits the binding of a
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an
 CC active component. This substance may be an antagonist to the receptor,
 CC or an antibody (preferably monoclonal) or antibody fragment,
 CC recognising PTHrP. The antibody is preferably humanised or chimeric.
 CC The present invention also describes a humanised antibody prepared
 CC by hybridoma 23-57-137-1 (FERM Bp-5631). The composition is used for
 CC the treatment of cachexia arising in connection with diseases such as
 CC cancer, thereby improving the quality of life of the patient. The
 CC present sequence represents a PCR primer used in an example from the
 CC present invention.
 XX
 XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;
 SQ

Query Match 94.7%; Score 28.4; DB 20; Length 132;
 Best Local Similarity 96.7%; Pred. No. 0.0028;
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX

QY 1 ggattcaccttcagtagctatgacatgtct 30
 DB 92 GGATTCACCTTCAGTAGCTATGGCATGTCT 63

RESULT 11
 AAZ58893/C
 ID AAZ58893 standard; DNA; 132 BP.
 XX
 AC AAZ58893;
 XX
 DT 26-APR-2000 (first entry)
 XX
 DE PCR primer MBC1HG2P.
 XX
 KW Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP;
 KW human; tumour; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200000219-A1.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-JP03433.
 XX
 PR 26-JUN-1998; 98JP-0180143.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Sato K, Tsunenari T;
 XX
 DR WPI; 2000-117115/10.
 XX
 PT Treatment of hypercalcemic crisis with a substance inhibiting binding
 PT of parathyroid hormone related peptide to its receptor -
 XX
 PS Example 4; Page 79; 120pp; Japanese.
 XX

CC The invention relates to a method of treatment of hypercalcemic crisis.
 CC A composition for the treatment of hypercalcemic crisis contains as
 CC active component a substance which inhibits the binding of parathyroid
 CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used
 CC for the treatment of hypercalcemic crisis, such as that associated with
 CC a malignant tumour.
 CC
 XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;
 SQ

Query Match 94.7%; Score 28.4; DB 21; Length 132;
 Best Local Similarity 96.7%; Pred. No. 0.0028;
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX

QY 1 ggattcaccttcagtagctatgacatgtct 30
 DB 92 GGATTCACCTTCAGTAGCTATGGCATGTCT 63

RESULT 12
 AAH75086/C
 ID AAH75086 standard; DNA; 132 BP.
 XX
 AC AAH75086;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of a PCR primer.
 XX
 KW Tissue decomposition inhibitor; parathyroid hormone; cancer cachexia;
 KW septicemia; injury; muscular dystrophy; cytokine; interleukin-6;
 KW granulocyte colony stimulating factor; interleukin-11;
 KW leukemia inhibitory factor; weight loss; PCR primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200164249-A1.
 XX
 PD 07-SEP-2001.
 XX
 PF 30-AUG-2000; 2000WO-JP05886.
 XX
 PR 28-FEB-2000; 2000JP-0052414.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Saito H, Tsunenari T, Onuma E, Sato K;
 XX
 DR WPI; 2001-550131/61.
 XX
 PT Tissue decomposition inhibitor that prevents parathyroid hormone
 PT associated proteins from binding to its receptor -
 XX
 PS Example 1; Page 87; 132pp; Japanese.
 XX

CC The specification describes a tissue decomposition inhibitor, which
 CC comprises a substance that inhibits peptides associated with
 CC parathyroid hormone (PTH) from binding with their receptor. The method
 CC is used to inhibit tissue decomposition caused by cancer cachexia,
 CC septicemia, heavy external injury or muscular dystrophy, and for
 CC treating patients with elevated cytokine (interleukin-6, Granulocyte
 CC colony stimulating factor, Interleukin-11 and Leukemia inhibitory
 CC factor) levels. It may also be used for preventing weight loss caused
 CC by cancer cachexia. PCR primers AAH75086-87 were used in the course
 CC of the invention.
 XX
 XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;
 SQ

Query Match 94.7%; Score 28.4; DB 22; Length 132;
 Best Local Similarity 96.7%; Pred. No. 0.0028;
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX

QY 1 ggattcaccttcagtagctatgacatgtct 30
 DB 92 GGATTCACCTTCAGTAGCTATGGCATGTCT 63

RESULT 13
 AAH74265/C
 ID AAH74265 standard; DNA; 132 BP.
 XX
 AC AAH74265;
 XX

```
XX 15-OCT-2001 (first entry)
XX
XX Nucleotide sequence of an oligonucleotide.
DE
XX Parathyroid hormone-associated peptide; PThrP; dental disease; primer;
KW ss.
XX
XX Synthetic.
OS
XX WO200154725-A1.
XX
XX 02-AUG-2001.
XX
XX 14-DEC-2000; 2000WO-JP08875.
XX
XX 25-JAN-2000; 2000JP-0083034.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Kato A, Suzuki M, Sugimoto T;
PI
XX WPI; 2001-465459/50.
XX
XX Parathyroid hormone-associated peptide binding inhibitors useful for
PT treating dental disease
PT
XX
XX Example 4; Page 91; 140pp; Japanese.
XX
XX The present oligonucleotide was used in the course of the invention.
CC The specification describes a treatment for dental diseases. The
CC treatment comprises a substance that inhibits binding between
CC parathyroid hormone-associated peptide and its receptor.
XX
XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;
SQ

Query Match 94.7%; Score 28.4; DB 22; Length 132;
Best Local Similarity 96.7%; Pred. No. 0.0028;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30
   |||||
DB 92 GGATTCACCTTCAGTACGTATGGCATGTCT 63

RESULT 14
AAH76624/C
ID AAH76624 standard; DNA; 132 BP.
XX
XX AAH76624;
AC
XX
XX 08-OCT-2001 (first entry)
XX
XX Humanised anti-PThrP Ab VH CDR PCR primer MBC1HGP2, SEQ ID NO:25.
DE
XX
XX Parathyroid hormone-related peptide; PThrP; antagonist; antibody;
KW calcium regulation disorder; serum calcium concentration;
KW humoral hypercalcaemia of malignancy; cytostatic; analgesic;
KW PCR primer; ss.
XX
XX Synthetic.
OS
XX WO200147554-A1.
XX
XX 05-JUL-2001.
XX
XX 27-DEC-2000; 2000WO-JP09339.
XX
XX 28-DEC-1999; 99JP-0375203.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
```

```
PI Yamazaki T, Hayasaka A, Koga A;
XX
XX WPI; 2001-425590/45.
XX
XX Composition for treating diseases of calcium regulation and for use as
PT an analgesic, comprises an antibody recognizing parathyroid hormone
PT related peptide
PT
XX
XX Examples; Page 86; 128pp; Japanese.
XX
XX The invention relates to a stabilised composition of an antibody which
CC recognises parathyroid hormone-related peptide (PTHrP) - see AAG64793.
CC The composition consists of a solution of the antibody in a buffer of pH
CC 5-8 containing one or more of acetic acid, phosphoric acid, citric acid
CC and their salts. The composition has increased storage stability,
CC especially at elevated temperatures. The composition antagonises the
CC action of PTHrP, and may be used in the treatment of diseases involving
CC disturbances of calcium regulation (high or low serum calcium
CC concentration) such as humoral hypercalcaemia of malignancy and as an
CC analgesic. The present sequence represents a PCR primer used in the
CC exemplifications of the invention in the construction of polynucleotides
CC encoding humanised versions of the anti-human PTHrP murine monoclonal
CC antibody 23-57-137-1.
XX
XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;
SQ

Query Match 94.7%; Score 28.4; DB 22; Length 132;
Best Local Similarity 96.7%; Pred. No. 0.0028;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30
   |||||
DB 92 GGATTCACCTTCAGTACGTATGGCATGTCT 63

RESULT 15
AAF69109/c
ID AAF69109 standard; DNA; 132 BP.
XX
XX AAF69109;
AC
XX
XX 12-APR-2001 (first entry)
XX
XX Human H chain V region PCR primer MBC1HGP2 SEQ ID NO:25.
DE
XX
XX Human; mouse; parathyroid hormone-related peptide; PTHrP; vasopressin;
KW monoclonal antibody; antidiarrheic; antiemetic; antidiabetic;
KW antipyretic; cancer; dehydration; excessive urination; thirst;
KW vomiting; diarrhoea; fever; perspiration; diabetes; diabetes; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200102010-A1.
XX
XX 11-JAN-2001.
XX
XX 03-JUL-2000; 2000WO-JP04413.
XX
XX 02-JUL-1999; 99JP-0189322.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Ogata E, Onuma E, Tsunenari T, Saito H, Azuma Y;
PI
XX
XX WPI; 2001-112507/12.
XX
XX Inhibitor of parathyroid hormone related peptide binding to its
PT receptor can ameliorate symptoms caused by a decrease in vasopressin
PT level due to cancer
XX
XX Example 2; Page 71; 114pp; Japanese.
XX
```

SQ Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
|||
Db 92 GGATTCACCTTCAGTAGCTATGGCATGTCT 63

Search completed: August 21, 2002, 10:08:24
Job time: 10042 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 08:11:20 ; Search time 174.26 Seconds
(without alignments)
42.287 Million cell updates/sec

Title: US-09-339-922A-33
Perfect score: 30
Sequence: 1 gattcaacttcagtagatgatgtct 30

Scoring table: IDENTITY_NUC
Gapop 10.0, Capext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26.8	89.3	354	5	PCT-US93-08435-9
2	26.8	89.3	357	5	PCT-US94-07659-5
3	26.8	89.3	519	1	US-08-339-582-1
4	26.8	89.3	717	2	US-08-553-497A-17
5	26.8	89.3	783	4	US-08-487-283A-19
6	26.8	89.3	923	5	PCT-US94-07659-1
7	25.4	84.7	335	2	US-08-477-553A-55
8	25.4	84.7	342	2	US-08-477-553A-51
9	25.4	84.7	378	4	US-09-240-274-94
10	25.4	84.7	378	4	US-09-240-274-95
11	25.4	84.7	378	4	US-09-240-274-192
12	25.4	84.7	378	4	US-09-240-274-196
13	25.4	84.7	453	3	US-08-724-752-12
14	25.4	84.7	512	3	US-08-545-809A-30
15	25.4	84.7	583	3	US-08-545-809A-33
16	25.2	84.0	96	4	US-08-976-183A-52
17	25.2	84.0	318	1	US-08-129-930B-94
18	25.2	84.0	318	4	US-08-976-288A-94
19	25.2	84.0	339	1	US-07-789-344A-9
20	25.2	84.0	345	3	US-08-483-749A-5
21	25.2	84.0	348	2	US-08-888-366-9
22	25.2	84.0	354	4	US-08-487-761-14
23	25.2	84.0	369	1	US-08-356-272-2
24	25.2	84.0	394	4	US-08-134-346A-14
25	25.2	84.0	405	4	US-08-579-378A-15
26	25.2	84.0	405	4	US-08-579-378A-19
27	25.2	84.0	413	1	US-08-253-877C-56

Sequence 56, Appl
Sequence 30, Appl
Sequence 49, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 5, Appl
Sequence 9, Appl
Patent No. 5455030
Sequence 3, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appl
Patent No. 5455030
Sequence 3, Appl
Patent No. 5455030
Patent No. 5455030

ALIGNMENTS

RESULT 1
PCT-US93-08435-9
; Sequence 9, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Conferring Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..354
PCT-US93-08435-9

Query Match 89.3%; Score 26.8; DB 5; Length 354;
 Best Local Similarity 93.3%; Pred. No. 0.0015;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagcatgtct 30
 ||||| ||||| ||||| ||||| |||||
 Db 64 GGATTCACCTTCAGTAGCATGTCT 93

RESULT 2
 PCT-US94-07659-5
 ; Sequence 5, Application PC/TUS9407659
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Peter
 ; APPLICANT: Gross, Mitchell
 ; APPLICANT: Jonak, Zdenka L.
 ; APPLICANT: Theisen, Timothy
 ; APPLICANT: Hurle, Mark
 ; APPLICANT: Jackson, Jeffrey R.
 ; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
 ; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
 ; TITLE OF INVENTION: Disorders in Man
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation - Corp.
 ; ADDRESSEE: Intellectual Property
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-2799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/07659
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/090,534
 ; FILING DATE: 09-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sutton, Jeffrey A.
 ; REGISTRATION NUMBER: 34,028
 ; REFERENCE/DOCKET NUMBER: P50171-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 270-5024
 ; TELEFAX: (610) 270-5090
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 357 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..357
 PCT-US94-07659-5

Query Match 89.3%; Score 26.8; DB 5; Length 357;
 Best Local Similarity 93.3%; Pred. No. 0.0015;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagcatgtct 30
 ||||| ||||| ||||| ||||| |||||
 Db 76 GGATTCATTTTCAGTAGCATGTCT 105

RESULT 3
 US-08-339-582-1
 ; Sequence 1, Application US/08339582
 ; Patent No. 555852
 ; GENERAL INFORMATION:
 ; APPLICANT: Bigner, Darrell D.
 ; APPLICANT: Zalutsky, Michael R.
 ; APPLICANT: Carrel, Stefan
 ; TITLE OF INVENTION: METHOD OF TREATMENT
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kenneth D. Sibley
 ; STREET: P.O. Drawer 34009
 ; CITY: Charlotte
 ; STATE: No. 555852th Carolina
 ; COUNTRY: USA
 ; ZIP: 28234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/339,582
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/033,864
 ; FILING DATE: 19-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sibley, Kenneth D.
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5405-89
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-420-2200
 ; TELEFAX: 919-881-3175
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 519 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 157..519
 US-08-339-582-1

Query Match 89.3%; Score 26.8; DB 1; Length 519;
 Best Local Similarity 93.3%; Pred. No. 0.0016;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagcatgtct 30
 ||||| ||||| ||||| ||||| |||||
 Db 244 GGATTCACCTTCAGTAGCATGTCT 273

RESULT 4
 US-08-553-497A-17
 ; Sequence 17, Application US/08553497A
 ; Patent No. 584093
 ; GENERAL INFORMATION:
 ; APPLICANT: KETTLEBOROUGH, C. A.
 ; APPLICANT: BENDIG, MARY M.
 ; APPLICANT: ANSELL, KEITH H.
 ; APPLICANT: GUSOW, DETLEF
 ; APPLICANT: ADAM, JAUME
 ; APPLICANT: MITJANS, FRANCESCA
 ; APPLICANT: ROSELL, ELISABET
 ; APPLICANT: BLASCO, FRANCESCA
 ; APPLICANT: PIULATS, JAUME
 ; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR

;; TITLE OF INVENTION: ANTIBODIES
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P.C.
;; STREET: 2200 CLARENDON BLVD. SUITE 1400
;; CITY: ARLINGTON
;; STATE: VA
;; COUNTRY: US
;; ZIP: 22201
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/553,497A
;; FILING DATE: 17-NOV-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/EP95/00978
;; FILING DATE: 16-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 94104160.0
;; FILING DATE: 17-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 94118970.6
;; FILING DATE: 02-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: HAMLET-KING, DIANA
;; REGISTRATION NUMBER: 33,302
;; REFERENCE/DOCKET NUMBER: MERCK 1726
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-243-6333
;; TELEFAX: 703-243-6410
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 717 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: mouse
;; STRAIN: Balb/c
;; DEVELOPMENTAL STAGE: adult
;; TISSUE TYPE: splenocytes
;; IMMEDIATE SOURCE:
;; CLONE: 4 B 2
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..717
;;
US-08-553-497A-17

Query Match 89.3%; Score 26.8; DB 2; Length 717;
Best Local Similarity 93.3%; Pred. No. 0.0017;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30
||||| ||||||| ||||||| ||||||| |||||||
Db 76 GGATTCACCTTCAGTAGCTATGGCATGTCT 105

RESULT 5
US-08-487-283A-19
; Sequence 19, Application US/08487283A
; Patent No. 6355245
; GENERAL INFORMATION:
; APPLICANT: Evans, Mark J.
; ADDRESSEE: Matis, Louis A.

;; APPLICANT: Mueller, Eileen Elliott
;; APPLICANT: Nye, Steven H.
;; APPLICANT: Rollins, Scott
;; APPLICANT: Rother, Russell P.
;; APPLICANT: Springhorn, Jeremy P.
;; APPLICANT: Squinto, Stephen P.
;; APPLICANT: Thomas, Thomas C.
;; APPLICANT: Wilkins, James A.
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
;; OF INFLAMMATORY DISEASES
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seth A. Fidel
;; STREET: 25 Science Park (Alexion)
;; CITY: New Haven
;; STATE: Connecticut
;; COUNTRY: USA
;; ZIP: 06511
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.4mb storage
;; COMPUTER: Macintosh Cetrus 610
;; OPERATING SYSTEM: System 7
;; SOFTWARE: WordPerfect 3.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/487,283A
;; FILING DATE: June 7, 1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/236,208
;; FILING DATE: 02-MAY-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seth A. Fidel
;; REGISTRATION NUMBER: 38,449
;; REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (203)776-1790
;; TELEFAX: (203)772-3655
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 783 base pairs
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Double
;; TOPOLOGY: linear
;; MOLECULE TYPE: Other nucleic acid
;; DESCRIPTION: N19/8 scfv (His Tagged)
;;
US-08-487-283A-19

Query Match 89.3%; Score 26.8; DB 4; Length 783;
Best Local Similarity 93.3%; Pred. No. 0.0017;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30
||||| ||||||| ||||||| ||||||| |||||||
Db 466 GGATTCACCTTCAGTAGCTATTAATGTCT 495

RESULT 6
PCT-US94-07659-1
; Sequence 1, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
APPLICATION NUMBER: PCT/US94/07659
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 923 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 169..909
PCT-US94-07659-1

Query Match 89.3%; Score 26.8; DB 5; Length 923;
Best Local Similarity 93.3%; Pred. No. 0.0018;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcccttcagtagcatgtct 30
||||| | ||||| ||||| ||||| |||||

Db 301 GGATTCCTTCAGTAGCATGTCT 330

RESULT 7
US-08-477-553A-55
Sequence 55, Application US/08477553A
Patent No. 5919910
GENERAL INFORMATION:
APPLICANT: HUGHES-JONES, Nevin C
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,553A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,034
FILING DATE: 23-JUNE-1992

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8925590.5
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 007330-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..335
OTHER INFORMATION: /note= "Nucleotides 1-375 corres.
to nucleotides 24-359 of Fig. 14/14. Nucleotides
1-23 and 360-375 represent PCR primers."
US-08-477-553A-55

Query Match 84.7%; Score 25.4; DB 2; Length 335;
Best Local Similarity 96.3%; Pred. No. 0.0063;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagcatgtc 27
||||| | ||||| ||||| ||||| |||||

Db 52 GGATTCACCTTCAGTAGCATGTC 78

RESULT 8
US-08-477-553A-51
Sequence 51, Application US/08477553A
Patent No. 5919910
GENERAL INFORMATION:
APPLICANT: HUGHES-JONES, Nevin C
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,553A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,034
FILING DATE: 23-JUNE-1992
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8925590.5
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 007330-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620

```
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..342
; OTHER INFORMATION: /note= "Nucleotides 1-381 corres.
; OTHER INFORMATION: to nucleotides 24-365 of Fig. 10/14. Nucleotides
; OTHER INFORMATION: 1-23 and 366-381 represent PCR primers."
US-08-477-553A-51

Query Match      84.7%; Score 25.4; DB 2; Length 342;
Best Local Similarity 96.3%; Pred. No. 0.0064;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
   |||||
DB 53 GGATTCACCTTCAGTAGCTATGGCATG 79

RESULT 9
US-09-240-274-94
; Sequence 94, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D30
US-09-240-274-94

Query Match      84.7%; Score 25.4; DB 4; Length 378;
Best Local Similarity 96.3%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
   |||||
DB 76 ggattcaccttcagtagctatggcatg 102

RESULT 10
US-09-240-274-95
; Sequence 95, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; EARLIER APPLICATION NUMBER: 60/081,380
```

```
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-95

Query Match      84.7%; Score 25.4; DB 4; Length 378;
Best Local Similarity 96.3%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
   |||||
DB 76 ggattcaccttcagtagctatggcatg 102

RESULT 11
US-09-240-274-192
; Sequence 192, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 192
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH39
US-09-240-274-192

Query Match      84.7%; Score 25.4; DB 4; Length 378;
Best Local Similarity 96.3%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
   |||||
DB 79 ggattcaccttcagtagctatggcatg 105

RESULT 12
US-09-240-274-196
; Sequence 196, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
```

NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 196
LENGTH: 378
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-196

Query Match 84.7%; Score 25.4; DB 4; Length 378;
Best Local Similarity 96.3%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
|||||
Db 76 ggattcaccttcagtagctatgacatg 102

RESULT 13
US-08-724-752-12
Sequence 12, Application US/08724752
Patent No. 6150584
GENERAL INFORMATION:
APPLICANT: Kucheralapati, Raju
APPLICANT: Jakobovits, Aya
APPLICANT: Brenner, Daniel G.
APPLICANT: Capon, Daniel J.
APPLICANT: Klaphoz, Sue
TITLE OF INVENTION: HUMAN ANTIBODIES DERIVED FROM IMMUNIZED
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,752
FILING DATE: 02-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05928
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cell 4.17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

Query Match 84.7%; Score 25.4; DB 3; Length 453;
Best Local Similarity 96.3%; Pred. No. 0.0067;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
|||||
Db 31 GGATTACCTTCAGTAGCTATGGCATG 57

RESULT 14
US-08-545-809A-30
Sequence 30, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
US-08-545-809A-30

Query Match 84.7%; Score 25.4; DB 3; Length 512;
Best Local Similarity 96.3%; Pred. No. 0.0059;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
|||||
Db 243 GGATTACCTTCAGTAGCTATGGCATG 269

RESULT 15
US-08-545-809A-33
Sequence 33, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
US-08-545-809A-30

Query Match 84.7%; Score 25.4; DB 3; Length 512;
Best Local Similarity 96.3%; Pred. No. 0.0059;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

;
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
;
US-08-545-809A-33

```

```

Query Match      84.7%; Score 25.4; DB 3; Length 583;
Best Local Similarity 96.3%; Pred. No. 0.007;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 ggattcaccttcagtagctatgacatg 27
   |||
Db 254 GGATTACACCTTCAGTAGCTATGGCATG 280

```

```

Search completed: August 21, 2002, 10:52:11
Job time: 9651 sec

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:48:56 ; Search time 2408.76 Seconds
(without alignments)
234.567 Million cell updates/sec

Title: US-09-339-922A-89
Perfect score: 27
Sequence: 1 caacagatggcagctggcctctgacg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	27	100.0	27	6	AX060868
2	25.4	94.1	27	6	AX060870
3	23.8	88.1	27	6	AX060824
4	23.8	88.1	57	6	AX060797
5	23.8	88.1	57	6	AX060806
6	23.8	88.1	321	6	AX060782
7	23.8	88.1	321	6	AX060786
8	23.8	88.1	321	6	AX060810
9	22.2	82.2	228	10	MDIGKVAV
10	22.2	82.2	236	10	MDIGKVAV
11	22.2	82.2	297	10	AF137617
12	22.2	82.2	306	10	MMVL3B6
13	22.2	82.2	317	10	MMIG1KL4
14	22.2	82.2	321	10	AF163757
15	22.2	82.2	420	10	MUSIGKCKN
16	22.2	82.2	5238	6	A07699
17	21.2	78.5	253	9	HS426269
18	21.2	78.5	318	10	MMIGKVR4
19	21.2	78.5	361	10	MMIGKBP5
20	21.2	78.5	181088	2	AC097733
21	20.8	77.0	101447	2	AC097994
22	20.6	76.3	243	10	MMU19309
23	20.6	76.3	300	10	MUSIGKABJ
24	20.6	76.3	313	10	MUSIGVABU
25	20.6	76.3	313	10	MUSIGVABW
26	20.6	76.3	317	10	MMIG1KL3
27	20.6	76.3	321	10	AF113242
28	20.6	76.3	321	10	AF113243
29	20.6	76.3	321	10	MMALCVR26
30	20.6	76.3	321	10	MMU277216
31	20.6	76.3	324	10	AF087031
32	20.6	76.3	324	10	AF139844
33	20.6	76.3	324	10	AF139845
34	20.6	76.3	324	10	AF139846
35	20.6	76.3	324	10	AF139847
36	20.6	76.3	324	10	AF139848
37	20.6	76.3	324	10	AF139849
38	20.6	76.3	324	10	MMU60469
39	20.6	76.3	370	10	MUSIGKAD
40	20.6	76.3	381	6	E07933
41	20.6	76.3	381	10	MUSIGRAQA
42	20.6	76.3	582	10	MMU26998
43	20.6	76.3	178274	2	AC008763
44	20.2	74.8	52809	2	AC100034
45	20.2	74.8	131948	2	AC034183

ALIGNMENTS

RESULT	1	AX060868	Sequence 89 from Patent WO0078815.	27 bp	DNA	linear	PAT 22-JAN-2001
LOGUS		AX060868					
DEFINITION		AX060868					
ACCESSION		AX060868.1	GI:12406246				
VERSION							
KEYWORDS			synthetic construct.				
SOURCE			synthetic construct				
ORGANISM			artificial sequence.				
REFERENCE			1 (bases 1 to 27)				
AUTHORS			Huse,W.D. and Wu,H.				
TITLE			Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use				
JOURNAL			Patent: WO 0078815-A 89 28-DEC-2000;				
FEATURES			Applied Molecular Evolution (US)				
source			Location/Qualifiers				
			1..27				
			/organism="synthetic construct"				
			/db_xref="taxon:32630"				
			<1..>27				
			/note="Mutated complementarity determining region (CDR)"				
			/codon_start=1				
CDS							

```

/transl_table=11
/protein_id="CAC24920.1"
/db_xref="GI:12406247"
/translation="QQSGSWPLT" 4 t
BASE COUNT      6 a      8 c      9 g
ORIGIN

Query Match      100.0%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caacagagtgccagctggcctctgacg 27
    |||||
Db 1 CAACAGAGTGGCAGCTGGCCTCTGACG 27

RESULT 2
LOCUS AX060870 27 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 91 from Patent WO0078815.
ACCESSION AX060870
VERSION AX060870.1 GI:12406248
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial construct.
artificial sequence.
1 (bases 1 to 27)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 91 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source
1..27
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>27
/codon_start=1
/transl_table=11
/protein_id="CAC24921.1"
/db_xref="GI:12406249"
/translation="QQSGSWPQT" 3 t
BASE COUNT      7 a      8 c      9 g
ORIGIN

Query Match      94.1%; Score 25.4; DB 6; Length 27;
Best Local Similarity 96.3%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 caacagagtgccagctggcctctgacg 27
    |||||
Db 1 CAACAGAGTGGCAGCTGGCCTCTGACG 27

RESULT 3
LOCUS AX060824 27 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 45 from Patent WO0078815.
ACCESSION AX060824
VERSION AX060824.1 GI:12406202
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 45 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source
1..27
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>27
/codon_start=1
/transl_table=11
/protein_id="CAC24920.1"
/db_xref="GI:12406247"
/translation="QQSGSWPLT" 4 t
BASE COUNT      6 a      8 c      9 g
ORIGIN

Query Match      100.0%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caacagagtgccagctggcctctgacg 27
    |||||
Db 1 CAACAGAGTGGCAGCTGGCCTCTGACG 27

RESULT 4
LOCUS AX060797 57 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 18 from Patent WO0078815.
ACCESSION AX060797
VERSION AX060797.1 GI:12406177
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial construct.
artificial sequence.
1 (bases 1 to 57)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 18 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source
1..57
/organism="synthetic construct"
/db_xref="taxon:32630"
/translation="oligonucleotide" 8 t
BASE COUNT     16 a     12 c     21 g
ORIGIN

Query Match      88.1%; Score 23.8; DB 6; Length 57;
Best Local Similarity 92.6%; Pred. No. 1.6;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caacagagtgccagctggcctctgacg 27
    |||||
Db 1 CAACAGAGTGGCAGCTGGCCTCTGACG 27

RESULT 5
LOCUS AX060806 57 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 27 from Patent WO0078815.
ACCESSION AX060806
VERSION AX060806.1 GI:12406186
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial construct.
artificial sequence.
1 (bases 1 to 57)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 27 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source
1..27
/organism="synthetic construct"
/db_xref="taxon:32630"
/translation="oligonucleotide" 8 t
BASE COUNT     16 a     12 c     21 g
ORIGIN

Query Match      88.1%; Score 23.8; DB 6; Length 57;
Best Local Similarity 92.6%; Pred. No. 1.6;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caacagagtgccagctggcctctgacg 27
    |||||
Db 1 CAACAGAGTGGCAGCTGGCCTCTGACG 27

RESULT 6
LOCUS AX060806 57 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 27 from Patent WO0078815.
ACCESSION AX060806
VERSION AX060806.1 GI:12406186
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial construct.
artificial sequence.
1 (bases 1 to 57)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 27 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source
1..27
/organism="synthetic construct"
/db_xref="taxon:32630"
/translation="oligonucleotide" 8 t
BASE COUNT     16 a     12 c     21 g
ORIGIN

```



```

SOURCE          western European house mouse.
ORGANISM        Mus musculus domesticus
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE          1 (bases 1 to 228)
JOURNAL        Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
MEDLINE        Both IgM and IgG anti-DNA antibodies are the products of clonally
REFERENCE       selective B cell stimulation in (NZB x NZW)F1 mice
AUTHORS        J. Exp. Med. 176 (3), 761-779 (1992)
TITLE          92381444
JOURNAL        2 (bases 1 to 228)
MEDLINE        Marion,T.N.
AUTHORS        Direct Submission
TITLE          Submitted (23-MAR-1993) Tony N. Marion, Microbiology and
JOURNAL        Immunology, University of, Tennessee, Memphis, 858 Madison Avenue,
               Memphis, TN, 38163, USA
FEATURES       Location/Qualifiers
               1..228
               /organism="Mus musculus domesticus"
               /strain="(NZB x NZW)F1"
               /isolate="mouse #165"
               /db_xref="taxon:10092"
               /chromosome="6"
               /sex="Female"
               /cell_line="165.6"
               /cell_type="hybridoma"
               /tissue_type="spleen"
               /dev_stage="somatic variant"
               1..228
               /gene="Igk"
               <1..>228
               /gene="Igk"
               /function="kappa light chain variable region for anti-DNA
               antibody; Vκ23 family"
               /codon_start=1
               /product="immunoglobulin variable region"
               /protein_id="CAA80047.1"
               /db_xref="GI:297640"
               /translation="NLHWYQQKSDSPRLIKYASKISGIPRFGSGSGTDTLTLSI
               NSVETEDFMVFCQSNWNPQTFGGKLEIK"
BASE COUNT    67 a 52 c 53 g 54 t
ORIGIN
|||||||
Query Match      82.2%; Score 22.2; DB 10; Length 228;
Best Local Similarity 88.9%; Pred. No. 8.2;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
|||||||
Db 172 CAACAGAGTAACAGCTGGCCTCAGACG 198

RESULT 10
MDIGKAV        236 bp      mRNA      linear      ROD 05-NOV-1994
LOCUS          Mus musculus Igk variable region.
DEFINITION     M.domesticus Igk variable region.
ACCESSION      222072
VERSION        222072.1 GI:297637
KEYWORDS       anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.
SOURCE         western European house mouse.
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 236)
REFERENCE      Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
AUTHORS        Both IgM and IgG anti-DNA antibodies are the products of clonally
TITLE          selective B cell stimulation in (NZB x NZW)F1 mice
JOURNAL        J. Exp. Med. 176 (3), 761-779 (1992)
MEDLINE        92381444
REFERENCE      2 (bases 1 to 236)
AUTHORS        Marion,T.N.
TITLE          Direct Submission

```

```

JOURNAL        Submitted (23-MAR-1993) Tony N. Marion, Microbiology and
               Immunology, University of, Tennessee, Memphis, 858 Madison Avenue,
               Memphis, TN, 38163, USA
FEATURES       Location/Qualifiers
               1..236
               /organism="Mus musculus domesticus"
               /strain="(NZB x NZW)F1"
               /isolate="mouse #165"
               /db_xref="taxon:10092"
               /chromosome="6"
               /sex="Female"
               /cell_line="165.60"
               /cell_type="hybridoma"
               /tissue_type="spleen"
               /dev_stage="somatic variant"
               1..236
               /gene="Igk"
               <1..>236
               /gene="Igk"
               /function="kappa light chain variable region for anti-DNA
               antibody; Vκ23 family"
               /codon_start=1
               /product="immunoglobulin variable region"
               /protein_id="CAA80046.1"
               /db_xref="GI:297638"
               /translation="LATYTGINKNHSLOQFSSMLPSPSLGSPPGSVAYDQGQISL
               SVSTVRLKILICISVNRVTAGLRVSVEAPSWKS"
BASE COUNT    68 a 57 c 53 g 58 t
ORIGIN
|||||||
Query Match      82.2%; Score 22.2; DB 10; Length 236;
Best Local Similarity 88.9%; Pred. No. 8.2;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
|||||||
Db 180 CAACAGAGTAACAGCTGGCCTCAGACG 206

RESULT 11
AF137617       297 bp      mRNA      linear      ROD 03-JUN-1999
LOCUS          Mus musculus clone 6C10F12 anti-fluorescein immunoglobulin light
DEFINITION     chain mRNA, partial cds.
ACCESSION      AF137617
VERSION        AF137617.1 GI:4972840
KEYWORDS       house mouse.
SOURCE         Mus musculus
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 297)
REFERENCE      van der Keyl,H., Gellad,Z.F. and Owen,J.A.
AUTHORS        Disparity in the kinetics of onset of hypermutation in
TITLE          immunoglobulin heavy and light chains
JOURNAL        Unpublished
AUTHORS        2 (bases 1 to 297)
TITLE          van der Keyl,H., Gellad,Z.F. and Owen,J.A.
JOURNAL        Direct Submission
AUTHORS        Submitted (25-MAR-1999) Biology, Haverford College, 370 Lancaster
TITLE          Avenue, Haverford, PA 19041-1392, USA
FEATURES       Location/Qualifiers
               1..297
               /organism="Mus musculus"
               /strain="Balb/c"
               /db_xref="taxon:10090"
               /clone="6C10F12"
               /cell_type="hybridoma"
               <1..>297
               /note="from primary IgM antibody"
               /codon_start=1
               /product="anti-fluorescein immunoglobulin light chain"

```



```

/protein_id="AAD34812.1"
/db_xref="GI:4972841"
/translation="QSPATLSVTPGDSVLSCRASQISNNLHWYQQKSHSPRLLIK
YASQISGIPSRFSGSGGDFTLINSVEXEDGMYFCQDSNPOTFGGGTKL"
BASE COUNT      76 a      69 g      72 t      2 others
ORIGIN

Query Match      82.2%; Score 22.2; DB 10; Length 297;
Best Local Similarity 88.9%; Pred. No. 8;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 250 CAACAGAGTAACAGCTGGCCTCTCAGC 276

RESULT 12
MMVL3E6
LOCUS      306 bp      mRNA      linear      ROD 26-JAN-1998
DEFINITION M.musculus mRNA for immunoglobulin light chain variable region
(VL3E6).
ACCESSION      X86546
VERSION      X86546.1 GI:809059
KEYWORDS      immunoglobulin; immunoglobulin light chain; kappa chain; light
chain; variable region.
SOURCE      house mouse.
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 306)
AUTHORS      Cerato,E., Birkle,S., Portoukalian,J., Mezazigh,A., Chatal,J.F. and
Aubry,J.
TITLE      Variable region gene segments of nine monoclonal antibodies
specific to disialogangliosides (GD2, GD3) and their O-acetylated
derivatives
JOURNAL      Hybridoma 16 (4), 307-316 (1997)
MEDLINE      97455038
REFERENCE      2 (bases 1 to 306)
AUTHORS      Cerato,E.M.
TITLE      Direct Submission
JOURNAL      Submitted (24-APR-1995) E.M. Cerato, INSERM U211, Institut de
Biologie, 9 quai Moncousu, 44035 Nantes Cedex 01, FRANCE
FEATURES
source
1..306
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/chromosome="12"
/rearranged
/dev_stage="adult"
/tissue_type="spleen"
/cell_type="B cell hybridoma"
/cell_line="3E6 hybridoma"
V_region 16..306
/note="anti-ganglioside GD3 immunoglobulin"
/product="immunoglobulin light chain variable region VL
3E6"
BASE COUNT      79 a      79 c      71 g      77 t
ORIGIN

Query Match      82.2%; Score 22.2; DB 10; Length 306;
Best Local Similarity 88.9%; Pred. No. 8;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 250 CAACAGAGTAACAGCTGGCCTCTCAGC 276

RESULT 13
MMIG1KL4
LOCUS      317 bp      mRNA      linear      ROD 04-AUG-1992
DEFINITION Mouse mRNA fragment for Gl kappa immunoglobulin A 20/44 light chain
(V-J).
ACCESSION      X02556
VERSION      X02556.1 GI:51646
KEYWORDS      Ig kappa light chain; immunoglobulin; joining region; variable
region.
SOURCE      house mouse.
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 317)
AUTHORS      Sablitzky,F. and Rajewsky,K.
TITLE      Molecular basis of an isogeneic anti-idiotypic response
JOURNAL      EMBO J. 3 (12), 3005-3012 (1984)
MEDLINE      85126904
FEATURES
Location/Qualifiers
1..317
/organism="Mus musculus"
/db_xref="taxon:10090"
misc_feature 1..285
/note="V(K) region"
mRNA <1..>317
/note="light chain fragment of A20/44"
misc_feature 286..317
/note="J(K) region"
BASE COUNT      80 a      84 c      70 g      82 t      1 others
ORIGIN

Query Match      82.2%; Score 22.2; DB 10; Length 317;
Best Local Similarity 88.9%; Pred. No. 8;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 265 CAACAGAGTAACAGCTGGCCTCTCAGC 291

RESULT 14
AF163757
LOCUS      321 bp      mRNA      linear      ROD 20-JUL-2001
DEFINITION Mus musculus mAb 101.4.1 immunoglobulin light chain variable region
mRNA, partial cds.
ACCESSION      AF163757
VERSION      AF163757.1 GI:5690320
KEYWORDS      house mouse.
SOURCE      house mouse.
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 321)
AUTHORS      Mertens,N.M., Galvin,J.E., Adderson,E.E. and Cunningham,M.W.
TITLE      Molecular analysis of cross-reactive anti-myoisin/anti-streptococcal
mouse monoclonal antibodies
JOURNAL      Mol. Immunol. 37 (15), 901-913 (2000)
MEDLINE      11282394
PUBMED      11282394
REFERENCE      2 (bases 1 to 321)
AUTHORS      Mertens,N.M. and Cunningham,M.W.
TITLE      Direct Submission
JOURNAL      Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma
University Health Sciences Center, 940 St. Young Blvd, Oklahoma
City, OK 73190, USA
FEATURES
Location/Qualifiers
1..321
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/note="mAb 101.4.1"
<1..>321
/note="V-J segments"
/codon_start=1
CDS

```

BASE COUNT83 a83 c73 g82 t

ORIGIN

/product="immunoglobulin light chain variable region"
/protein_id="AAD47036.1"
/db_xref="GI:5690321"
/translation="DIVLTQSPATLSVTFPGDSVLSCSRASQSIISNNLHWYQQKSHESP
RLIKYASQISGIPSRFSGSGTDFTLINSVETEDFGMYFCQQSNSWPLTFGAGT
KLELK"

Query Match82.2%; Score 22.2; DB 10; Length 321;
Best Local Similarity88.9%; Pred. No. 8;
Matches24; Conservative0; Mismatches3; Indels0; Gaps0;

QY1caacagagtggcagctggcctctgacg27
||||||| ||||||| |||

Db265CAACAGAGTAACAGCTGGCCTCTCACG291

RESULT15

MUSIGKCKN420 bp mRNA linear ROD 27-APR-1993
LOCUSMouse Ig kappa-chain mRNA VC-region (VJ5C) from hybridoma MAK33.
DEFINITIONM16162
ACCESSIONM16162
VERSIONM16162.1 GI:196893
KEYWORDSC-region; J-region; V-region; immunoglobulin kappa-chain;
immunoglobulin light chain; processed gene.
SOURCEMouse creatine kinase-specific monoclonal antibody producing
hybridoma (MAK33), cDNA to mRNA.
ORGANISMMus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE1 (bases 1 to 420)
AUTHORSBuckel,P.; Huebner-Parajsz,C.; Mattes,R.; Lenz,H.; Haug,H. and
Beaucamp,K.
TITLECloning and nucleotide sequence of heavy- and light-chain cDNAs
from a creatine-kinase-specific monoclonal antibody
JOURNALGene 51, 13-19 (1987)
MEDLINE87248058
COMMENTDraft entry for [1] kindly provided by P.Buckel, 31-JUL-1987.
FEATURES
Location/Qualifiers
1..420
/organism="Mus musculus"
/db_xref="taxon:10090"
7..66
/note="Ig-kappa chain signal peptide"
7..>420
/note="Ig-kappa-chain (VJ5C) precursor"
/codon_start=1
/protein_id="AAA38823.1"
/db_xref="GI:196894"
/translation="MVETPQILGLMFWISASRGDIVLTQSPATLSVTPRDSVLSLSCR
ASQSLSNLHWYQQKSHESPRLLIKYASQISGIPSRFSGSGTDFTLINSVETED
FGMYFCQQSNSWPLTFGAGTKLELKRAADAPIVSIF"
67..>420
/product="Ig-kappa chain"
BASE COUNT105 a107 c93 g115 t
ORIGINChromosome 6.

Query Match82.2%; Score 22.2; DB 10; Length 420;
Best Local Similarity88.9%; Pred. No. 7.8;
Matches24; Conservative0; Mismatches3; Indels0; Gaps0;

QY1caacagagtggcagctggcctctgacg27
||||||| ||||||| |||

Db331CAACAGAGTAACAGCTGGCCTCTCACG357

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run On: August 21, 2002, 09:55:34 ; Search time 6260.2 seconds
(without alignments)
58.212 Million cell updates/sec

Title: US-09-339-922a-89

Perfect score: 27
Sequence: 1 caacagatggcagctgcctctgacg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.2	82.2	772	10	BI105452
2	22.2	82.2	833	10	BG966582
3	21.8	80.7	961	12	CNS031KL
4	20.6	76.3	835	10	BI083006
5	20.6	76.3	868	10	BG539952
6	20.6	76.3	874	10	BG539326
7	20.6	76.3	1138	10	BG536825
8	20.4	75.6	385	12	AZ311061
9	20.2	74.8	191	12	AZ309067
10	20.2	74.8	558	12	AZ304616
11	19.8	73.3	477	9	AW035934
12	19.8	73.3	611	12	AZ018356
13	19.8	73.3	662	10	BZ232947
14	19.6	72.6	711	10	BG484755
15	19.6	72.6	1035	12	CNS054YD
16	19.6	72.6	1077	10	BF569518
17	19.4	71.9	846	10	BI555572
					BI05452 602891971
					BG966582 602834412
					AL223662 Tetraodon
					BI083006 602874524
					BG539952 602567464
					BG539326 602567937
					BG536825 602566362
					AZ311061 1M0026L13
					AZ309067 1M0012G13
					AZ304616 1M0004G13
					AW035934 EST282793
					AZ018356 RPCI-23-2
					BZ232947 602023450
					BG484755 60205642
					AL321358 Tetraodon
					BF569518 602186012
					BI555572 603239386

18	19.2	71.1	234	9	AI103024
19	19.2	71.1	389	9	AW786966
20	19.2	71.1	389	9	AW786967
21	19.2	71.1	473	12	AQ633034
22	19.2	71.1	530	12	BH118115
23	19.2	71.1	645	12	AG059962
24	19.2	71.1	738	10	BF582153
25	19.2	71.1	791	9	AL576123
26	19	70.4	519	9	AW405183
27	19	70.4	600	10	BF031314
28	19	70.4	1043	10	BI869360
29	18.8	69.6	311	12	AZ02801
30	18.6	68.9	166	9	AA066242
31	18.6	68.9	166	9	AI614002
32	18.6	68.9	272	9	AW186570
33	18.6	68.9	331	9	AA062406
34	18.6	68.9	342	10	BG937558
35	18.6	68.9	362	10	T97665
36	18.6	68.9	383	9	AA118430
37	18.6	68.9	390	9	AA475298
38	18.6	68.9	396	9	AI036201
39	18.6	68.9	406	12	AQ174932
40	18.6	68.9	414	9	AI596454
41	18.6	68.9	414	9	AV664865
42	18.6	68.9	418	9	AA832758
43	18.6	68.9	434	9	AA238817
44	18.6	68.9	438	9	AV753666
45	18.6	68.9	449	12	AF046306

ALIGNMENTS

RESULT 1

BI105452
LOCUS 602891971 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5037137 5',
DEFINITION mRNA sequence.
ACCESSION BI105452
VERSION BI105452.1 GI:14556345
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 772)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1102 row: n column: 18
High quality sequence stop: 771.
Location/Qualifiers
1..772
/organism="Mus musculus"
/strain="C57BL/6J (f1)"
/db_xref="taxon:10090"
/clone="IMAGE:5037137"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary stem cell origin"
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1; SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator

```

BASE COUNT      214 a 208 c 173 g 177 t
ORIGIN
    providing samples: Gilbert Smith, NIH"

Query Match      82.2%; Score 22.2; DB 10; Length 772;
Best Local Similarity 88.9%; Pred. No. 38;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27
    ||||| ||||| ||||| ||||| |||||
Db 330 CAACAGAGTAACAGCTGGCGCTCGGACG 356.

RESULT 2
LOCUS      BG966582      833 bp mRNA linear EST 12-JUN-2001
DEFINITION 602834412F1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4988955 5',
    mRNA sequence.
ACCESSION  BG966582
VERSION     BG966582.1 GI:14354219
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 833)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-remail.nih.gov
    Tissue Procurement: Jeffrey E. Green, M.D.
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM1002 row: g column: 04
    High quality sequence stop: 830.
    Location/Qualifiers
        1..833
            /organism="Mus musculus"
            /strain="FVB/N"
            /db_xref="taxon:10090"
            /clone_lib="NCI_CGAP_C024"
            /lab_host="DH10B (T1 phage-resistant)"
            /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.6 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      227 a 227 c 186 g 193 t
ORIGIN
    providing samples: Gilbert Smith, NIH"

Query Match      82.2%; Score 22.2; DB 10; Length 833;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27
    ||||| ||||| ||||| ||||| |||||
Db 329 CAACAGAGTGACAGCTGGCGCGCTCAGC 355.

RESULT 3
LOCUS      CNS031KL      961 bp DNA linear GSS 15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
    205K05 of library G from Tetraodon nigroviridis, genomic survey
    sequence.
ACCESSION  AL223662

```

```

AL223662.1 GI:7882493
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 961)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 961)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 961)
Genoscope.
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
    1..961
        /organism="Tetraodon nigroviridis"
        /db_xref="taxon:99883"
        /clone="205K05"
        /clone_lib="G"
        /note="Genoscope sequence ID : COAG205AF03SP1-end :
        PUC-Ori"

BASE COUNT      230 a 204 c 241 g 284 t 2 others
ORIGIN
    Query Match      80.7%; Score 21.8; DB 12; Length 961;
    Best Local Similarity 92.0%; Pred. No. 61;
    Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctga 25
    ||||| ||||| ||||| ||||| |||||
Db 515 CAACAGAGTGGCAGCTACCCCTCTGA 539

RESULT 4
LOCUS      BT083006      835 bp mRNA linear EST 20-JUN-2001
DEFINITION  602874524F2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
    mRNA sequence.
ACCESSION  BT083006
VERSION     BT083006.1 GI:14501336
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 835)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```

by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH/MGC Library."

Query Match	75.3%	Score 20.6;	DB 10;	Length 868;
Best Local Similarity	85.2%;	Pred. No. 1.9e+02;		
Matches 23; Conservative	0; Mismatches 4;	Indels 0; Gaps 0;		

KEYWORDS	EST.
SOURCE	human.
VERSION	BGG39320.1
GI:	13331339

REFERENCE
1 (bases 1 to 874)
AUTHORS
NTH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LECMI513 row: 1 column: 10
 High quality sequence stop: 588.

```

FEATURES
location/qualifiers
1. .874
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:4692561"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCATTTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGGGCGGCACATG-3' (30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

```

BASE CO

```

BASE COUNT      211 a      270 c      213 g      180 t
ORIGIN
Query Match      76.3%;   Score 20.6;   DB 10;   Length 874;
Best Local Similarity 85.2%;   Pred. No. 1.9e+02;
Matches 23;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;
QY      1 caacagagtggcagctggcctctgacg 27
      || ||| ||||| ||||| ||| |||
Db      358 CAGCAGCGGTGGCAGCTGGCCTCCGAGG 384

```

RESULT 7	BG536825	1138 bp	mrna	linear	EST 03-APR-2001
LOCUS	6025636362F1 NIH_MGC_77	1138 bp	mrna	linear	EST 03-APR-2001
DEFINITION	6025636362F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691079 5', mRNA sequence.				
ACCESSION	BG536825				
VERSION	BG536825.1	GI:13528371			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1138)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
CONTACT	Contact: Robert Strausberg, Ph.D.				
EMAIL	Email: cgapbs-femail.nih.gov				
TISSUE	Tissue Procurement: CLONTECH Laboratories, Inc.				
CDNA	CDNA Library Preparation: CLONTECH Laboratories, Inc.				
CDNA	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
DNA	DNA Sequencing by: Incyte Genomics, Inc.				
CLONE	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov				
PLATE	Plate: L1CM1509 row: k column: 16				
HIGH	High quality sequence stop: 657.				
FEATURES	Location/Qualifiers				
SOURCE	1. 1138				
ORGANISM	/organism="Homo sapiens"				
DB_XREF	/db_xref="taxon:9606"				
CLONE	/clone="IMAGE:4691079"				
CLONE_LIB	/clone_lib="NIH_MGC_77"				
LAB_HOST	/lab_host="DH10B (T1 phage-resistant)"				
NOTE	/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcgctatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGCCGACATG-dn(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."				
BASE	317 a	340 c	297 g	184 t	
ORIGIN					
Query	Match	76.3%	Score	20.6;	DB 10; Length 1138;
Best	Local	Similarity	85.2%	Pred. No.	2.1e+02;
Matches	23;	Conservative	0;	Mismatches	4; Indels 0; Gaps 0;
QY	1	caacagatgagcagctgacctctgacg	27		
Db	360	CACGAGCTGGCAGCTGGCCTCCGAGG	386		
RESULT 8	AZ311061	385 bp	DNA	linear	GSS 29-SEP-2000
LOCUS	1M0026L13F	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0026L13 F, DNA sequence.				
ACCESSION	AZ311061				
VERSION	AZ311061.1	GI:10353645			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
EUKARYOTA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 385)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.				
and Wright,D., Weiss,R.					
Mouse whole genome scaffolding with paired end reads from 10kb					
plasmid inserts					
Unpublished (2000)					
Contact: Robert B. Weiss					
University of Utah Genome Center					
University of Utah					
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT					
84112, USA					
Tel: 801 585 5606					
Fax: 801 585 7177					
Email: dunn@genetics.utah.edu					
Insert length: 10000					
Std Error: 0.00					
Plate: 0026					
row: L					
column: 13					
Seq primer: CGTTGTAACACGACGCCAGT					
Class: plasmid ends					
High quality sequence stop: 385.					
FEATURES	Location/Qualifiers				
SOURCE	1. 385				
ORGANISM	/organism="Mus musculus"				
STRAIN	/strain="C57BL/6J"				
DB_XREF	/db_xref="taxon:10090"				
CLONE	/clone="UUGC1M0026L13"				
CLONE_LIB	/clone_lib="Mouse 10kb plasmid UUGC1M library"				
SEX	/sex="Male"				
LAB_HOST	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"				
NOTE	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
BASE	COUNT	100 a	74 c	95 g	116 t
ORIGIN					
Query	Match	75.6%	Score	20.4;	DB 12; Length 385;
Best	Local	Similarity	95.5%	Pred. No.	1.6e+02;
Matches	21;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
QY	1	caacagatggcagctggcctc	22		
Db	149	CAACAGAGTGTGAGCTGGCCTC	128		
RESULT 9	AZ309067/c	191 bp	DNA	linear	GSS 29-SEP-2000
LOCUS	1M0012G13R	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0012G13 R, DNA sequence.				
ACCESSION	AZ309067				
VERSION	AZ309067.1	GI:10349686			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
EUKARYOTA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 191)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.				

Lycopersicon.

REFERENCE 1 (bases 1 to 477)
 AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 TITLE Generation of ESTs from tomato callus tissue
 JOURNAL Unpublished (1999)
 COMMENT Contact: CUGI
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES

source

1. .477
 Location/Qualifiers
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cLEC37J24"
 /clone_lib="tomato callus, TAMU"
 /tissue_type="callus"
 /dev_stage="25-40 days old"
 /lab_host="X11-Blue MRP"
 /note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 134 a 97 c 105 g 141 t
 ORIGIN

Query Match 73.3%; Score 19.8; DB 9; Length 477;
 Best Local Similarity 91.3%; Pred. No. 3.2e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aacagagtgcagctggcctctg 24
 |||||

DB 291 AACAGAGTGCAGCGGACCTCTG 269
 |||||

RESULT 12

AZ018356
 LOCUS RPci-23-298M6.TJ RPci-23 611 bp DNA linear GSS 25-FEB-2000
 DEFINITION RPci-23-298M6.TJ RPci-23 Mus musculus genomic clone RPci-23-298M6, DNA sequence.
 ACCESSION AZ018356
 VERSION AZ018356.1 GI:7093740
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 611)
 AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.
 TITLE Mouse BAC End Sequences from Library RPci-23

JOURNAL

COMMENT Unpublished (1999)
 Other_GSSs: RPci-23-298M6.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPci-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 298 row: M column: 6
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1. .611
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCi-23-298M6"
 /clone_lib="RPCi-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 158 a 98 c 141 g 214 t
 ORIGIN

Query Match 73.3%; Score 19.8; DB 12; Length 611;
 Best Local Similarity 91.3%; Pred. No. 3.5e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 acagagtgcagctggcctctga 25
 |||||

DB 431 AGACAGTGCAGCTGGCCTCTGA 453
 |||||

RESULT 13

BF232947
 LOCUS 60203450F1 NCI_CGAP_Li9 662 bp mRNA linear EST 14-NOV-2000
 DEFINITION mRNA sequence.
 ACCESSION BF232947
 VERSION BF232947.1 GI:11142629
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 662)
 AUTHORS NTH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM9435 row: d column: 14
 High quality sequence start: 2
 High quality sequence stop: 650.

FEATURES

source

Location/Qualifiers
 1. .662
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4158685"
 /clone_lib="NCI_CGAP_Li9"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."


```

BASE COUNT      139 a   143 c   209 g   171 t
ORIGIN

Query Match          73.3%; Score 19.8; DB 10; Length 662;
Best Local Similarity 91.3%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  4  cacagtggtgcagctggcctctgac 26
    ||| ||| ||||| ||||| |||
Db   349 CAGGGTGCACGCTGGCCTCTGAC 371

RESULT 14
BG484755
LOCUS              711 bp     mRNA       linear     EST 21-MAR-2001
DEFINITION         602505642F1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4619074 5',
                    mRNA sequence.
ACCESSION          BG484755
VERSION            BG484755.1 GI:13417034
KEYWORDS           EST.
SOURCE             human.
ORGANISM           Homo sapiens
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE          1 (bases 1 to 711)
AUTHORS            NIH-MGC http://mgc.ncl.nih.gov/.
TITLE              National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL            Unpublished (1999)
COMMENT            Contact: Robert Strausberg, Ph.D.
                   Email: cgabps@remail.nih.gov
                   Tissue Procurement: CLONTECH Laboratories, Inc.
                   CDNA Library Preparation: CLONTECH Laboratories, Inc.
                   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
                   DNA Sequencing by: Incyte Genomics, Inc.
                   Clone distribution: MGC clone distribution information can be
                   found through the I.M.A.G.E. Consortium/LNLN at:
                   http://image.lnl.gov
                   Plate: LLCMI378 row: c column: 11
                   High quality sequence stop: 564.
FEATURES           source
                   1..711
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:4619074"
                   /clone_lib="NIH_MGC_77"
                   /lab_host="DH10B (T1 phage-resistant)"
                   /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

BASE COUNT      177 a   206 c   192 g   136 t
ORIGIN

Query Match          72.6%; Score 19.6; DB 10; Length 711;
Best Local Similarity 84.6%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  1  cacacagtggtgcagctggcctctgac 26
    ||| ||| ||||| ||||| |||
Db   310 CAGCAGCGTCGCAGCTGGCCTCTCAC 335

RESULT 15
CN5054YD/c
LOCUS              1035 bp     DNA       linear     GSS 26-JUL-2000
DEFINITION         Tetraodon nigroviridis genome survey sequence T7 end of clone
                   041J22 of library A from Tetraodon nigroviridis, genomic survey
                   sequence.
ACCESSION          AL321358.1 GI:9554242
VERSION            AL321358
KEYWORDS           GSS; genome survey sequence.
SOURCE             Tetraodon nigroviridis.
ORGANISM           Tetraodon nigroviridis
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                   Tetraodontidae; Tetraodon.
REFERENCE          1 (bases 1 to 1035)
AUTHORS            Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                   Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                   Saurin,W. and Weissenbach,J.
TITLE              Estimate of human gene number provided by genome-wide analysis
                   using Tetraodon nigroviridis DNA sequence
JOURNAL            Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE            20296633
REFERENCE          2 (bases 1 to 1035)
AUTHORS            Crolius,H.R., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C.,
                   Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W.,
                   Bernot,A. and Weissenbach,J.
TITLE              Characterization and repeat analysis of the compact genome of the
                   freshwater pufferfish tetraodon nigroviridis
JOURNAL            Genome Res. 10 (7), 939-949 (2000)
MEDLINE            20359837
REFERENCE          3 (bases 1 to 1035)
AUTHORS            Genoscope.
TITLE              Direct Submission
JOURNAL            Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT            This sequence is a single read and was generated as part of a large
                   scale clone-end sequencing project of the Tetraodon nigroviridis
                   genome. For more information, please take a look at
                   http://www.genoscope.cns.fr/Tetraodon.
FEATURES           source
                   1..1035
                   /organism="Tetraodon nigroviridis"
                   /db_xref="taxon:99883"
                   /clone="041J22"
                   /clone_lib="A"
                   /note="Genoscope sequence ID : COAA041DE11C1-end : T7"

BASE COUNT      247 a   266 c   241 g   228 t   53 others
ORIGIN

Query Match          72.6%; Score 19.6; DB 12; Length 1035;
Best Local Similarity 84.6%; Pred. No. 5.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  1  caacagagtgcagctggcctctgac 26
    ||||| ||||| ||||| |||
Db   420 CACAGAGTGCGACTTTGCCCTCCGCC 395

Search completed: August 21, 2002, 09:55:42
Job time: 9305 sec

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:24 ; Search time 754.01 Seconds
(without alignments)
61.480 Million cell updates/sec

Title: US-09-339-922A-89

Perfect score: 27

Sequence: 1 caacagatggcagctggcctctgacg 27

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

1:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1980.DAT.*
2:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1981.DAT.*
3:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1982.DAT.*
4:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1983.DAT.*
5:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1984.DAT.*
6:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1985.DAT.*
7:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1986.DAT.*
8:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1987.DAT.*
9:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1988.DAT.*
10:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1989.DAT.*
11:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1990.DAT.*
12:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1991.DAT.*
13:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1992.DAT.*
14:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1993.DAT.*
15:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1994.DAT.*
16:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1995.DAT.*
17:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1996.DAT.*
18:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1997.DAT.*
19:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1998.DAT.*
20:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1999.DAT.*
21:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA2000.DAT.*
22:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA2001A.DAT.*
23:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA2001B.DAT.*
24:	/SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	19	AAV49872
2	27	100.0	27	22	AAV28228
3	25.4	94.1	27	19	AAV49873
4	25.4	94.1	27	22	AAV28229
5	23.8	88.1	27	19	AAV49850
6	23.8	88.1	27	22	AAV28206
7	23.8	88.1	57	19	AAV49842
8	23.8	88.1	57	19	AAV49833
9	23.8	88.1	57	22	AAH74636

10	23.8	88.1	57	22	AAF28188	Oligonucleotide #1	
11	23.8	88.1	57	22	AAF28197	Grafted light chain	
12	23.8	88.1	321	19	AAV49843	LM609 antibody lig	
13	23.8	88.1	321	19	AAV49821	Vitaxin antibody l	
14	23.8	88.1	321	19	AAV49823	LM609 antibody lig	
15	23.8	88.1	321	22	AAH74624	DNA encoding light	
16	23.8	88.1	321	22	AAH74626	DNA encoding light	
17	23.8	88.1	321	22	AAF28176	Vitaxin light chain	
18	23.8	88.1	321	22	AAF28178	Antibody LM609 lig	
19	23.8	88.1	321	22	AAF28199	DNA encoding light	
20	22.2	82.2	5238	11	AAQ04654	Plasmid pBT111 enc	
21	20.6	76.3	69	20	AAQ59221	PCR primer CR510 u	
22	20.6	76.3	72	20	AAQ59220	PCR primer CR508 u	
23	20.6	76.3	73	20	AAQ59218	PCR primer CR503 u	
24	20.6	76.3	98	20	AAV71819	Alpha-v beta-3 MAB	
25	20.6	76.3	321	20	AAV71800	Humanised anti-alp	
26	20.6	76.3	324	20	AAV71798	Murine vitronectin	
27	20.6	76.3	338	20	AAV71802	Vitronectin alpha-	
28	20.6	76.3	381	15	AAQ64167	Sequence of mouse	
29	20.6	76.3	381	21	AAZ35242	Mouse anti-verotoxin	
30	20.6	76.3	381	21	AAZ35244	Humanised anti-ver	
c	31	19.2	71.1	276	22	ABA53976	Human foetal liver
c	32	19.2	71.1	276	22	ABA53976	Probe #2192 for ge
c	33	19.2	71.1	276	22	AAK02242	Human brain expres
c	34	19.2	71.1	276	22	AAK27692	Human bone marrow
c	35	19.2	71.1	276	22	AAI33626	Probe #2312 used t
c	36	19.2	71.1	276	22	AAI02187	Probe #2178 used t
c	37	19.2	71.1	424	22	ABA44443	Human breast cell
c	38	19.2	71.1	424	22	ABA54890	Human foetal liver
c	39	19.2	71.1	424	22	ABA24656	Probe #3122 for ge
c	40	19.2	71.1	424	22	AAK03166	Human brain expres
c	41	19.2	71.1	424	22	AAK28616	Human bone marrow
c	42	19.2	71.1	424	22	AAI13190	Probe #3123 for ge
c	43	19.2	71.1	424	22	AAI34542	Probe #3228 used t
c	44	19.2	71.1	424	22	AAI03095	Probe #3086 used t
c	45	19.2	71.1	566	22	ABA66550	Human foetal liver

ALIGNMENTS

RESULT 1

AAV49872
ID AAV49872 standard; DNA; 27 BP.

XX AAV49872;

XX AAV49872;

DT 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-L region CDR3 DNA fragment #4.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region; ss.

OS Mus sp.

XX WO9833919-A2.

PN PD

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSV-) IXSVS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR P-PSDB; AAW76035.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

XX Disclosure; Page 42; 129pp; English.

XX

XX AAV49844-V49877 are nucleotide fragments of the grafted monoclonal

CC antibody LM609 heavy and light chain variable region. LM609 and the

CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used

CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX

SQ Sequence 27 BP; 6 A; 8 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 27; DB 19; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.014; 0; Mismatches 0; Gaps 0;

Matches 27; Conservative 0;

QY 1 caacagagtggcagctggcctctgacg 27

|||||

Db 1 caacagagtggcagctggcctctgacg 27

|||||

RESULT 2

AAF28228

ID AAF28228 standard; DNA; 27 BP.

XX

XX AAF28228;

XX

XX 03-APR-2001 (first entry)

XX

DE DNA encoding mutant VL CDR3 peptide #3.

XX

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX

XX Unidentified.

OS

PN WO200078815-A1.

XX

XX 28-DEC-2000.

XX

XX 23-JUN-2000; 2000WO-US17454.

PF

XX

XX 24-JUN-1999; 99US-0339922.

PR

XX

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA

XX

XX Huse WD, Wu H;

PI

XX

XX WPI; 2001-050110/06.

DR

XX

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta3 integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

XX Claim 16; Page 42; 132pp; English.

PS

XX

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 27 BP; 6 A; 8 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 27; DB 22; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.014; 0; Mismatches 0; Gaps 0;

Matches 27; Conservative 0;

QY 1 caacagagtggcagctggcctctgacg 27

|||||

Db 1 caacagagtggcagctggcctctgacg 27

|||||

RESULT 3

AAV49873

ID AAV49873 standard; DNA; 27 BP.

XX

XX AAV49873;

AC

XX

DT 02-NOV-1998 (first entry)

XX

XX LM609 grafted antibody V-L region CDR3 DNA fragment #5.

DE

XX

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-L region; CDR;

KW complementarity determining region; ss.

XX

OS Mus sp.

XX

XX WO9833919-A2.

PN

XX

XX 06-AUG-1998.

PD

XX

XX 30-JAN-1998; 98WO-US01826.

PF

XX

XX 30-JAN-1997; 97US-0791391.

PR

XX

XX (IXSY-) IXSYS INC.

PA

XX

XX Glaser SM, Huse WD;

PI

XX

XX WPI; 1998-437472/37.

DR

DR P-PSDB; AAW76036.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Disclosure; Page 42; 129pp; English.

XX

XX AAV49844-V49877 are nucleotide fragments of the grafted monoclonal

CC antibody LM609 heavy and light chain variable region. LM609 and the

CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used

CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 27 BP; 7 A; 8 C; 9 G; 3 T; 0 other;

Query Match 94.1%; Score 25.4; DB 19; Length 27;
 Best Local Similarity 96.3%; Pred. No. 0.067;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27
 |||||
 Db 1 caacagagtggcagctggcctctgacg 27

RESULT 4

AAAF28229
 ID AAF28229 standard; DNA; 27 BP.

XX AC AAF28229;

XX DT 03-APR-2001 (first entry)

XX DE DNA encoding mutant VL CDR3 peptide #4.

XX KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 XX KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX PS WPI; 2001-050110/06.

XX DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 XX PT osteoporosis -

XX PS Disclosure; Page 42; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX SQ Sequence 27 BP; 7 A; 8 C; 9 G; 3 T; 0 other;

Query Match 94.1%; Score 25.4; DB 22; Length 27;
 Best Local Similarity 96.3%; Pred. No. 0.067;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27
 |||||

Db 1 caacagagtggcagctggcctctgacg 27

RESULT 5

AAV49850

ID AAV49850 standard; DNA; 27 BP.

XX AC AAV49850;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-L region CDR2 DNA fragment #1.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region; ss.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Disclosure; Page 40; 129pp; English.

XX CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal
 CC antibody LM609 heavy and light chain variable region. LM609 and the
 CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used
 CC to inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

XX SQ Sequence 27 BP; 7 A; 9 C; 8 G; 3 T; 0 other;

Query Match 88.1%; Score 23.8; DB 19; Length 27;

Best Local Similarity 92.6%; Pred. No. 0.33;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27
 |||||

Db 1 caacagagtggcagctggcctctgacg 27

RESULT 6

AAF28206

ID AAF28206 standard; DNA; 27 BP.

XX AC AAF28206;

XX DT 03-APR-2001 (first entry)

XX DNA encoding LM609 VL CDR3 peptide.
 DE LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;
 XX inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 KW Unidentified.
 OS WO200078815-A1.
 XX 28-DEC-2000.
 PN 23-JUN-2000; 2000WO-US17454.
 XX 24-JUN-1999; 99US-0339922.
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA Huse WD, Wu H;
 PI WPI; 2001-050110/06.
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 XX to alpha(V)beta₃ integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Disclosure; Page 40; 132pp; English.
 PS The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX Sequence 27 BP; 7 A; 9 C; 8 G; 3 T; 0 other;
 SQ

Query Match 88.1%; Score 23.8; DB 22; Length 27;
 Best Local Similarity 92.6%; Pred. No. 0.33;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
 |||||
 Db 1 caacagagtggcagctggcctctgacg 27

RESULT 7
 AAV49842
 ID AAV49842 standard; DNA; 57 BP.
 AC AAV49842;
 XX 02-NOV-1998 (first entry)
 DT LM609 grafted antibody light chain variable region oligonucleotide #5.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; ss.
 XX Synthetic.
 OS Mus sp.
 XX WO9833919-A2.
 PN

XX 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta₃
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Example 5; Page 80; 129pp; English.
 PS AAV49838-V49842 are oligonucleotides used in the construction of grafted
 XX LM609 monoclonal antibody light chain variable regions. LM609 and the
 CC antibody vitaxin bind selectively to integrin alphavbeta₃ and can be
 CC used to inhibit binding of alphavbeta₃ to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta₃-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;
 SQ

Query Match 88.1%; Score 23.8; DB 19; Length 57;
 Best Local Similarity 92.6%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
 |||||
 Db 1 caacagagtggcagctggcctctgacg 27

RESULT 8
 AAV49833
 ID AAV49833 standard; DNA; 57 BP.
 AC AAV49833;
 XX 02-NOV-1998 (first entry)
 DT LM609 grafted antibody variable region oligonucleotide #10.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; ss.
 XX Synthetic.
 OS Mus sp.
 XX WO9833919-A2.
 PN 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA

XX PI Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Example 2; Page 65; 129pp; English.
 XX AAV49824-V49833 are oligonucleotides used in the construction of grafted
 CC LM609 monoclonal antibody heavy and light chain variable regions. LM609
 CC and the antibody vitaxin bind selectively to integrin alphavbeta3 and
 CC can be used to inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;
 SQ

Query Match 88.1%; Score 23.8; DB 19; Length 57;
 Best Local Similarity 92.6%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtgccagctggcctctgacg 27
 |||||
 Db 1 caacagagtgccagctggcctcacag 27

RESULT 9
 AAH74636
 ID AAH74636 standard; DNA; 57 BP.
 XX AC
 XX AAH74636;
 XX 15-OCT-2001 (first entry)
 XX PCR primer for light chain variable region of LM609 antibody.
 DE Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer; PCR primer; ss.
 XX Mus sp.
 XX OS
 XX US2001011125-A1.
 XX PN
 XX 02-AUG-2001.
 XX PD
 XX 30-JAN-1997; 97US-0790540.
 XX PF
 XX 30-JAN-1997; 97US-0790540.
 XX PR
 XX (HUSE/) HUSE W D.
 XX PA
 XX Huse WD;
 XX PI
 XX WPI; 2001-496171/54.
 XX DR
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX

PS Example 2; Page 17; 25pp; English.
 XX PCR primers AAH74632-36 were used to amplify DNA encoding fragments
 CC of the light chain variable region of the monoclonal antibody LM609.
 CC LM609 is a murine antibody which specifically recognises the integrin
 CC alphavbeta3, and inhibits its functional activity. The specification
 CC describes a LM609 grafted antibody which has the complementarity
 CC determining regions (CDRs) substituted into a non-murine framework.
 CC Nucleic acids encoding LM609 substituted heavy and light chain polypeptides
 CC and fragments are useful in diagnostic and therapeutic purposes, such
 CC as in the production of LM609 grafted antibodies and fragments having
 CC binding specificity and inhibitory activity against the integrin
 CC alphavbeta3. The antibody can be used for the diagnosis or treatment
 CC of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic
 CC articular rheumatism, psoriasis, disorders associated with inappropriate
 CC or inopportune invasion of vessels such as diabetic retinopathy,
 CC neovascular glaucoma and capillary proliferation in atherosclerotic
 CC plaques, or cancers), and to inhibit binding activity of alphavbeta3
 CC that are necessary for progression of an alphavbeta3-mediated disease.
 XX Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;
 SQ

Query Match 88.1%; Score 23.8; DB 22; Length 57;
 Best Local Similarity 92.6%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtgccagctggcctctgacg 27
 |||||
 Db 1 caacagagtgccagctggcctcacag 27

RESULT 10
 AAH28188
 ID AAH28188 standard; DNA; 57 BP.
 XX AC
 XX AAH28188;
 XX 03-APR-2001 (first entry)
 XX DE Oligonucleotide #10.
 XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 XX Unidentified.
 XX OS
 XX WO200078815-A1.
 XX PN
 XX 28-DEC-2000.
 XX PD
 XX 23-JUN-2000; 2000WO-US17454.
 XX PF
 XX 24-JUN-1999; 99US-0339922.
 XX PR
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX PA
 XX Huse WD, Wu H;
 XX PI
 XX WPI; 2001-050110/06.
 XX DR
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Example 2; Page 67; 132pp; English.
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;

Query Match 88.1%; Score 23.8; DB 22; Length 57;
 Best Local Similarity 92.6%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27
 |||||
 Db 1 caacagagtggcagctggcctcacg 27

RESULT 11
 AAF28197
 ID AAF28197 standard; DNA; 57 BP.
 XX
 AC AAF28197;

XX 03-APR-2001 (first entry)

XX Grafted light chain variable region oligonucleotide #5.

XX LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 to alpha(V)beta₃ integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

PS Example 4; Page 81; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;

Query Match 88.1%; Score 23.8; DB 22; Length 57;
 Best Local Similarity 92.6%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27
 |||||
 Db 1 caacagagtggcagctggcctcacg 27

RESULT 12
 AAV49843
 ID AAV49843 standard; DNA; 321 BP.
 XX
 AC AAV49843;

XX 02-NOV-1998 (first entry)

XX LM609 antibody light chain variable region DNA grafted fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; ss.

XX Mus sp.

XX Key Location/Qualifiers
 FH CDS 1..321
 FT /*tag= a
 FT /product= "LM609 grafted antibody light chain variable
 FT region"
 FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX P-PSDB; AAW76006.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta₃
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 24; Fig 7; 129pp; English.

XX This sequence encodes a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphaVbeta₃ and can be used to inhibit binding of alphaVbeta₃ to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphaVbeta₃-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 88.1%; Score 23.8; DB 19; Length 321;
 Best Local Similarity 92.6%; Pred. No. 0.46;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27

Db 265 caacagagtgccagctggcctcacgc 291

RESULT 13

AAV49821
ID AAV49821 standard; DNA; 321 BP.

AC AAV49821;

XX 02-NOV-1998 (first entry)

DE Vitaxin antibody light chain variable region DNA.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; ss.

OS Mus sp.

Key Location/Qualifiers

CDS 1..321

FT /*tag= a

FT /product= "vitaxin antibody light chain variable region"

FT /note= "partial sequence, no start or stop codon given"

PN WO9833919-A2.

XX 06-AUG-1998.

PD 30-JAN-1998; 98WO-US01826.

PF 30-JAN-1997; 97US-0791391.

PR (IXSY-) IXSYS INC.

PA Glaser SM, Huse WD;

PI WPI; 1998-437472/37.

DR P-PSDB; AAW76002.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis

Claim 6; Fig 1b; 129pp; English.

CC This sequence encodes the vitaxin antibody variable light chain region.
CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.

XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Query Match 88.1%; Score 23.8; DB 19; Length 321;

Best Local Similarity 92.6%; Pred. No. 0.46;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtgccagctggcctctgacg 27

|||||

Db 265 caacagagtgccagctggcctcacgc 291

RESULT 14

AAV49823

ID AAV49823 standard; DNA; 321 BP.

AC AAV49823;

XX 02-NOV-1998 (first entry)

DE LM609 antibody light chain variable region DNA fragment.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; ss.

OS Mus sp.

Key Location/Qualifiers

CDS 1..321

FT /*tag= a

FT /product= "LM609 antibody light chain variable region"

FT /note= "partial sequence, no start or stop codon given"

PN WO9833919-A2.

XX 06-AUG-1998.

PD 30-JAN-1998; 98WO-US01826.

PF 30-JAN-1997; 97US-0791391.

PR (IXSY-) IXSYS INC.

PA Glaser SM, Huse WD;

PI WPI; 1998-437472/37.

DR P-PSDB; AAW75004.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis

Claim 40; Fig 2b; 129pp; English.

CC This sequence encodes the LM609 antibody variable light chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.

XX Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 88.1%; Score 23.8; DB 19; Length 321;

Best Local Similarity 92.6%; Pred. No. 0.46;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtgccagctggcctctgacg 27

|||||

Db 265 caacagagtgccagctggcctcacgc 291

RESULT 15

AAH74624

Search completed: August 21, 2002, 10:08:26
Job time: 10044 sec

AAH74624 standard; DNA; 321 BP.
AAH74624;
15-OCT-2001 (first entry)
DNA encoding light chain variable region of LM609 grafted antibody.
Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
chronic articular rheumatism; psoriasis; diabetic retinopathy;
neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
cancer; ss.
Synthetic.
Mus sp.
Key Location/Qualifiers
CDS 1..321
/tag= a
/transl_except= "(pos: 145..147, aa: Xaa)"
/note= "Xaa is unspecified"
US2001011125-A1.
02-AUG-2001.
30-JAN-1997; 97US-0790540.
30-JAN-1997; 97US-0790540.
(HUSE/) HUSE W D.
Huse WD;
WPI: 2001-496171/54.
P-PSDB; AAC63588.
New LM609 grafted antibody exhibiting selective binding affinity to
alphavbeta3, comprising at least one LM609 grafted heavy and light
chain polypeptide, useful for diagnosing and treating e.g. inflammatory
disorders or cancer -
Claim 6: Fig 1B; 25pp; English.
The present sequence encodes the light chain variable region of the
grafted monoclonal antibody LM609. LM609 is a murine antibody which
specifically recognises the integrin alphavbeta3, and inhibits its
functional activity. The LM609 grafted antibody has the
complementarity determining regions (CDRs) substituted into a non-murine
framework. Nucleic acids encoding LM609 grafted heavy and light chain
polypeptides and fragments are useful in diagnostic and therapeutic
purposes, such as in the production of LM609 grafted antibodies and
fragments having binding specificity and inhibitory activity against
the integrin alphavbeta3. The antibody can be used for the diagnosis
or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
disorders, chronic articular rheumatism, psoriasis, disorders
associated with inappropriate or inopportune invasion of vessels such
as diabetic retinopathy, neovascular glaucoma and capillary
proliferation in atherosclerotic plaques, or cancers), and to inhibit
binding activity of alphavbeta3 that are necessary for progression of
an alphavbeta3-mediated disease.
Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 88.1%; Score 23.8; DB 22; Length 321;
Best Local Similarity 92.6%; Pred. No. 0.46;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1- caacagatggcagctggcctctgacg 27
Db 265 caacagatggcagctggcctcacacg 291

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:11 ; Search time 174.26 Seconds
(without alignments)
38.059 Million cell updates/sec

Title: US-09-339-922A-89

Perfect score: 27

Sequence: 1 caacagagtggcagctgcctctgacg 27

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.2	82.2	5238	6	Patent No. 5453363
2	20.6	76.3	424	1	US-08-436-463-3
3	19	70.4	27	2	US-08-232-081B-32
C 4	19	70.4	116	1	US-07-634-278-93
C 5	19	70.4	116	1	US-08-477-728-93
C 6	19	70.4	116	1	US-08-474-040-93
C 7	19	70.4	116	1	US-08-487-200-93
C 8	19	70.4	116	4	US-08-484-537-93
9	19	70.4	321	2	US-08-232-081B-35
10	19	70.4	321	2	US-08-232-081B-36
11	19	70.4	321	2	US-08-232-081B-39
12	19	70.4	381	1	US-07-634-278-82
13	19	70.4	381	1	US-08-477-728-82
14	19	70.4	381	1	US-08-474-040-82
15	19	70.4	381	1	US-08-487-200-82
16	19	70.4	381	4	US-08-484-537-82
C 17	17.6	65.2	2074	2	US-09-018-576-2
C 18	17.6	65.2	2074	2	US-09-018-576-11
C 19	17.6	65.2	2074	3	US-09-248-137-2
C 20	17.6	65.2	2074	3	US-09-248-137-11
21	17.4	64.4	3867	3	US-08-762-428A-5
22	17.4	64.4	4016	3	US-08-762-428A-7
23	17	63.0	2476	4	US-09-008-271A-23
C 24	17	63.0	2920	3	US-09-276-400-1
C 25	17	63.0	2920	4	US-09-448-076-1
C 26	16.8	62.2	26664	4	US-09-364-805-28
C 27	16.6	61.5	516	2	US-08-756-387B-12

c	28	16.6	61.5	516	4	US-09-285-873-12	Sequence 12, Appl
	29	16.6	61.5	568	3	US-08-985-950-9	Sequence 9, Appl
	30	16.6	61.5	591	2	US-08-756-387B-10	Sequence 10, Appl
	31	16.6	61.5	591	3	US-08-788-934-1	Sequence 1, Appl
	32	16.6	61.5	591	4	US-09-285-873-10	Sequence 10, Appl
	33	16.6	61.5	699	2	US-08-756-387B-7	Sequence 7, Appl
	34	16.6	61.5	699	4	US-09-285-873-7	Sequence 7, Appl
	35	16.6	61.5	713	2	US-08-238-027-3	Sequence 3, Appl
	36	16.6	61.5	774	2	US-08-756-387B-4	Sequence 4, Appl
c	37	16.6	61.5	774	2	US-08-756-387B-5	Sequence 5, Appl
	38	16.6	61.5	774	4	US-09-285-873-5	Sequence 4, Appl
c	39	16.6	61.5	774	4	US-09-285-873-5	Sequence 5, Appl
	40	16.6	61.5	1174	1	US-07-869-933-10	Sequence 10, Appl
	41	16.6	61.5	1174	4	US-09-103-663-10	Sequence 10, Appl
	42	16.6	61.5	1198	2	US-08-756-387B-1	Sequence 1, Appl
c	43	16.6	61.5	1198	2	US-08-756-387B-3	Sequence 3, Appl
	44	16.6	61.5	1198	4	US-09-285-873-1	Sequence 1, Appl
c	45	16.6	61.5	1198	4	US-09-285-873-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
5453363-1
; Patent No. 5453363
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MARTES, RALF
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
; ING AFTER GENETIC EXPRESSION IN PROKARYOTES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,044
; FILING DATE: 02-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 942,370
; FILING DATE: 09-SEP-1992
; APPLICATION NUMBER: 498,500
; FILING DATE: 23-MAR-1990
; APPLICATION NUMBER: 76,207
; FILING DATE: 23-OCT-1986
; SEQ ID NO:1:
; LENGTH: 5238
5453363-1

Query Match 82.2%; Score 22.2; DB 6; Length 5238;
Best Local Similarity 88.9%; Pred. No. 0.5;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 caacagagtggcagctgcctctgacg 27
Db 271 caacagagttaacagctggcctctcacg 297
RESULT 2
US-08-436-463-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 28-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992.
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..403
; US-08-436-463-3

Query Match 76.3%; Score 20.6; DB 1; Length 424;
Best Local Similarity 85.2%; Pred. No. 2;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
||||||| ||||||| |||
DB 347 CAACAGAGTAACAGCTGGCCTCACG 373

RESULT 3
US-08-232-081B-32
; Sequence 32, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WJDNES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-232-081B-32

Query Match 70.4%; Score 19; DB 2; Length 27;
Best Local Similarity 81.5%; Pred. No. 8.2;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
||||||| ||||||| |||
DB 1 CAACAAGTAGTAGCTGGCCTCACG 27

RESULT 4
US-07-634-278-93/C
; Sequence 93, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLET, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)

US-07-634-278-93

Query Match 70.4%; Score 19; DB 1; Length 116;
Best Local Similarity 81.5%; Pred. No. 9.1;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
||||| ||| ||||| |||
Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

RESULT 5

US-08-477-728-93/c
; Sequence 93, Application US/08477728
; Patent No. 5585089

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.

APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto

STATE: California
COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:

LENGTH: 116 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (oligonucleotide)
US-08-477-728-93

Query Match 70.4%; Score 19; DB 1; Length 116;
Best Local Similarity 81.5%; Pred. No. 9.1;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
||||| ||| ||||| |||

Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

RESULT 6

US-08-474-040-93/c

; Sequence 93, Application US/08474040
; Patent No. 5693761

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue

CITY: Palo Alto
STATE: California

COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995

CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 93:

SEQUENCE CHARACTERISTICS:
LENGTH: 116 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)

US-08-474-040-93

Query Match 70.4%; Score 19; DB 1; Length 116;
Best Local Similarity 81.5%; Pred. No. 9.1;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
||||| ||| ||||| |||

Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

RESULT 7

US-08-487-200-93/c

; Sequence 93, Application US/08487200
; Patent No. 5693762

```

; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-487-200-93

```

```

Query Match 70.4%; Score 19; DB 1; Length 116;
Best Local Similarity 81.5%; Pred. No. 9.1;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 caacagagtggcagctggcctctgacg 27
||||| ||| ||||| |||
Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

```

```

RESULT 8
US-08-484-537-93/c
; Sequence 93, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.

```

```

; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-484-537-93

```

```

Query Match 70.4%; Score 19; DB 4; Length 116;
Best Local Similarity 81.5%; Pred. No. 9.1;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 caacagagtggcagctggcctctgacg 27
||||| ||| ||||| |||
Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

```

```

RESULT 9
US-08-232-081B-35
; Sequence 35, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJDENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA

```

ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-232-081B-35

Query Match 70.4%; Score 19; DB 2; Length 321;
Best Local Similarity 81.5%; Pred. No. 9.7;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
||||| ||| | ||||| || |||
DB 265 CAACAAAGTAGTAGTGGCGCTCAGC 291

RESULT 10

US-08-232-081B-36
Sequence 36, Application US/082322081B
Patent No. 5886152

GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDNES, JOHN
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA

ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-232-081B-36

Query Match 70.4%; Score 19; DB 2; Length 321;
Best Local Similarity 81.5%; Pred. No. 9.7;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
||||| ||| | ||||| || |||
DB 265 CAACAAAGTAGTAGTGGCGCTCAGC 291

RESULT 11

US-08-232-081B-39
Sequence 39, Application US/082322081B
Patent No. 5886152

GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDNES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
US-08-232-081B-39

Query Match 70.4%; Score 19; DB 2; Length 321;
Best Local Similarity 81.5%; Pred. No. 9.7;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
||||| ||| | ||||| || |||
DB 265 CAACAAAGTAGTAGTGGCGCTCAGC 291

RESULT 12

US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-07-634-278-82

Query Match 70.4%; Score 19; DB 1; Length 381;
Best Local Similarity 81.5%; Pred. No. 9.8;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 caacagagtggcagctggcctctgacg 27
||||||| ||| ||||| |||
Db 325 CAACAGAGTAACAGTGGCCTCATACG 351

RESULT 13
US-08-477-728-82
; Sequence 82, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.

; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-477-728-82

Query Match 70.4%; Score 19; DB 1; Length 381;
Best Local Similarity 81.5%; Pred. No. 9.8;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 caacagagtggcagctggcctctgacg 27
||||||| ||| ||||| |||
Db 325 CAACAGAGTAACAGTGGCCTCATACG 351

RESULT 14
US-08-474-040-82
; Sequence 82, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-474-040-82

Query Match 70.4%; Score 19; DB 1; Length 381;
Best Local Similarity 81.5%; Pred. No. 9.8;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctgcctctgacg 27
||||| ||| ||||| |||
Db 325 CAACAGAGTAAACAGTTGGCCTCATACG 351

RESULT 15
US-08-487-200-82
Sequence 82, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELING, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto

STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-487-200-82

Query Match 70.4%; Score 19; DB 1; Length 381;
Best Local Similarity 81.5%; Pred. No. 9.8;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctgcctctgacg 27
||||| ||| ||||| |||
Db 325 CAACAGAGTAAACAGTTGGCCTCATACG 351

Search completed: August 21, 2002, 10:52:13
Job time: 9653 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:48:59 ; Search time 2408.76 seconds

(without alignments)
443.072 Million cell updates/sec

Title: US-09-339-922A-101

Perfect score:

Sequence: 1 aaagttagtagtggtggtgg.....atttagacactgtgcagggc 51

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Minimum DB seq	length: 0
Maximum DB seq	length: 200000000

THE FIRST BOOK OF SAMUEL

Post-processing: Minimum Match 08

Maximum Match 100%

Database :

GenEmbl: ★

1: qb_ba:

2: gb_htg

3: gb_in:

4: gb_om:

5: gb_ov:

6: gb_pat

7: gb_ph:

8: gb-pl:

9: gb_pr:

10: gb_ro

11: gb_st:

```
12: gb_sy
13: gb_un
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result	Query	Score	Length	ID	Description
No.	Match		DB		

Result	Score	Match	Length	DB	ID	Description
1	100	100	100	100	100	100
2	95	95	95	95	95	95
3	90	90	90	90	90	90
4	85	85	85	85	85	85
5	80	80	80	80	80	80
6	75	75	75	75	75	75
7	70	70	70	70	70	70
8	65	65	65	65	65	65
9	60	60	60	60	60	60
10	55	55	55	55	55	55
11	50	50	50	50	50	50
12	45	45	45	45	45	45
13	40	40	40	40	40	40
14	35	35	35	35	35	35
15	30	30	30	30	30	30
16	25	25	25	25	25	25
17	20	20	20	20	20	20
18	15	15	15	15	15	15
19	10	10	10	10	10	10
20	5	5	5	5	5	5

1	51	100.0	51	6	AX060880	Sequence
2	51	100.0	87	6	AX060790	Sequence
3	51	100.0	351	6	AX060780	Sequence
4	51	100.0	351	6	AX060784	Sequence
5	47.8	93.7	51	6	AX060882	Sequence
6	42.2	82.7	339	10	MMTGH4	
7	42.2	82.7	375	10	MMACHVR15	
8	41.2	80.8	345	10	MMAX229172	
9	40.6	79.6	85	6	A62608	
10	40.6	79.6	345	10	MUSIGVAAS	
11	40.6	79.6	345	10	MUSIGVAAB	
12	40.6	79.6	348	10	MUSIGVABB	
13	40.6	79.6	351	10	MUSIGVAAZ	
14	40.6	79.6	441	6	A62635	
15	40.6	79.6	445	6	A62635	
16	40.6	79.6	457	6	A6219	
17	39.8	78.0	337	10	MUSIGVAAZ	
18	39.8	78.0	344	10	MUSIGVABA	
19	39.8	78.0	363	10	MDIGGVAB	
20	39.6	77.6	290	10	AF318441	
21	39.6	77.6	363	10	MMHCVR2	
22	39	76.5	261	10	MM718313	
23	39	76.5	262	10	AF023214	
24	39	76.5	317	10	AF290963	
25	39	76.5	321	10	AF004399	
26	39	76.5	321	10	AF163750	
27	39	76.5	351	10	MM026468	
28	39	76.5	354	10	AF285276	
29	39	76.5	355	10	MDTGMVAF	
30	39	76.5	413	6	A38870	
31	39	76.5	413	6	AR013776	
32	39	76.5	416	6	AR174700	
33	39	76.5	482	6	I08289	
34	39	76.5	488	10	S45356	
35	39	76.5	721	6	AR027762	
36	39	76.5	721	6	AR088763	
37	39	76.5	733	6	AR027763	
38	39	76.5	733	6	AR088764	
39	38.8	76.1	348	10	MDTGGVBF	
40	38.2	74.9	354	10	MMTHPL911	
41	38	74.5	51	6	AR041111	
42	38	74.5	51	6	AR066005	
43	38	74.5	51	6	AR072747	
44	38	74.5	90	6	A38888	
45	38	74.5	90	6	AR013789	

ALIGNMENTS

```

RESULT      1
AX060880
LOCUS       AX060880            51 bp          DNA           linear         PAT 22-JAN-2001
DEFINITION Sequence 101 from Patent WO0078815.
ACCESSION   AX060880
VERSION     AX060880.1 GI:12406258
KEYWORDS    .
SOURCE      synthetic construct.
            synthetic construct.
            artificial sequence.
            1 (bases 1 to 51)
            Huse,W.D. and Wu,H.
            Anti-g(a) v $\gamma$ g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use.
            Patent: WO 0078815-A 101 28-DEC-2000;
            Applied Molecular Evolution (US)
            Location/Qualifiers
                source             1..51
                                   /organism="synthetic construct"
                                   /db_xref="taxon:32630"
                                   <1..>51
                                   /note="Mutated complementarity determining region (CDR)"
                                   /codon_start=1

```

/transl_table=11
/protein_id="CAC24926.1"
/db_xref="GI:12406259"
/translation="KVSSGGSTYYLDTVQG"
13 a 8 c 16 g 14 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51
|||||
Db 1 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGCG 51

RESULT 2

AX060790 AX060790 87 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 11 from Patent WO0078815.
ACCESSION AX060790
VERSION AX060790.1 GI:12406170

KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE
AUTHORS Huse, W.D. and Wu, H.

TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use

JOURNAL Patent: WO 0078815-A 11 28-DEC-2000;
Applied Molecular Evolution (US)

FEATURES
source 1..87
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligonucleotide"

BASE COUNT 23 a 18 c 24 g 22 t
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51
|||||
Db 10 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGCG 60

RESULT 3

AX060780 AX060780 351 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0078815.
ACCESSION AX060780
VERSION AX060780.1 GI:12406160

KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE
AUTHORS Huse, W.D. and Wu, H.

TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use

JOURNAL Patent: WO 0078815-A 1 28-DEC-2000;
Applied Molecular Evolution (US)

FEATURES
source 1..351
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="grafted antibody variable region"

BASE COUNT
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51
|||||
Db 10 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGCG 60

/codon_start=1
/transl_table=11
/protein_id="CAC24888.1"
/db_xref="GI:12406161"
/translation="QVOLVESGGVWOPGRSLRLSCAASGFTSSYDMSWVROAPGKG
LEWAKVSSGGSTYYLDTVQGRFTISRDNKNTLYLOMNSLASEDTAMYYCARHNYG
SFAYWGGTIVTVSS"
80 a 82 c 104 g 85 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51
|||||
Db 148 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGCG 198

RESULT 4

AX060784 AX060784 351 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 5 from Patent WO0078815.
ACCESSION AX060784
VERSION AX060784.1 GI:12406164

KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use

JOURNAL Patent: WO 0078815-A 5 28-DEC-2000;
Applied Molecular Evolution (US)

FEATURES
source 1..351
/organism="Mus musculus"
/db_xref="taxon:10090"
/note="unnamed protein product"

BASE COUNT 83 a 81 c 102 g 85 t
ORIGIN

CDS

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51
|||||
Db 148 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGCG 198

BASE COUNT
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51
|||||
Db 148 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGCG 198

RESULT 5

AX060882 AX060882 51 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 103 from Patent WO0078815.
ACCESSION AX060882
VERSION AX060882.1 GI:12406260

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 51)

AUTHORS Huse, W. D. and Wu, H.
 TITLE Anti-_3(a) v2_g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use
 JOURNAL Patent: WO 0078815-A 103 28-DEC-2000; Applied Molecular Evolution (US)
 FEATURES Location/Qualifiers
 source 1..51
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 <1..>51
 /note="Mutated complementarity determining region (CDR)"
 /codon_start=1
 /transl_table=11
 /protein_id="CAC24927.1"
 /db_xref="GI:12406261"
 /translation="KVSSGGSTYYPDVTVG"
 13 a 10 c 16 g 12 t
 BASE COUNT 13 a 10 c 16 g 12 t
 ORIGIN

Query Match 93.7%; Score 47.8; DB 6; Length 51;
 Best Local Similarity 96.1%; Pred. No. 2.8e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcactactatttagacactgtgcagggc 51
 |||||
 Db 1 AAAGTTAGTGGTGGTAGCACCCTACTATCCAGACACTGTGCAGGC 51

RESULT 6
 MMIGH4
 LOCUS M.musculus mRNA (L14-2G9) for IgH heavy chain V region.
 DEFINITION X59107
 ACCESSION
 VERSION X59107.1 GI:51944
 KEYWORDS Ig heavy chain; Ig variable region; immunoglobulin; rearranged.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 Kavalier, J.
 AUTHORS
 TITLE Direct Submission
 JOURNAL Submitted (15-APR-1991) J. Kavalier, Wistar Institute, 3601 Spruce Street, Philadelphia PA 19104, USA
 REFERENCE 2 (bases 1 to 339)
 AUTHORS Kavalier, J.
 JOURNAL Unpublished
 FEATURES Location/Qualifiers
 source 1..339
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /cell_line="L14-2G9"
 /tissue_type="B cell"
 /dev_stage="12 weeks old"
 /codon_start=1
 /product="IgH heavy chain V region"
 /protein_id="CAA41833.1"
 /db_xref="GI:51945"
 /translation="AVSSGSLVPGGSLKSCAASGAFSSYDMSWVROTPEKRLWY AVSSGSGSTYYPDVTVKGRFTISRDNAKNTLYLQMSLSKSDTAMYYCARHPYGNYYA MDYWGQSVT"
 84 a 83 c 92 g 80 t
 BASE COUNT 84 a 83 c 92 g 80 t
 ORIGIN

Query Match 82.7%; Score 42.2; DB 10; Length 339;
 Best Local Similarity 93.6%; Pred. No. 6.4e-07;
 Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AUTHORS Huse, W. D. and Wu, H.
 TITLE Anti-_3(a) v2_g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use
 JOURNAL Patent: WO 0078815-A 103 28-DEC-2000; Applied Molecular Evolution (US)
 FEATURES Location/Qualifiers
 source 1..51
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 <1..>51
 /note="Mutated complementarity determining region (CDR)"
 /codon_start=1
 /transl_table=11
 /protein_id="CAC24927.1"
 /db_xref="GI:12406261"
 /translation="KVSSGGSTYYPDVTVG"
 13 a 10 c 16 g 12 t
 BASE COUNT 13 a 10 c 16 g 12 t
 ORIGIN

Query Match 93.7%; Score 47.8; DB 6; Length 51;
 Best Local Similarity 96.1%; Pred. No. 2.8e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcactactatttagacactgtgcagggc 51
 |||||
 Db 1 AAAGTTAGTGGTGGTAGCACCCTACTATCCAGACACTGTGCAGGC 51

RESULT 6
 MMIGH4
 LOCUS M.musculus mRNA (L14-2G9) for IgH heavy chain V region.
 DEFINITION X59107
 ACCESSION
 VERSION X59107.1 GI:51944
 KEYWORDS Ig heavy chain; Ig variable region; immunoglobulin; rearranged.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 Kavalier, J.
 AUTHORS
 TITLE Direct Submission
 JOURNAL Submitted (15-APR-1991) J. Kavalier, Wistar Institute, 3601 Spruce Street, Philadelphia PA 19104, USA
 REFERENCE 2 (bases 1 to 339)
 AUTHORS Kavalier, J.
 JOURNAL Unpublished
 FEATURES Location/Qualifiers
 source 1..339
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /cell_line="L14-2G9"
 /tissue_type="B cell"
 /dev_stage="12 weeks old"
 /codon_start=1
 /product="IgH heavy chain V region"
 /protein_id="CAA41833.1"
 /db_xref="GI:51945"
 /translation="AVSSGSLVPGGSLKSCAASGAFSSYDMSWVROTPEKRLWY AVSSGSGSTYYPDVTVKGRFTISRDNAKNTLYLQMSLSKSDTAMYYCARHPYGNYYA MDYWGQSVT"
 84 a 83 c 92 g 80 t
 BASE COUNT 84 a 83 c 92 g 80 t
 ORIGIN

Query Match 82.7%; Score 42.2; DB 10; Length 339;
 Best Local Similarity 93.6%; Pred. No. 6.4e-07;
 Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcactactatttagacactgtgcagggc 51
 |||||
 Db 140 TTAGTAGTGGTGGTAGCACCCTACTATCCAGACACTGTGAAGGC 186

RESULT 7
 MMAHCVR15
 LOCUS M.musculus antibody heavy chain variable region (375bp).
 DEFINITION X90890
 ACCESSION
 VERSION X90890.1 GI:1518290
 KEYWORDS antibody heavy chain; variable region.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 Geiser, M. and Kretschmar, T.
 AUTHORS
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 375)
 AUTHORS Geiser, M.
 TITLE Direct Submission
 JOURNAL Submitted (17-AUG-1995) M. Geiser, CIBA-GEIGY LTD, CDDT, K-681.5.46, CH-4002, Basel, SWITZERLAND
 FEATURES Location/Qualifiers
 source 1..375
 /organism="Mus musculus"
 /strain="Balb/c"
 /db_xref="taxon:10090"
 /cell_type="lymphocytes"
 /tissue_type="spleen"
 /dev_stage="12 weeks old"
 <1..>375
 /codon_start=1
 /product="antibody heavy chain variable region"
 /protein_id="CAA62398.1"
 /db_xref="GI:1518291"
 /translation="EVKLESGLVPGGSLKSCAASGAFSSYDMSWVROTPEKR LEWAYISSGGSTYYPDVTVKGRFTISRDNAKNTLYLQMSLSKSDTAMYYCARQKGF YDYLTRNWFVWGAGTLVTSS"
 90 a 91 c 107 g 87 t
 BASE COUNT 90 a 91 c 107 g 87 t
 ORIGIN

Query Match 82.7%; Score 42.2; DB 10; Length 375;
 Best Local Similarity 93.6%; Pred. No. 6.4e-07;
 Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcactactatttagacactgtgcagggc 51
 |||||
 Db 152 TTAGTAGTGGTGGTAGCACCCTACTATCCAGACACTGTGAAGGC 198

RESULT 8
 MMA229172
 LOCUS Mus musculus rearranged cDNA for VH region of anti arsonate antibody (B cell hybridoma A22).
 DEFINITION AJ229172
 ACCESSION
 VERSION AJ229172.1 GI:3135848
 KEYWORDS anti arsonate antibody; diversity segment; heavy chain; immunoglobulin; joining segment; variable segment.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 345)
 Ismaili, J., RazanaJaona, D., Van Acker, A., Wuilmart, C., Mancini, I., Heinen, E., Leo, O., Lebecque, S., Urbain, J. and Brait, M.
 TITLE Molecular and cellular basis of the altered immune response against arsonate in irradiated A/J mice autologously reconstituted Int. Immunol. 11 (7), 1157-1167 (1999)
 JOURNAL
 MEDLINE 99315320

```

REFERENCE 2 (bases 1 to 345)
AUTHORS  Urbain,J.J.
TITLE     Direct Submission
JOURNAL   Submitted (13-MAY-1998) Urbain J.J., Biologie moleculaire,
          Universite Libre de Bruxelles, 67 rue des chevaux, Rhode-St-Genese,
          1640, BELGIUM
FEATURES  Location/Qualifiers
           source
           1..345
           /organism="Mus musculus"
           /strain="A/J"
           /db_xref="taxon:10090"
           /rearranged
           /cell_line="B cell"
           /cell_type="B cell hybridoma"
           /clone="A22"
           <1..276
           /gene="IGHF"
           /evidence=experimental
           /product="variable segment of immunoglobulin heavy chain"
           1..276
           /gene="IGHF"
           D_segment 277..300
           /gene="DSP2.7"
           /evidence=experimental
           /product="diversity region of immunoglobulin heavy chain"
           277..300
           /gene="DSP2.7"
           301..345
           /gene="JH2"
           J_segment 301..345
           /gene="JH2"
           /evidence=experimental
           /product="joining region of immunoglobulin heavy chain"
           80 a 92 c 89 g 81 t 3 others
BASE COUNT 80 a 92 c 89 g 81 t
ORIGIN
Query Match      80.8%; Score 41.2; DB 10; Length 345;
Best Local Similarity 91.5%; Pred. No. 1.7e-06;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 134 TTAGTAGTGGTGGTGTAGCACCTACTATCCAGACACTGTGNAGGCC 180

RESULT 9
A62608/c A62608 85 bp DNA linear PAT 12-MAR-1998
LOCUS Sequence 27 from Patent EP0781847.
ACCESSION A62608
VERSION A62608.1 GI:3716515
KEYWORDS  unidentified.
SOURCE  unidentified.
        unclassified.
        ORGANISM
REFERENCE 1 (bases 1 to 85)
AUTHORS  Bendig,M.D., Saldana,J.D. and Jones,T.D.
TITLE     Humanized monoclonal antibody
JOURNAL   Patent: EP 0781847-A 27 02-JUL-1997;
          MERCK PATENT GMBH (DE)
COMMENT   Other publication JP 9183799 19970715.
FEATURES  Location/Qualifiers
           source
           1..85
           /organism="unidentified"
           /db_xref="taxon:32644"
BASE COUNT 19 a 23 c 21 g 22 t
ORIGIN
Query Match      79.6%; Score 40.6; DB 6; Length 85;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 73 TTAGTAGAGGTGGTGGTAGCACCTACTATCCAGACACTGTGAAGGCC 27

RESULT 10
MUSIGVAAS 345 bp mRNA linear ROD 27-APR-1993
LOCUS Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
DEFINITION sequence.
ACCESSION L08991
VERSION L08991.1 GI:197989
KEYWORDS V-region; Immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 345)
AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
          Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
TITLE     V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
          mice
JOURNAL J Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES  Location/Qualifiers
           source
           1..345
           /organism="Mus musculus"
           /strain="mrl/mp-lpr/lpr"
           /db_xref="taxon:10090"
           /cell_line="anti-Sm hybridoma 14C10"
           /cell_type="B-cell"
           /tissue_type="spleen"
           /dev_stage="adult"
BASE COUNT 80 a 85 c 102 g 78 t
ORIGIN
Query Match      79.6%; Score 40.6; DB 10; Length 345;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 151 TTAGTAGTGGTGGTGGTAGCACCTACTATCCAGACACTGTGAAGGCC 197

RESULT 11
MUSIGVAAX 345 bp mRNA linear ROD 27-APR-1993
LOCUS Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
DEFINITION sequence.
ACCESSION L08996
VERSION L08996.1 GI:197994
KEYWORDS V-region; Immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 345)
AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
          Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
TITLE     V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
          mice
JOURNAL J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES  Location/Qualifiers
           source
           1..345
           /organism="Mus musculus"
           /strain="mrl/mp-lpr/lpr"
           /db_xref="taxon:10090"
           /cell_line="anti-Sm hybridoma 22F6"
           /cell_type="B-cell"

```

```

/tissue_type="spleen"
/dev_stage="adult"
BASE COUNT      80 a      86 c      102 g      77 t
ORIGIN

Query Match      79.6%; Score 40.6; DB 10; Length 345;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
Db 152 TTAGTAGTGGTGGTGTAGCACCTACTATCCACAGACAGTGTGAAGGC 198

RESULT 12
MUSIGVABB
LOCUS      MUSIGVABB      348 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
sequence.
ACCESSION L09000
VERSION L09000.1 GI:197998
KEYWORDS V-region; immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 348)
Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
mice
JOURNAL J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES
source
1..348
/organism="Mus musculus"
/strain="mrl/mp-lpr/lpr"
/db_xref="taxon:10090"
/cell_line="anti-Sm hybridoma 4D12"
/cell_type="B-cell"
/tissue_type="spleen"
/dev_stage="adult"
BASE COUNT      80 a      87 c      102 g      79 t
ORIGIN

Query Match      79.6%; Score 40.6; DB 10; Length 348;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
Db 152 TTAGTAGTGGTGGTGTAGCACCTACTATCCACAGACAGTGTGAAGGC 198

RESULT 13
MUSIGVAAV
LOCUS      MUSIGVAAV      351 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
sequence.
ACCESSION L08997
VERSION L08997.1 GI:197995
KEYWORDS V-region; immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 351)
Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
mice

```

```

J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES
source
1..351
/organism="Mus musculus"
/strain="mrl/mp-lpr/lpr"
/db_xref="taxon:10090"
/cell_line="anti-Sm hybridoma 2E10"
/cell_type="B-cell"
/tissue_type="spleen"
/dev_stage="adult"
BASE COUNT      82 a      87 c      103 g      79 t
ORIGIN

Query Match      79.6%; Score 40.6; DB 10; Length 351;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
Db 152 TTAGTAGTGGTGGTGTAGCACCTACTATCCACAGACAGTGTGAAGGC 198

RESULT 14
A62623
LOCUS      A62623      441 bp      DNA      linear      PAT 12-MAR-1998
DEFINITION Sequence 42 from Patent EP0781847.
ACCESSION A62623
VERSION A62623.1 GI:3716530
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 441)
AUTHORS Bendig,M.D., Saldana,J.D. and Jones,T.D.
TITLE Humanized monoclonal antibody
JOURNAL Patent: EP 0781847-A 42 02-JUL-1997;
MERCK PATENT GMBH (DE)
COMMENT Other publication JP 9183799 19970715.
FEATURES
source
1..441
/organism="unidentified"
/db_xref="taxon:32644"
misc_signal
1..11
sig_peptide
12..68
CDS
12..>428
/function="FR'S, CDR'S"
/codon_start=1
/product="CHIMERIC MAB 15, HEAVY CHAIN VARIABLE REGION"
/protein_id="CAA03670.1"
/db_xref="GI:4530024"
/translation="MNRGLSLIFLVILKGVKCEVQVVESSGGLVKGSGSLKLSCAAS
GFAPSDYDMWVROTPEKRLEWVAYLSRGSGSTYPDPVTKGRFTISRDNKAKILFLQM
TSLSKSDAAMYICARHGEEVRFDFYWGQGTLTVSA"
BASE COUNT      98 a      99 c      130 g      114 t
ORIGIN

Query Match      79.6%; Score 40.6; DB 6; Length 441;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
Db 220 TTAGTAGAGTGGTGGTGTAGCACCTACTATCCACAGACACTGTGAAGGC 266

RESULT 15
A62635
LOCUS      A62635      445 bp      DNA      linear      PAT 12-MAR-1998
DEFINITION Sequence 54 from Patent EP0781847.
ACCESSION A62635

```

```
Query Match      79.6%; Score 40.6; DB 6; Length 445;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Search completed: August 21, 2002, 10:49:01
Job time: 9756 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 09:55:42 ; Search time 6260.2 Seconds
(without alignments)
109.956 Million cell updates/sec

Title: US-09-339-922a-101
Perfect score: 51
Sequence: 1 aaagttagtagtggtggtg.....atttagacactgtgcagggc 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	37.4	73.3	861	10	BI455668 603173862
2	35.8	70.2	333	10	BI336517 AR097E07S
3	35.8	70.2	424	10	BI337375 AR089G02P
4	35.8	70.2	469	9	AI645111 ms87g10.y
5	35.8	70.2	650	10	BF579001 602096117
6	35.8	70.2	823	9	AA170256 ms87g10.r
7	35.8	70.2	837	10	BG966355 602832843
8	35.2	69.0	662	10	BF163874 601772386
9	35.2	69.0	883	10	BI151077 602917012
10	35.2	69.0	908	10	BF161883 601766819
11	35.2	69.0	913	10	BF162056 601768714
12	34.8	68.2	338	9	BB868286 BB868286
13	34.8	68.2	404	10	BF452207 uz85h05.y
14	34.8	68.2	548	9	AW408295 UI-HF-BK0
15	34.8	68.2	877	10	BF144493 601790133
16	34.2	67.1	689	10	BF579926 602095194
17	34.2	67.1	758	10	BM083708 imageqc_2

18	33.6	65.9	898	10	BG757960
19	33.2	65.1	342	9	BB869694
20	33.2	65.1	406	9	AW403983
21	33.2	65.1	494	10	BG145342
22	32.6	63.9	308	10	BF844139
23	32.6	63.9	330	10	F14516
24	32.6	63.9	332	10	BF155433
25	32.6	63.9	367	10	BI305075
26	32.6	63.9	372	9	AA581192
27	32.6	63.9	454	9	AW824857
28	32.6	63.9	648	10	BG340670
29	32.6	63.9	652	10	BG965201
30	32.6	63.9	718	10	BF136279
31	32.6	63.9	735	10	BG745292
32	32.6	63.9	737	10	BF974929
33	32.6	63.9	774	10	BF581450
34	32.6	63.9	862	10	BF143948
35	32.6	63.9	875	10	BG340548
36	32.6	63.9	954	10	BG963956
37	32.6	63.9	966	10	BG745389
38	32.6	63.9	1012	10	BF142302
39	31.6	62.0	624	12	BH021317
40	31.6	62.0	1559	10	BF138708
41	31	60.8	294	9	AW606245
42	31	60.8	406	9	AW401971
43	31	60.8	412	9	AW800162
44	31	60.8	434	9	AW630702
45	31	60.8	440	9	AW408304

ALIGNMENTS

RESULT 1
BI455668

LOCUS 861 bp mRNA linear EST 21-AUG-2001
DEFINITION 603173862F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5253279 5', mRNA sequence.

ACCESSION BI455668
VERSION BI455668.1 GI:15246324

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 861)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM1639 Row: 1 Column: 16
High quality sequence stop: 780.

Location/Qualifiers
1. 861
/organism="Mus musculus"

/db_xref="taxon:10090"
/clone="IMAGE:5253279"

/tissue_type="tumor, gross tissue"
/dev_stage="7 months"

/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1; Salt; Site:2; NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

```

providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 205 a 239 c 211 g 206 t
ORIGIN

Query Match 73.3%; Score 37.4; DB 10; Length 861;
Best Local Similarity 87.2%; Pred. No. 0.0015;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 tttagtagtggtgtagcaccattatttagacactgtgcaggcc 51
||||| ||||||| ||||||| ||| ||||||| |||||
Db 279 TTAGTAATGCTGTTGCTAGCACCCTATTATCCAGACACTGTGAAGGCC 325

RESULT 2
BI336517
LOCUS BI336517 333 bp mRNA linear EST 01-SEP-2001
DEFINITION AR097E07SPD09S Porcine Spleen cDNA library Sus scrofa cDNA, mRNA
sequence.
ACCESSION BI336517
VERSION BI336517.1 GI:15417813
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 333)
AUTHORS Rink A., Santschi, E.M. and Beattie, C.W.
TITLE Amplified, Normalized cDNA Libraries from a Porcine Model of
Orthopedic Implant Associated Staphylococcus aureus Infection
Unpublished (2001)
JOURNAL
COMMENT Contact: Rink A
Department of Animal Biotechnology
College of Agriculture, Biotechnology and Natural Resources,
University of Nevada, Reno
MS 202, FA 103, 1664 N Virginia St, Reno, NV 89557-0236, USA
Tel: 775 784 1705
Fax: 775 784 1375
Email: arink@cabnr.unr.edu
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCACGAG'.
FEATURES
Location/Qualifiers
source
1..333
/organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone_lib="Porcine Spleen cDNA library"
/tissue_type="Spleen"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/note="Vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGGCACGAG'."

BASE COUNT 69 a 84 c 101 g 69 t 10 others
ORIGIN

Query Match 70.2%; Score 35.8; DB 10; Length 333;
Best Local Similarity 85.1%; Pred. No. 0.0042;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 tttagtagtggtgtagcaccattatttagacactgtgcaggcc 51
||||| ||||||| ||||||| ||| ||||||| |||||
Db 236 TTAGTAATGCTGTTGCTAGCACCCTATTATCCAGACACTGTGAAGGCC 282

RESULT 4
BI337375
LOCUS BI337375 424 bp mRNA linear EST 01-SEP-2001
DEFINITION AR089G02PBC0G02S Porcine Peripheral Blood Cell cDNA library Sus
scrofa cDNA, mRNA sequence.
ACCESSION BI337375
VERSION BI337375.1 GI:15418671
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 424)
AUTHORS Rink A., Santschi, E.M. and Beattie, C.W.
TITLE Amplified, Normalized cDNA Libraries from a Porcine Model of
Orthopedic Implant Associated Staphylococcus aureus Infection
Unpublished (2001)
JOURNAL
COMMENT Contact: Rink A
Department of Animal Biotechnology
College of Agriculture, Biotechnology and Natural Resources,
University of Nevada, Reno
MS 202, FA 103, 1664 N Virginia St, Reno, NV 89557-0236, USA
Tel: 775 784 1705
Fax: 775 784 1375
Email: arink@cabnr.unr.edu
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCACGAG'.
FEATURES
Location/Qualifiers
source
1..424
/organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone_lib="Porcine Peripheral Blood Cell cDNA library"
/tissue_type="Peripheral Blood Cell"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/note="Vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGGCACGAG'."

BASE COUNT 88 a 101 c 133 g 92 t 10 others
ORIGIN

Query Match 70.2%; Score 35.8; DB 10; Length 424;
Best Local Similarity 85.1%; Pred. No. 0.0045;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 tttagtagtggtgtagcaccattatttagacactgtgcaggcc 51
||||| ||||||| ||||||| ||| ||||||| |||||
Db 236 TTAGTAATGCTGTTGCTAGCACCCTATTATCCAGACACTGTGAAGGCC 282

RESULT 4
BI645111
LOCUS BI645111 469 bp mRNA linear EST 15-MAR-2000
DEFINITION ms87g10.y1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:616594
5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION
(HUMAN); gb:U23089 Mus musculus CB17 SCID immunoglobulin heavy
chain V region mRNA, (MOUSE);, mRNA sequence.

```

```

||||| | ||||||| ||||||| |||| | ||||| |||||
Db 148 TTAGTAATGCTGTTGCTAGCACCCTACTACGCAGACTGTGAAGGCC 194

RESULT 3
BI337375
LOCUS BI337375 424 bp mRNA linear EST 01-SEP-2001
DEFINITION AR089G02PBC0G02S Porcine Peripheral Blood Cell cDNA library Sus
scrofa cDNA, mRNA sequence.
ACCESSION BI337375
VERSION BI337375.1 GI:15418671
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 424)
AUTHORS Rink A., Santschi, E.M. and Beattie, C.W.
TITLE Amplified, Normalized cDNA Libraries from a Porcine Model of
Orthopedic Implant Associated Staphylococcus aureus Infection
Unpublished (2001)
JOURNAL
COMMENT Contact: Rink A
Department of Animal Biotechnology
College of Agriculture, Biotechnology and Natural Resources,
University of Nevada, Reno
MS 202, FA 103, 1664 N Virginia St, Reno, NV 89557-0236, USA
Tel: 775 784 1705
Fax: 775 784 1375
Email: arink@cabnr.unr.edu
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCACGAG'.
FEATURES
Location/Qualifiers
source
1..424
/organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone_lib="Porcine Peripheral Blood Cell cDNA library"
/tissue_type="Peripheral Blood Cell"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/note="Vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGGCACGAG'."

BASE COUNT 88 a 101 c 133 g 92 t 10 others
ORIGIN

Query Match 70.2%; Score 35.8; DB 10; Length 424;
Best Local Similarity 85.1%; Pred. No. 0.0045;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 tttagtagtggtgtagcaccattatttagacactgtgcaggcc 51
||||| ||||||| ||||||| ||| ||||||| |||||
Db 236 TTAGTAATGCTGTTGCTAGCACCCTACTACGCAGACTGTGAAGGCC 282

RESULT 4
BI645111
LOCUS BI645111 469 bp mRNA linear EST 15-MAR-2000
DEFINITION ms87g10.y1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:616594
5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION
(HUMAN); gb:U23089 Mus musculus CB17 SCID immunoglobulin heavy
chain V region mRNA, (MOUSE);, mRNA sequence.

```



```

FEATURES
source
    Location/Qualifiers
    1. .837
    /organism="Mus musculus"
    /strain="FVB/N"
    /db_xref="taxon:10090"
    /clone_image="4987379"
    /clone_lib="NCL_CGAP_Co24"
    /lab_host="PH10B (T1 phage-resistant)"

```



```

BASE COUNT      218 a      248 c      260 g      187 t
ORIGIN
    providing samples: Gilbert Smith, NIH"

Query Match      69.0%; Score 35.2; DB 10; Length 913;
Best Local Similarity 83.3%; Pred. No. 0.0097;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 agttagtggtggtgtagcaccctactatttagacactgtgcagg 50
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 273 AGCCATTAGTAGTGGTGGTACCTACTATCCAGACAGTGTGAAGG 320

RESULT 12
LOCUS      BB868286      338 bp      mRNA      linear      EST 27-NOV-2001
DEFINITION BB868286 RIKEN full-length enriched, pooled tissues, intestinal
            mucosa, etc. Mus musculus cDNA clone G630003K04 5', mRNA sequence.
ACCESSION  BB868286
VERSION     BB868286.1 GI:17114496
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 338)
AUTHORS     Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
            Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
            ,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
            , Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shinaawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
            ,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
            Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
            2001)
TITLE       Unpublished (2001)
JOURNAL     Contact: Yoshihide Hayashizaki
COMMENT     Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center (GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
            e mouse tissues.
            Location/Qualifiers
            1. .338
            /organism="Mus musculus"
            /strain="C57BL/6"
            /db_xref="taxon:10090"
            /clone="G630003K04"

FEATURES
source
    Location/Qualifiers
    1. .404
    /organism="Mus musculus"
    /strain="CZECH II (feral)"
    /db_xref="taxon:10090"
    /clone="IMAGE:3675897"
    /clone_lib="NCI_CGAP_Lu29"
    /tissue_type="spontaneous tumor, metastatic to mammary.

/clone_lib="RIKEN full-length enriched, pooled tissues,
intestinal mucosa, etc."
/note="pooled tissues", (tissue_type=intestinal mucosa,
dev_stage=adult, sex=male), (tissue_type=accessory
axillary lymph node, dev_stage=adult, sex=male),
(tissue_type=jejunal and colic lymph node, dev_stage=adult
, sex=male), (tissue_type=gall bladder, dev_stage=adult,
sex=male), (tissue_type=vesicular gland, dev_stage=adult,
embryo), (tissue_type=spinal cord, dev_stage=11 days
embryo), (tissue_type=brain, dev_stage=13 days embryo),
(tissue_type=spinal cord, dev_stage=13 days embryo),
(tissue_type=lung, dev_stage=14 days embryo),
(tissue_type=brain, dev_stage=15 days embryo),
(tissue_type=ovary and uterus, dev_stage=10 days pregnant
adult, sex=female), (tissue_type=cortex, dev_stage=0 day
neonate), (tissue_type=cerebellum, dev_stage=1 month
neonate), (tissue_type=diencephalon, dev_stage=16 days
neonate, sex=male), (tissue_type=medulla oblongata,
dev_stage=16 days neonate, sex=male),
(tissue_type=cerebellum, dev_stage=21 days neonate),
(tissue_type=testis, dev_stage=8 days neonate, sex=male)"
BASE COUNT      70 a      80 c      100 g      88 t
ORIGIN
    Query Match      68.2%; Score 34.8; DB 9; Length 338;
    Best Local Similarity 84.8%; Pred. No. 0.0098;
    Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccctactatttagacactgtgcagg 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 289 TCAGTAGTGGTGGTGGTTCACCGATTATTAGACAGTGTGAAGG 334

RESULT 13
LOCUS      BF452207      404 bp      mRNA      linear      EST 29-DEC-2000
DEFINITION uz85h05.y1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3675897 5',
            similar to SW:HV55_MOUSE P18526 IG HEAVY CHAIN V REGION 345
            PRECURSOR. , mRNA sequence.
ACCESSION  BF452207
VERSION     BF452207.1 GI:11518376
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 404)
REFERENCE   1 (bases 1 to 404)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapsof@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Cloning Arrayed by: Washington University Genome Sequencing Center
            Cloning distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml

MGI:1436665
Seq primer: -40RP from Gibco
High quality sequence stop: 399.
Location/Qualifiers
    1. .404
    /organism="Mus musculus"
    /strain="CZECH II (feral)"
    /db_xref="taxon:10090"
    /clone="IMAGE:3675897"
    /clone_lib="NCI_CGAP_Lu29"
    /tissue_type="spontaneous tumor, metastatic to mammary.

```

```
Stem cell origin."
/lab_host="DH10B"
/Note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
96 a 94 c 109 g 105 t
BASE COUNT
ORIGIN

Query Match 68.2%; Score 34.8; DB 10; Length 404;
Best Local Similarity 84.8%; Pred. No. 0.01;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 257 TTAGTGATGTTGGTGTACACCTACTACTATCTAGACAGTGTGAAGG 302

RESULT 14
AW408295 548 bp mRNA linear EST 16-FEB-2000
LOCUS
DEFINITION
IMAGE:3056327 5', mRNA sequence.
ACCESSION
AW408295
VERSION
AW408295.1 GI:6927352
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
REFERENCE
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Sequencing by: M.B. Soares Lab
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbfp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1..548
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3056327"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/Note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
109 a 148 c 156 g 135 t
BASE COUNT
ORIGIN

Query Match 68.2%; Score 34.8; DB 9; Length 548;
Best Local Similarity 84.8%; Pred. No. 0.012;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 276 TTAGTTGGGATGTTGGTGTAGCACCCTACTATGCAGACTCTGTGAAGG 321
```

```
RESULT 15
BF144493 877 bp mRNA linear EST 24-OCT-2000
LOCUS
DEFINITION
601790133F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4020753 5',
mRNA sequence.
ACCESSION
BF144493
VERSION
BF144493.1 GI:10983533
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 877)
REFERENCE
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9275 row: a column: 10
High quality sequence stop: 644.
Location/Qualifiers
1..877
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4020753"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/Note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dt. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
198 a 233 c 254 g 192 t
BASE COUNT
ORIGIN

Query Match 68.2%; Score 34.8; DB 10; Length 877;
Best Local Similarity 84.8%; Pred. No. 0.013;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 245 TTAGTAGTGGTGTAGTTACACCTACTATCCAGACAGTGTGAAGG 290

Search completed: August 21, 2002, 09:55:46
Job time: 9309 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:26 ; Search time 754.01 seconds
(without alignments)
116.129 Million cell updates/sec

Title: US-09-339-922A-101

Perfect score: 51

Sequence: 1 aaagttagtggtgtgtg.....atttagacactgtgcaggcc 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

```

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	51	22	AAF28234
2	51	100.0	87	19	AAV49826
3	51	100.0	87	22	AAH74629
4	51	100.0	87	22	AAF28181
5	51	100.0	351	19	AAV49820
6	51	100.0	351	19	AAV49822
7	51	100.0	351	22	AAH74623
8	51	100.0	351	22	AAH74625
9	51	100.0	351	22	AAF28175

10	51	100.0	351	22	AAF28177	Antibody LM609 hea
11	47.8	93.7	51	22	AAF28235	DNA encoding enhan
12	40.6	79.6	85	18	AAV72258	Mouse MAb 15 heavy
13	40.6	79.6	369	19	AAV07642	anti-CD22 monoclon
14	40.6	79.6	441	18	AAV72269	Chimeric MAB 15 PC
15	40.6	79.6	445	18	AAV72237	Humanised reshaped
16	40.6	79.6	457	18	AAV72267	Mouse MAB 15 heavy
17	40.6	79.6	923	16	AAV51436	Murine MAB SK48-E2
18	39	76.5	413	15	AAQ68650	MAB A33 heavy chai
19	39	76.5	482	11	AAQ55555	Sequence encoding
20	39	76.5	721	20	AAV99765	A33/212 single-cha
21	39	76.5	721	21	AAZ37397	Linked fusion prot
22	39	76.5	733	20	AAV99766	A33/218 single-cha
23	39	76.5	733	21	AAZ37398	Linked fusion prot
24	39	76.5	1938	19	AAV58929	A33 chimeric recep
25	38	74.5	51	19	AAV44992	15D3 antibody heav
26	38	74.5	51	20	AAZ10944	15D3 VH chain CDR2
27	38	74.5	357	19	AAV44997	15D3 antibody heav
28	38	74.5	357	20	AAZ10957	15D3 VH chain codi
29	38	74.5	357	20	AAV08933	Antibody 15D3 heav
30	38	74.5	480	13	AAQ20070	MRK16-H chain. Ch
31	37.4	73.3	97	22	AAF68679	Ganglioside GD3 sp
32	37.4	73.3	351	16	AAQ96282	Human Ige receptor
33	37.4	73.3	351	18	AAV90025	cDNA encoding heav
34	37.4	73.3	354	14	AAQ48765	Monoclonal antibod
35	37.4	73.3	357	17	AAV28000	B5 immunoglobulin
36	37.4	73.3	360	17	AAV33445	Egf receptor chime
37	37.4	73.3	363	18	AAV75583	Monoclonal antibod
38	37.4	73.3	363	18	AAV71325	Thyroid hormone sp
39	37.4	73.3	363	20	AAV81002	Murine 340 Vh DNA
40	37.4	73.3	363	24	AAV25246	Mouse monoclonal a
41	37.4	73.3	403	14	AAQ37057	Rat immunoglobulin
42	37.4	73.3	403	15	AAQ45439	KM641 L chain vari
43	37.4	73.3	403	20	AAV99482	pKM641 HA3 immunog
44	37.4	73.3	403	21	AAA51003	Murine immunoglobu
45	37.4	73.3	474	18	AAV70808	Mouse anti-idiotyp

ALIGNMENTS

RESULT 1

ID AAF28234 standard; DNA; 51 BP.
XX AAF28234;
XX AC
XX
DT 03-APR-2001 (first entry)
XX
DE DNA encoding enhanced 6H6LH heavy chain CDR2.
XX
KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

```

PT osteoporosis -
PS Claim 16; Page 105; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 51 BP; 13 A; 8 C; 16 G; 14 T; 0 other;

Query Match 100.0%; Score 51; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 9.8e-11;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacctactatttagacactgtgcaggc 51
   |||||
DB 1 aaagttagtagtggtggtgtagcacctactatttagacactgtgcaggc 51

RESULT 2
AAV49826
ID AAV49826 standard; DNA; 87 BP.
XX
AC AAV49826;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody variable region oligonucleotide #3.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Example 2; Page 65; 129pp; English.
XX
CC AAV49824-V49833 are oligonucleotides used in the construction of grafted
CC LM609 monoclonal antibody heavy and light chain variable regions. LM609
CC and antibody vitaxin bind selectively to integrin alphaVbeta3 and
CC can be used to inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,

```

```

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
XX greater than that of parent the parent antibody.
SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 100.0%; Score 51; DB 19; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacctactatttagacactgtgcaggc 51
   |||||
DB 10 aaagttagtagtggtggtgtagcacctactatttagacactgtgcaggc 60

RESULT 3
AAH74629
ID AAH74629 standard; DNA; 87 BP.
XX
AC AAH74629;
XX
DT 15-OCT-2001 (first entry)
XX
DE PCR primer for heavy chain variable region of LM609 antibody.
XX
KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW cancer; PCR primer; ss.
XX
OS Mus sp.
XX
PN US2001011125-A1.
XX
PD 02-AUG-2001.
XX
PF 30-JAN-1997; 97US-0790540.
XX
PR 30-JAN-1997; 97US-0790540.
XX
PA (HUSE/) HUSE W D.
XX
PI Huse WD;
XX
DR WPI; 2001-496171/54.
XX
XX New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer
XX
PS Example 2; Page 16; 25pp; English.
XX
CC PCR primers AAH74627-31 were used to amplify DNA encoding fragments
CC of the heavy chain variable region of the monoclonal antibody LM609.
CC LM609 is a murine antibody which specifically recognises the integrin
CC alphavbeta3, and inhibits its functional activity. The specification
CC describes a LM609 grafted antibody which has the complementarity
CC determining regions (CDRs) substituted into a non-murine framework.
CC Nucleic acids encoding LM609 grafted heavy and light chain polypeptides
CC and fragments are useful in diagnostic and therapeutic purposes, such
CC as in the production of LM609 grafted antibodies and fragments having
CC binding specificity and inhibitory activity against the integrin
CC alphavbeta3. The antibody can be used for the diagnosis or treatment
CC of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic
CC articular rheumatism, psoriasis, disorders associated with inappropriate
CC or inopportune invasion of vessels such as diabetic retinopathy,
CC neovascular glaucoma and capillary proliferation in atherosclerotic

```

CC plaques, or cancers), and to inhibit binding activity of alphavbeta3
 CC that are necessary for progression of an alphavbeta3-mediated disease.
 XX
 SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 100.0%; Score 51; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 51
 |||
 Db 10 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 60

RESULT 4

AAAF28181
 ID AAF28181 standard; DNA; 87 BP.

XX AAF28181;

XX 03-APR-2001 (first entry)

XX Oligonucleotide #3.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

OS Unidentified.

PN WO200078815-A1.

XX 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.

PR 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;

DR WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis.

PS Example 2; Page 67; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 100.0%; Score 51; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 51
 |||
 Db 10 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 60

RESULT 5

AAV49820
 ID AAV49820 standard; DNA; 351 BP.

XX AAV49820;

XX 02-NOV-1998 (first entry)

XX Vitaxin antibody heavy chain variable region DNA.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; ss.

OS Mus sp.

XX Location/Qualifiers

FT Key 1..351

FT CDS /*tag= a

FT /product= "vitaxin antibody heavy chain variable region"

FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX P-PSDB; AAW76001.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 3; Fig 1a; 129pp; English.

XX This sequence encodes the vitaxin antibody variable heavy chain region.
 CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 100.0%; Score 51; DB 19; Length 351;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 51
 |||

Db 148 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 198

RESULT 6


```

AAV49822
ID  AAV49822 standard; DNA; 351 BP.
AC  AAV49822;
XX
DT  02-NOV-1998 (first entry)
XX
DE  LM609 antibody heavy chain variable region DNA fragment.
XX
KW  Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW  LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW  diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW  neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW  macular degeneration; osteoporosis; ss.
XX
OS  Mus sp.
XX
FH  Key Location/Qualifiers
FT  CDS 1..351
FT  /*tag= a
FT  /product= "LM609 antibody heavy chain variable region"
FT  /note= "partial sequence, no start or stop codon given"
XX
PN  WO9833919-A2.
XX
PD  06-AUG-1998.
XX
PF  30-JAN-1998; 98WO-US01826.
XX
PR  30-JAN-1997; 97US-0791391.
XX
PA  (IXSY-) IXSYS INC.
XX
PI  Glaser SM, Huse WD;
XX
DR  WPI; 1998-437472/37.
XX
PT  Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT  integrin - and related grafted antibodies based on murine monoclonal
PT  LM609, also related nucleic acid, used to treat, prevent or diagnose
PT  angiogenesis or restenosis
XX
PS  Claim 37; Fig 2a; 129pp; English.
XX
CC  This sequence encodes the LM609 antibody variable heavy chain region.
CC  LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC  and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC  block integrin-mediated signal transduction. This is useful in the
CC  treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC  specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC  inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC  psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC  etc.). The antibodies contain non-murine framework regions so are
CC  suitable for use in humans. Enhanced types of LM609 have affinity more
CC  than 90 times greater than that of parent the parent antibody.
XX
SQ  Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

Query Match 100.0%; Score 51; DB 19; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 51
|||||
Db 148 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 198

RESULT 17
AAH74623
ID AAH74623 standard; DNA; 351 BP.
XX
AC AAH74623;
XX
DT 15-OCT-2001 (first entry)
XX
DE DNA encoding heavy chain variable region of LM609 grafted antibody.
XX
KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW cancer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN US200101125-A1.
XX
PD 02-AUG-2001.
XX
PF 30-JAN-1997; 97US-0790540.
XX
PR 30-JAN-1997; 97US-0790540.
XX
PA (HUSE/) HUSE W D.
XX
PI Huse WD;
XX
DR WPI; 2001-496171/54.
DR P-PSDB; AAG63587.
XX
PT New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer
XX
PS Claim 3; Fig 1A; 25pp; English.
XX
CC The present sequence encodes the heavy chain variable region of the
CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC specifically recognises the integrin alphavbeta3, and inhibits its
CC functional activity. The LM609 grafted antibody has the
CC complementarity determining regions (CDRs) substituted into a non-murine
CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC polypeptides and fragments are useful in diagnostic and therapeutic
CC purposes, such as in the production of LM609 grafted antibodies and
CC fragments having binding specificity and inhibitory activity against
CC the integrin alphavbeta3. The antibody can be used for the diagnosis
CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC disorders, chronic articular rheumatism, psoriasis, disorders
CC associated with inappropriate or inopportune invasion of vessels such
CC as diabetic retinopathy, neovascular glaucoma and capillary
CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC binding activity of alphavbeta3 that are necessary for progression of
CC an alphavbeta3-mediated disease.
XX
SQ Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 100.0%; Score 51; DB 22; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 51
|||||
Db 148 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 198

RESULT 8
AAH74625
ID AAH74625 standard; DNA; 351 BP.
XX
AC AAH74625;
XX
DT 15-OCT-2001 (first entry)
XX

```

DE DNA encoding heavy chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;

KW chronic articular rheumatism; psoriasis; diabetic retinopathy;

KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;

KW cancer; ss.

XX Mus sp.

OS

XX US200101125-A1.

PN

XX 02-AUG-2001.

PD

XX 30-JAN-1997; 97US-0790540.

PF

XX 30-JAN-1997; 97US-0790540.

PR

XX (HUSE/) HUSE W D.

PA

XX Huse WD;

PI

XX WPI; 2001-496171/54.

DR

XX P-PSDB; AAG63589.

DR

XX New LM609 grafted antibody exhibiting selective binding affinity to

PT alphavbeta3, comprising at least one LM609 grafted heavy and light

PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory

PT disorders or cancer -

XX

XX Disclosure; Fig 2A; 25pp; English.

PS

XX The present sequence encodes the heavy chain variable region of the

CC monoclonal antibody LM609. LM609 is a murine antibody which specifically

CC recognises the integrin alphavbeta3, and inhibits its functional activity.

CC The specification describes a LM609 grafted antibody which has the

CC complementarity determining regions (CDRs) substituted into a non-murine

CC framework. Nucleic acids encoding LM609 grafted heavy and light chain

CC polypeptides and fragments are useful in diagnostic and therapeutic

CC purposes, such as in the production of LM609 grafted antibodies and

CC fragments having binding specificity and inhibitory activity against

CC the integrin alphavbeta3. The antibody can be used for the diagnosis

CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory

CC disorders, chronic articular rheumatism, psoriasis, disorders

CC associated with inappropriate or inopportune invasion of vessels such

CC as diabetic retinopathy, neovascular glaucoma and capillary

CC proliferation in atherosclerotic plaques, or cancers), and to inhibit

CC binding activity of alphavbeta3 that are necessary for progression of

CC an alphavbeta3-mediated disease.

XX

XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

SQ

Query Match 100.0%; Score 51; DB 22; Length 351;

Best Local Similarity 100.0%; Pred. No. 1.5e-10;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcaccctactatttagacactgtgcaggcc 51

|||||

Db 148 aaagttagtggtggtgtagcaccctactatttagacactgtgcaggcc 198

|||||

RESULT 9

AAF28175

ID AAF28175 standard; DNA; 351 BP.

XX

XX AAF28175;

AC

XX 03-APR-2001 (first entry)

DT

XX Vitaxin heavy chain variable region DNA.

DE

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

XX Unidentified.

OS

XX WO200078815-A1.

PN

XX 28-DEC-2000.

PD

XX 23-JUN-2000; 2000WO-US17454.

PF

XX 24-JUN-1999; 99US-0339922.

PR

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA

XX Huse WD, Wu H;

PI

XX WPI; 2001-050110/06.

DR

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin; useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

XX Disclosure; Fig 1; 132pp; English.

PS

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

SQ

Query Match 100.0%; Score 51; DB 22; Length 351;

Best Local Similarity 100.0%; Pred. No. 1.5e-10;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcaccctactatttagacactgtgcaggcc 51

|||||

Db 148 aaagttagtggtggtgtagcaccctactatttagacactgtgcaggcc 198

|||||

RESULT 10

AAF28177

ID AAF28177 standard; DNA; 351 BP.

XX

XX AAF28177;

AC

XX 03-APR-2001 (first entry)

DT

XX Antibody LM609 heavy chain variable region DNA.

DE

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

KW

XX Unidentified.

OS

XX WO200078815-A1.

PN

XX 28-DEC-2000.

PD

XX 23-JUN-2000; 2000WO-US17454.

PF

XX 24-JUN-1999; 99US-0339922.

PR

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA

XX

PI Huse WD, Wu H;
 DR WPI; 2001-050110/06.
 XX
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Fig 2; 132pp; English.
 XX
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;
 Query Match 100.0%; Score 51; DB 22; Length 351;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcagggc 51
 Db 148 aaagttagtagtggtggtgtagcactactatttagacactgtgcagggc 198
 |||||
 RESULT 11
 AAF28235
 ID AAF28235 standard; DNA; 51 BP.
 XX
 AC AAF28235;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE DNA encoding enhanced 2236-38/ 6H6LH heavy chain CDR2.
 XX
 KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 DR WPI; 2001-050110/06.
 XX
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Claim 14; Page 105; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or

CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 51 BP; 13 A; 10 C; 16 G; 12 T; 0 other;
 Query Match 93.7%; Score 47.8; DB 22; Length 51;
 Best Local Similarity 96.1%; Pred. No. 1.8e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcagggc 51
 Db 1 aaagttagtagtggtggtgtagcactactatccagacactgtgcagggc 51
 |||||
 RESULT 12
 AAT7258/C
 ID AAT7258 standard; DNA; 85 BP.
 XX
 AC AAT7258;
 XX
 DT 03-JAN-1998 (first entry)
 XX
 DE Mouse MAb 15 heavy chain backward PCR primer 4.
 XX
 KW Humanised antibody; monoclonal antibody; MAb 15; tumour;
 KW lung cancer; therapy; polymerase chain reaction; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN EP781847-A1.
 XX
 PD 02-JUL-1997.
 XX
 PF 25-OCT-1996; 96EP-0117154.
 XX
 PR 06-NOV-1995; 95EP-0117407.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Bendig M, Jones T, Saldana J;
 XX
 DR WPI; 1997-334904/31.
 XX
 PT Humanised form of murine monoclonal antibody MAB 15 - useful for
 PT treating lung cancer
 XX
 PS Disclosure; Page 27; 71pp; English.
 XX
 XX This synthetic oligonucleotide comprises backward PCR primer 4
 CC that was used with other sense and antisense primers (AAT7255-60)
 CC to produce a sequence encoding a reshaped humanised monoclonal
 CC antibody (MAB) 15 heavy chain variable region VH sequence (see
 CC AAT7237). The full-length product was then amplified with external
 CC primers (see AAT7261-62) and subcloned into HCMV expression vector
 CC containing human heavy chain gamma-1 constant region. Humanised
 CC reshaped MAB 15 is claimed for use in the treatment of human
 CC tumours, especially lung cancer.
 XX
 SQ Sequence 85 BP; 19 A; 23 C; 21 G; 22 T; 0 other;
 Query Match 79.6%; Score 40.6; DB 18; Length 85;
 Best Local Similarity 91.5%; Pred. No. 1.3e-06;
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagggc 51
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 73 TTAGTAGAGGTGGTGGTAGCACCTACTATCCAGACACTGTGAAGGC 27

RESULT 13
 AAV07642
 ID AAV07642 standard; DNA; 369 BP.
 XX
 AC AAV07642;
 XX
 DT 10-DEC-1998 (first entry)
 XX
 DE anti-CD22 monoclonal antibody heavy chain variable region DNA sequence.
 XX
 KW anti-CD22 monoclonal antibody heavy chain variable region; VL;
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;
 KW malignant B-cell; immunodiagnosis; RFB4 IgG; ss.
 XX
 OS Mammalia.

XX
 FH Key Location/Qualifiers
 FT CDS 1..369
 FT FT /*tag= a
 FT FT /transl_except= (pos:361..363, aa:Thr)
 FT FT /note= "CDS does not contain a stop codon"
 XX
 PN WO9841641-A1.

XX
 PD 24-SEP-1998.
 XX
 PF 19-MAR-1998; 98WO-US05453.
 XX
 PR 20-MAR-1997; 97US-0041437.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
 PI Fitzgerald D, Kreitman R, Mansfield E, Pastan I;
 XX
 DR WPI; 1998-521227/44.
 DR P-PSDB; AAW66099.

XX
 PT Recombinant anti-CD22 antibodies and immuno-conjugates - of
 PT antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin
 PT or a label; for inhibiting malignant B-cells
 XX
 PS Claim 15; Fig 1; 71pp; English.
 CC The present sequence represents the anti-CD22 monoclonal antibody
 CC (RFB4 IgG) heavy chain variable region DNA sequence. The invention
 CC claims for a recombinant immunoconjugate comprising of a therapeutic
 CC agent (e.g. Pseudomonas exotoxin) or a detectable label peptide bonded
 CC to a recombinant anti-CD22 antibody having a variable heavy (VH;
 CC AAW66099) chain with a cysteine residue at amino acid 44 and a variable
 CC light (VL; AAW66098) chain with a cysteine residue at amino acid 100.
 CC The immunoconjugate is claimed to inhibit the growth of malignant
 CC B-cells in vivo, such as rodent, canine or primate B-cells. The
 CC anti-CD22 antibody is claimed useful for detecting CD22 protein in a
 CC sample or in vivo in a mammal, and can be used in diagnostic kits.

XX
 SQ Sequence 369 BP; 83 A; 85 C; 110 G; 91 T; 0 other;
 Query Match 79.6%; Score 40.6; DB 19; Length 369;
 Best Local Similarity 91.5%; Pred. No. 1.9e-06;
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagggc 51
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 152 ttagtagtggtggtgtagcacctactatttagacactgtgaagggc 198

RESULT 14

AAT72269
 ID AAT72269 standard; cDNA; 441 BP.
 XX
 AC AAT72269;
 XX
 DT 03-JAN-1998 (first entry)
 XX
 DE Chimeric MAB 15 PCR-modified heavy chain variable region cDNA.

XX
 KW Humanised antibody; monoclonal antibody; MAB 15; tumour;
 KW lung cancer; therapy; ds.
 XX
 OS Chimeric Mus musculus.
 OS Chimeric synthetic.

XX
 FH Key Location/Qualifiers
 FT sig_peptide 12..68
 FT FT /*tag= a
 FT FT mat_peptide 69..428
 FT FT /*tag= b
 XX
 PN EP781847-A1.

XX
 PD 02-JUL-1997.
 XX
 PF 25-OCT-1996; 96EP-0117154.
 XX
 PR 06-NOV-1995; 95EP-0117407.

XX
 PA (MERE) MERCK PATENT GMBH.

XX
 PI Bendig M, Jones T, Saldana J;
 XX
 DR WPI; 1997-334904/31.

XX
 DR P-PSDB; AAW21656.

XX
 PT Humanised form of murine monoclonal antibody MAB 15 - useful for
 PT treating lung cancer
 XX
 PS Disclosure; Fig 5; 71pp; English.

XX
 CC This cDNA sequence comprises the heavy chain variable region VH
 CC sequence of murine monoclonal antibody (MAB) 15 (DSM ACC2117),
 CC modified for the expression of chimeric 15 antibody. The 5' and
 CC 3' ends of the VH sequence (see also AAT72267) were modified by
 CC PCR (see AAT72245-46) to provide a Kozak sequence for efficient
 CC translation, a 5' HindIII site for cloning into HCMV vectors, a
 CC 3' splice donor site at the J-C junction for splicing the mouse
 CC variable regions to human constant regions and a 3' BamHI site for
 CC cloning into HCMV vectors. The VL sequence was similarly modified
 CC (see AAT72268). The modified VH and VL sequences were used in a
 CC claimed process to model and design novel humanised, reshaped MAB
 CC 15 having humanised, reshaped VH and VL sequences (see AAW21652 and
 CC AAW21651), which can be used for treating tumours, especially lung
 CC cancer, and for the manufacture of a drug related to tumours,
 CC especially lung cancer.

XX
 SQ Sequence 441 BP; 98 A; 99 C; 130 G; 114 T; 0 other;

Query Match 79.6%; Score 40.6; DB 18; Length 441;
 Best Local Similarity 91.5%; Pred. No. 1.9e-06;
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagggc 51
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 220 ttagtagaggggtggtgtagcacctactatttagacactgtgaagggc 266

RESULT 15
 AAT72237
 ID AAT72237 standard; cDNA; 445 BP.
 XX

17

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run On: August 21, 2002, 10:52:13 ; Search time 174.26 Seconds
(without alignments)
71.889 Million cell updates/sec

Title: US-09-339-922A-101
Perfect score: 51
Sequence: 1 aaagttagtggtggtgg.....atttagacactgtgcagggc 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.6	79.6	923	5	PCT-US94-07659-1
2	39	76.5	413	1	US-08-253-877C-56
3	39	76.5	413	2	US-08-452-164A-56
4	39	76.5	416	4	US-08-976-183A-30
5	39	76.5	721	2	US-08-224-591-15
6	39	76.5	721	2	US-08-926-789-15
7	39	76.5	733	2	US-08-224-591-17
8	39	76.5	733	2	US-08-926-789-17
9	38	74.5	51	1	US-08-475-000-2
10	38	74.5	51	2	US-08-483-199-2
11	38	74.5	51	2	US-08-484-508-2
12	38	74.5	90	1	US-08-253-877C-70
13	38	74.5	90	2	US-08-452-164A-70
14	38	74.5	90	4	US-08-976-183A-49
15	38	74.5	357	1	US-08-475-000-15
16	38	74.5	357	2	US-08-483-199-15
17	38	74.5	357	2	US-08-484-508-15
18	37.4	73.3	354	1	US-08-326-362-1
19	37.4	73.3	357	1	US-08-331-398A-21
20	37.4	73.3	357	2	US-08-331-397B-21
21	37.4	73.3	357	2	US-08-759-804A-21
22	37.4	73.3	357	2	US-09-227-693-21
23	37.4	73.3	375	1	US-08-331-398A-59
24	37.4	73.3	375	2	US-08-331-397B-59
25	37.4	73.3	375	2	US-08-759-804A-58
26	37.4	73.3	403	1	US-08-408-133-4
27	37.4	73.3	403	1	US-08-454-683-4

28	37.4	73.3	403	2	US-08-116-778E-20	Sequence 20, Appli
29	37.4	73.3	403	2	US-08-454-680-4	Sequence 4, Appli
30	37.4	73.3	403	2	US-08-438-582-20	Sequence 20, Appli
31	37.4	73.3	403	2	US-08-483-528B-20	Sequence 20, Appli
32	37.4	73.3	403	3	US-08-673-799C-20	Sequence 5, Appli
33	37.4	73.3	474	2	US-08-653-402B-5	Sequence 9, Appli
34	37.4	73.3	474	2	US-08-653-402B-9	Sequence 19, Appli
35	35.8	70.2	783	4	US-08-487-283A-19	Sequence 5, Appli
36	34.2	67.1	357	5	PCT-US94-07659-5	Sequence 43, Appli
37	34.2	67.1	870	3	US-08-545-809A-43	Sequence 17, Appli
38	34	66.7	51	5	PCT-US93-08435-17	Sequence 48, Appli
39	34	66.7	102	5	PCT-US93-08435-48	Sequence 94, Appli
40	34	66.7	318	1	US-08-129-930B-94	Sequence 94, Appli
41	34	66.7	318	4	US-08-976-288A-94	Sequence 9, Appli
42	34	66.7	354	5	PCT-US93-08435-9	Sequence 11, Appli
43	34	66.7	389	5	PCT-US93-08435-11	Sequence 13, Appli
44	34	66.7	389	5	PCT-US93-08435-13	Sequence 14, Appli
45	34	66.7	394	4	US-08-134-346A-14	

ALIGNMENTS

RESULT 1
PCT-US94-07659-1
; Sequence 1, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurlie, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 923 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS


```
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELEPHONE: (202) 672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..416
; US-08-976-183A-30

Query Match 76.5%; Score 39; DB 4; Length 416;
Best Local Similarity 89.4%; Pred. No. 1.4e-06;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtgtggtgtagcacctactatttagacactgtgcaggc 51
|||||
Db 214 TTAGTAGTGGTGTAGTTACACTACTATTATAGACAGTGTGAAGGC 260

RESULT 5
US-08-224-591-15
; Sequence 15, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..711)
; US-08-224-591-15

Query Match 76.5%; Score 39; DB 2; Length 721;
Best Local Similarity 89.4%; Pred. No. 1.6e-06;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtgtggtgtagcacctactatttagacactgtgcaggc 51
|||||
Db 515 TTAGTAGTGGTGTAGTTACACTACTATTATAGACAGTGTGAAGGC 561

RESULT 6
US-08-926-789-15
; Sequence 15, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
```



```
;
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..711)
US-08-926-789-15

Query Match 76.5%; Score 39; DB 2; Length 721;
Best Local Similarity 89.4%; Pred. No. 1.6e-06;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
Db 515 TTAGTAGTGGTGGTAGTTACACCTACTATTATTTAGACAGTGTGAAGGCC 561

RESULT 7
US-08-224-591-17
; Sequence 17, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..723)
US-08-224-591-17
```

US-08-224-591-17

```
Query Match 76.5%; Score 39; DB 2; Length 733;
Best Local Similarity 89.4%; Pred. No. 1.6e-06;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
Db 527 TTAGTAGTGGTGGTAGTTACACCTACTATTATTTAGACAGTGTGAAGGCC 573

RESULT 8
US-08-926-789-17
; Sequence 17, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..723)
US-08-926-789-17

Query Match 76.5%; Score 39; DB 2; Length 733;
Best Local Similarity 89.4%; Pred. No. 1.6e-06;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
Db 527 TTAGTAGTGGTGGTAGTTACACCTACTATTATTTAGACAGTGTGAAGGCC 573

RESULT 9
```

US-08-475-000-2
; Sequence 2, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-475-000-2

Query Match 74.5%; Score 38; DB 1; Length 51;
Best Local Similarity 89.1%; Pred. No. 2.3e-06;
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50
|||||
DB 5 TTAGTAGTGGTGGTGAACACCTACTATCCAGACAGTGTGAAGG 50

RESULT 10
US-08-483-199-2
; Sequence 2, Application US/08483199
; Patent No. 5849877
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,199
; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-483-199-2

Query Match 74.5%; Score 38; DB 2; Length 51;
Best Local Similarity 89.1%; Pred. No. 2.3e-06;
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50
|||||
DB 5 TTAGTAGTGGTGGTGAACACCTACTATCCAGACAGTGTGAAGG 50

RESULT 11
US-08-484-508-2
; Sequence 2, Application US/08484508
; Patent No. 5948647
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,508
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-585
; TELEFAX: (510) 695-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-484-508-2

Query Match 74.5%; Score 38; DB 2; Length 51;
Best Local Similarity 89.1%; Pred. No. 2.3e-06;
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50
|||||

Db 5 TTAGTAGTGGTGGTAAACCTACTATCCAGACAGTGTGAAGG 50

RESULT 12

US-08-253-877C-70
; Sequence 70, Application US/08253877C
; Patent No. 5773001

GENERAL INFORMATION:

APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.

TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor

TITLE OF INVENTION: Agents and Intermediates for Their Synthesis

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company

STREET: One Cyanamid Plaza

CITY: Wayne

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/253,877C

FILING DATE: 03-JUN-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Barnhard, Elizabeth M.

REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 32,368

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-831-3246

TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 90 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-253-877C-70

Query Match 74.5%; Score 38; DB 1; Length 90;

Best Local Similarity 89.1%; Pred. No. 2.6e-06;

Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcaccactatttagacactgtgcagg 50

Db 11 TTAGTAGTGGTGGTAAACCTACTATCCAGACAGTGTGAAGG 56

RESULT 13

US-08-452-164A-70

; Sequence 70, Application US/08452164A

; Patent No. 5877296

GENERAL INFORMATION:

APPLICANT: Hamann, Philip R.

APPLICANT: Hinman, Lois

APPLICANT: Hollander, Irwin

APPLICANT: Holcomb, Ryan

APPLICANT: Hallett, William

APPLICANT: Tsou, Hwei-Ru

APPLICANT: Weiss, Martin J.

TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor

TITLE OF INVENTION: Agents and Intermediates for Their Synthesis

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Home Products Corporation

STREET: One Campus Drive

CITY: Parsippany

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/452,164A

FILING DATE: 26-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Barnhard, Elizabeth M.

REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 32,368-04

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-683-2158

TELEFAX: 201-683-4117

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 90 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-452-164A-70

Query Match 74.5%; Score 38; DB 2; Length 90;

Best Local Similarity 89.1%; Pred. No. 2.6e-06;

Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcaccactatttagacactgtgcagg 50

Db 11 TTAGTAGTGGTGGTAAACCTACTATCCAGACAGTGTGAAGG 56

RESULT 14

US-08-976-183A-49

; Sequence 49, Application US/08976183A

; Patent No. 6307026

GENERAL INFORMATION:

APPLICANT: King, David J.

APPLICANT: Adair, John R.

APPLICANT: Owens, Raymond J.

TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

TITLE OF INVENTION: ANTIGEN

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K. Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,183A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/595,848

FILING DATE: 02-FEB-1996

APPLICATION NUMBER: PCT/GB93/02529

; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC"
US-08-976-183A-49

Query Match 74.5%; Score 38; DB 4; Length 90;
Best Local Similarity 89.1%; Pred. No. 2.6e-06;
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtgtggtggtgtagcacctactatttagacactgtgcagg 50
|||||
DB 11 TTAGTAGTGGTGTACACCTACTATTATTAGACAGTGTGAAGG 56

RESULT 15
US-08-475-000-15
; Sequence 15, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..357
US-08-475-000-15

Query Match 74.5%; Score 38; DB 1; Length 357;
Best Local Similarity 89.1%; Pred. No. 3.4e-06;
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5 ttagtgtggtggtgtagcacctactatttagacactgtgcagg 50
|||||
DB 152 TTAGTAGTGGTGTACACCTACTATTCCAGACAGTGTGAAGG 197

Search completed: August 21, 2002, 10:52:14
Job time: 9654 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:49:01 ; Search time 2408.76 Seconds
(without alignments)
443.072 Million cell updates/sec

Title: US-09-339-922A-103
Perfect score: 51
Sequence: 1 aaagttagtagtggtggtg.....atccagacactgtgcagggc 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	GenEmbl.*	
	1: gb_ba.*	
	2: gb_htg.*	
	3: gb_in.*	
	4: gb_om.*	
	5: gb_ov.*	
	6: gb_pat.*	
	7: gb_ph.*	
	8: gb_pl.*	
	9: gb_pr.*	
	10: gb_ro.*	
	11: gb_sts.*	
	12: gb_sy.*	
	13: gb_un.*	
	14: gb_vi.*	
	15: em_ba.*	
	16: em_fun.*	
	17: em_hum.*	
	18: em_in.*	
	19: em_mu.*	
	20: em_om.*	
	21: em_or.*	
	22: em_ov.*	
	23: em_pat.*	
	24: em_ph.*	
	25: em_pi.*	
	26: em_ro.*	
	27: em_sts.*	
	28: em_un.*	
	29: em_vi.*	
	30: em_htg_hum.*	
	31: em_htg_inv.*	
	32: em_htg_other.*	
	33: em_htgo_inv.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
------------	-------	-------	-------	--------	----	-------------

RESULT 1	AX060882	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	AX060882	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
DEFINITION	AX060882	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
ACCESSION	AX060882	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
VERSION	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
KEYWORDS	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
SOURCE	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
ORGANISM	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
REFERENCE	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
AUTHORS	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
TITLE	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
JOURNAL	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
FEATURES	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
source	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
CDS	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001

Result No.	Query	Score	Match	Length	ID	Description
------------	-------	-------	-------	--------	----	-------------

```
/transl_table=11
/protein_id="CAC24927.1"
/db_xref="GI:12406261"
/translation="KVSSGGSTYYPDTVQG"
BASE COUNT      13 a      10 c      16 g      12 t
ORIGIN

Query Match      100.0%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcacctactatccagacactgtgcagggc 51
|||||
Db 1 AAAGTTAGTAGTGGTGGTGTAGCACCCTACTATCCAGACACTGTGCAGGCG 51

RESULT 2
AX060880
LOCUS             AX060880             51 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION       Sequence 101 from Patent WO0078815.
ACCESSION        AX060880
VERSION          AX060880.1 GI:12406258
KEYWORDS         .
SOURCE           synthetic construct.
ORGANISM         synthetic construct
artificial sequence.
REFERENCE        1 (bases 1 to 51)
AUTHORS         Huse,W.D. and Wu,H.
TITLE           Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
                encoding same and methods of use
JOURNAL         Patent: WO 0078815-A 101 28-DEC-2000;
                Applied Molecular Evolution (US)
FEATURES         Location/Qualifiers
source           1..51
                 /organism="synthetic construct"
                 /db_xref="taxon:32630"
                 <1..>51
CDS              /codon_start=1
                 /transl_table=11
                 /protein_id="CAC24926.1"
                 /db_xref="GI:12406259"
                 /translation="KVSSGGSTYYLDTVQG"
BASE COUNT      13 a      8 c      16 g      14 t
ORIGIN

Query Match      93.7%; Score 47.8; DB 6; Length 51;
Best Local Similarity 96.1%; Pred. No. 2.1e-09;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcacctactatccagacactgtgcagggc 51
|||||
Db 1 AAAGTTAGTAGTGGTGGTGTAGCACCCTACTATTTAGACACTGTGCAGGCG 51

RESULT 3
AX060790
LOCUS             AX060790             87 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION       Sequence 11 from Patent WO0078815.
ACCESSION        AX060790
VERSION          AX060790.1 GI:12406170
KEYWORDS         .
SOURCE           synthetic construct.
ORGANISM         synthetic construct
artificial sequence.
REFERENCE        1 (bases 1 to 87)
AUTHORS         Huse,W.D. and Wu,H.
TITLE           Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
                encoding same and methods of use
JOURNAL         Patent: WO 0078815-A 11 28-DEC-2000;
                Applied Molecular Evolution (US)
FEATURES         Location/Qualifiers
source           1..87
                 /organism="synthetic construct"
                 /db_xref="taxon:32630"
                 <1..>87
CDS              /codon_start=1
                 /transl_table=11
                 /protein_id="CAC24927.1"
                 /db_xref="GI:12406261"
                 /translation="KVSSGGSTYYPDTVQG"
BASE COUNT      13 a      10 c      16 g      12 t
ORIGIN

Query Match      100.0%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcacctactatccagacactgtgcagggc 51
|||||
Db 1 AAAGTTAGTAGTGGTGGTGTAGCACCCTACTATCCAGACACTGTGCAGGCG 51

RESULT 4
AX060780
LOCUS             AX060780             351 bp     DNA      linear      PAT 22-JAN-2001
DEFINITION       Sequence 1 from Patent WO0078815.
ACCESSION        AX060780
VERSION          AX060780.1 GI:12406160
KEYWORDS         .
SOURCE           synthetic construct.
ORGANISM         synthetic construct
artificial sequence.
REFERENCE        1 (bases 1 to 351)
AUTHORS         Huse,W.D. and Wu,H.
TITLE           Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
                encoding same and methods of use
JOURNAL         Patent: WO 0078815-A 1 28-DEC-2000;
                Applied Molecular Evolution (US)
FEATURES         Location/Qualifiers
source           1..351
                 /organism="synthetic construct"
                 /db_xref="taxon:32630"
                 <1..>351
CDS              /codon_start=1
                 /note="grafted antibody variable region"
                 /transl_table=11
                 /protein_id="CAC24888.1"
                 /db_xref="GI:12406161"
                 /translation="QVQLVESGSGVQPGRSRLRSLCAASGFTFSSYDMSWVRQAPGKG
                 LEWVAKVSSGGSTYYLDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYG
                 SFAYWGQGTFTVYSS"
BASE COUNT      80 a      82 c      104 g      85 t
ORIGIN

Query Match      93.7%; Score 47.8; DB 6; Length 351;
Best Local Similarity 96.1%; Pred. No. 2.2e-09;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcacctactatccagacactgtgcagggc 51
|||||
Db 148 AAAGTTAGTAGTGGTGGTGTAGCACCCTACTATTTAGACACTGTGCAGGCG 198

RESULT 5
AX060784
LOCUS             AX060784             351 bp     DNA      linear      PAT 22-JAN-2001
DEFINITION       Sequence 5 from Patent WO0078815.
ACCESSION        AX060784
VERSION          AX060784.1 GI:12406164
KEYWORDS         .
SOURCE           house mouse.
ORGANISM         Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE        1 (bases 1 to 351)
AUTHORS         Huse,W.D. and Wu,H.
```

TITLE Anti-g(a) v2.g(b)3? recombinant human antibodies, nucleic acids
JOURNAL encoding same and methods of use
Patent: WO 0078815-A 5 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source Location/Qualifiers
1. .351
/organism="Mus musculus"
/db_xref="taxon:10090"
<1. .>351
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAC24890.1"
/db_xref="GI:12406165"
/translation="EVQLVESGGGLVPGGSLRLSCAASGFAFSSYDMSWVRQIPERR
LEWAKVSSGGSTYYPDIVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCARHNYG
SPAYWGQGLTVTSSA"
BASE COUNT 83 a 81 c 102 g 85 t
ORIGIN
Query Match 93.7%; Score 47.8; DB 6; Length 351;
Best Local Similarity 96.1%; Pred. No. 2.2e-09;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 aaagttagtagtggtgtagcactatccagacactgtgcagggc 51
|||||
DB 148 AAAGTTAGTAGTGGTGGTAGCCTACTATTATGACACTGTGCAGGCG 198
|||||

RESULT 6
MMIGH4
LOCUS M.musculus mRNA (L14-2G9) for IgH heavy chain V region.
DEFINITION X59107
ACCESSION
VERSION X59107.1 GI:51944
KEYWORDS Ig heavy chain; Ig variable region; immunoglobulin; rearranged.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Kavalier, J.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1991) J. Kavalier, Wistar Institute, 3601 Spruce
Street, Philadelphia PA 19104, USA
REFERENCE 2 (bases 1 to 339)
AUTHORS Kavalier, J.
JOURNAL Unpublished
FEATURES
source Location/Qualifiers
1. .339
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="L14-2G9"
/cell_type="B cell"
/tissue_type="hybridoma"
1. .339
/partial
/codon_start=1
/product="IgH heavy chain V region"
/protein_id="CAA41833.1"
/db_xref="GI:51945"
/translation="TVSLGSLVPGGSLKLSCAASGFAFSSYDMSWVRQTPPEKRLWV
AYISSGGSTYYPDIVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCARHPYGNYYA
MDYWQGTSTV"
BASE COUNT 84 a 83 c 92 g 80 t
ORIGIN
Query Match 89.0%; Score 45.4; DB 10; Length 339;
Best Local Similarity 97.9%; Pred. No. 2.3e-08;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ttagtagtggtgtagcactatccagacactgtgcagggc 51
|||||
DB 140 TTAGTAGTGGTGGTAGCCTACTATCCAGACACTGTGAAGGCG 186
|||||

RESULT 7
MMAHCVR15
LOCUS M.musculus antibody heavy chain variable region (375bp).
DEFINITION X90890
ACCESSION
VERSION X90890.1 GI:1518290
KEYWORDS antibody heavy chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Geiser, M. and Kretzschmar, T.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 375)
AUTHORS Geiser, M.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1995) M. Geiser, CIBA-GEIGY LTD, CDDT,
K-681.5.46, CH-4002, Basel, SWITZERLAND
FEATURES
source Location/Qualifiers
1. .375
/organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
/cell_type="lymphocytes"
/tissue_type="spleen"
/dev_stage="12 weeks old"
<1. .>375
/codon_start=1
/product="antibody heavy chain variable region"
/protein_id="CAA62398.1"
/db_xref="GI:1518291"
/translation="EVKLSEGGGLVPGGSLKLSCAASGFAFSSYDMSWVRQTPPEKR
LEWAYISSGGSTYYPDIVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCARQKGF
YDYLTRNWFVWGAGTLTVSS"
BASE COUNT 90 a 91 c 107 g 87 t
ORIGIN
Query Match 89.0%; Score 45.4; DB 10; Length 375;
Best Local Similarity 97.9%; Pred. No. 2.3e-08;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ttagtagtggtgtagcactatccagacactgtgcagggc 51
|||||
DB 152 TTAGTAGTGGTGGTAGCCTACTATCCAGACACTGTGAAGGCG 198
|||||

RESULT 8
MMA229172
LOCUS Mus musculus rearranged cDNA for VH region of anti arsonate
DEFINITION antibody (B cell hybridoma A22).
ACCESSION AJ229172
VERSION AJ229172.1 GI:3135848
KEYWORDS anti arsonate antibody; diversity segment; heavy chain;
immunoglobulin; joining segment; variable segment.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Ismaili, J., Razanaajona, D., Van Acker, A., Wuilmart, C., Mancini, I.,
Heinen, E., Leo, O., Lebecque, S., Urbain, J., and Braйт, M.
TITLE Molecular and cellular basis of the altered immune response against
arsonate in irradiated A/J mice autologously reconstituted
JOURNAL Int. Immunol. 11 (7), 1157-1167 (1999)
MEDLINE 99315320

```

REFERENCE      2 (bases 1 to 345)
AUTHORS        Urbain,J.J.
TITLE          Direct Submission
JOURNAL        Submitted (13-MAY-1998) Urbain J.J., Biologie moleculaire,
                Universite Libre de Bruxelles, 67 rue des chevaux, Rhode-St-Genese,
                1640, BELGIUM
FEATURES       Location/Qualifiers
                source
                1..345
                /organism="Mus musculus"
                /strain="A/J"
                /db_xref="taxon:10090"
                /rearranged
                /cell_line="B cell"
                /cell_type="B cell hybridoma"
                /clone="A22"
                <1..276
                /gene="IGHF"
                /evidence=experimental
                /product="variable segment of immunoglobulin heavy chain"
                V_segment
                1..276
                /gene="IGHF"
                /gene="DSP2.7"
                /evidence=experimental
                /product="diversity region of immunoglobulin heavy chain"
                gene
                277..300
                /gene="DSP2.7"
                /evidence=experimental
                /product="diversity region of immunoglobulin heavy chain"
                gene
                301..345
                /gene="JH2"
                /gene="JH2"
                J_segment
                301..345
                /gene="JH2"
                /evidence=experimental
                /product="joining region of immunoglobulin heavy chain"
                BASE COUNT      80 a   92 c   89 g   81 t   3 others
                ORIGIN
                5 ttagtagtggtggtgtagcactactatccagacactgtgcaggcc 51
                |||||||
                Db 134 TTAGTAGTGTGTTAGCACCCTACTATCCAGACAGTGTGAGGGC 180
                |||||||

Query Match      87.1%; Score 44.4; DB 10; Length 345;
Best Local Similarity 95.7%; Pred. No. 6.1e-08;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
A62608/c        A62608      85 bp      DNA      linear      PAT 12-MAR-1998
DEFINITION      Sequence 27 from Patent EP0781847.
ACCESSION       A62608
VERSION         A62608.1 GI:3716515
KEYWORDS        .
SOURCE          unidentified.
                ORGANISM   unidentified.
                1 (bases 1 to 85)
                Bendig,M.D., Saldana,J.D. and Jones,T.D.
                Humanized monoclonal antibody
                TITLE       Patent: EP 0781847-A 27 02-JUL-1997;
                JOURNAL     MERCK PATENT GMBH (DE)
                COMMENT     Other publication JP 9183799 19970715.
                FEATURES     Location/Qualifiers
                source
                1..85
                /organism="unidentified"
                /db_xref="taxon:32644"
                BASE COUNT      19 a   23 c   21 g   22 t
                ORIGIN
                5 ttagtagtggtggtgtagcactactatccagacactgtgcaggcc 51
                |||||||
                Db 134 TTAGTAGTGTGTTAGCACCCTACTATCCAGACAGTGTGAGGGC 180
                |||||||

Query Match      85.9%; Score 43.8; DB 6; Length 85;
Best Local Similarity 95.7%; Pred. No. 1e-07;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

REFERENCE      1 (bases 1 to 345)
AUTHORS        Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
                Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
                J. Immunol. 150, 1591-1610 (1993)
TITLE          V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
                mice
JOURNAL         J. Immunol. 150, 1591-1610 (1993)
MEDLINE        93163585
FEATURES       Location/Qualifiers
                source
                1..345
                /organism="Mus musculus"
                /strain="mrl/mp-lpr/lpr"
                /db_xref="taxon:10090"
                /cell_line="anti-Sm hybridoma 14C10"
                /cell_type="B-cell"
                /tissue_type="spleen"
                /dev_stage="adult"
                BASE COUNT      80 a   85 c   102 g   78 t
                ORIGIN
                5 ttagtagtggtggtgtagcactactatccagacactgtgcaggcc 51
                |||||||
                Db 151 TTAGTAGTGTGTTAGCACCCTACTATCCAGACAGTGTGAGGGC 197
                |||||||

Query Match      85.9%; Score 43.8; DB 10; Length 345;
Best Local Similarity 95.7%; Pred. No. 1.1e-07;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 11
MUSIGVAAAX
LOCUS          MUSIGVAAAX      345 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION      Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
                sequence.
ACCESSION       L08996
VERSION         L08996.1 GI:197994
KEYWORDS        V-region; immunoglobulin V region; processed gene.
SOURCE          Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
                ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 345)
                Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
                Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
                J. Immunol. 150, 1591-1610 (1993)
TITLE          V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
                mice
JOURNAL         J. Immunol. 150, 1591-1610 (1993)
MEDLINE        93163585
FEATURES       Location/Qualifiers
                source
                1..345
                /organism="Mus musculus"
                /strain="mrl/mp-lpr/lpr"
                /db_xref="taxon:10090"
                /cell_line="anti-Sm hybridoma 22F6"
                /cell_type="B-cell"

```

```

QY 5 ttagtagtggtggtgtagcactactatccagacactgtgcaggcc 51
|||||
Db 73 TTAGTAGAGGTGGTGTAGCACCCTACTATCCAGACAGTGTGAGGGC 27
|||||

RESULT 10
MUSIGVAAAX
LOCUS          MUSIGVAAAX      345 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION      Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
                sequence.
ACCESSION       L08991
VERSION         L08991.1 GI:197989
KEYWORDS        V-region; immunoglobulin V region; processed gene.
SOURCE          Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
                ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 345)
                Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
                Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
                J. Immunol. 150, 1591-1610 (1993)
TITLE          V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
                mice
JOURNAL         J. Immunol. 150, 1591-1610 (1993)
MEDLINE        93163585
FEATURES       Location/Qualifiers
                source
                1..345
                /organism="Mus musculus"
                /strain="mrl/mp-lpr/lpr"
                /db_xref="taxon:10090"
                /cell_line="anti-Sm hybridoma 14C10"
                /cell_type="B-cell"
                /tissue_type="spleen"
                /dev_stage="adult"
                BASE COUNT      80 a   85 c   102 g   78 t
                ORIGIN
                5 ttagtagtggtggtgtagcactactatccagacactgtgcaggcc 51
                |||||||
                Db 151 TTAGTAGTGTGTTAGCACCCTACTATCCAGACAGTGTGAGGGC 197
                |||||||

Query Match      85.9%; Score 43.8; DB 10; Length 345;
Best Local Similarity 95.7%; Pred. No. 1.1e-07;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 11
MUSIGVAAAX
LOCUS          MUSIGVAAAX      345 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION      Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
                sequence.
ACCESSION       L08996
VERSION         L08996.1 GI:197994
KEYWORDS        V-region; immunoglobulin V region; processed gene.
SOURCE          Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
                ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 345)
                Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
                Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
                J. Immunol. 150, 1591-1610 (1993)
TITLE          V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
                mice
JOURNAL         J. Immunol. 150, 1591-1610 (1993)
MEDLINE        93163585
FEATURES       Location/Qualifiers
                source
                1..345
                /organism="Mus musculus"
                /strain="mrl/mp-lpr/lpr"
                /db_xref="taxon:10090"
                /cell_line="anti-Sm hybridoma 22F6"
                /cell_type="B-cell"

```


BASE COUNT 80 a 86 c 102 g 77 t
 ORIGIN /tissue_type="spleen"
 /dev_stage="adult"

Query Match 85.9%; Score 43.8; DB 10; Length 345;
 Best Local Similarity 95.7%; Pred. No. 1.1e-07;
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccactactatccagacactgtgcagggc 51
 |||||
 Db 152 TTAGTAGTGGTGGTGTAGCACCCTACTATCCAGACACTGTGAAGGC 198

RESULT 12
 MUSIGVABB
 LOCUS 348 bp mRNA linear ROD 27-APR-1993
 DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
 sequence.

ACCESSION L09000
 VERSION L09000.1 GI:197998
 KEYWORDS V-region; immunoglobulin V region; processed gene.
 SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 348)
 AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
 Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
 TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
 mice

JOURNAL J. Immunol. 150, 1591-1610 (1993)
 MEDLINE 93163585
 FEATURES Location/Qualifiers
 1. .348
 /organism="Mus musculus"
 /strain="mrl/mp-lpr/lpr"
 /db_xref="taxon:10090"
 /cell_line="anti-Sm hybridoma 4D12"
 /cell_type="B-cell"
 /tissue_type="spleen"
 /dev_stage="adult"

BASE COUNT 80 a 87 c 102 g 79 t
 ORIGIN

Query Match 85.9%; Score 43.8; DB 10; Length 348;
 Best Local Similarity 95.7%; Pred. No. 1.1e-07;
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccactactatccagacactgtgcagggc 51
 |||||
 Db 152 TTAGTAGTGGTGGTGTAGCACCCTACTATCCAGACACTGTGAAGGC 198

RESULT 13
 MUSIGVAAV
 LOCUS 351 bp mRNA linear ROD 27-APR-1993
 DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
 sequence.

ACCESSION L08997
 VERSION L08997.1 GI:197995
 KEYWORDS V-region; immunoglobulin V region; processed gene.
 SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 351)
 AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
 Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
 TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
 mice

JOURNAL J. Immunol. 150, 1591-1610 (1993)
 MEDLINE 93163585
 FEATURES Location/Qualifiers
 1. .351
 /organism="Mus musculus"
 /strain="mrl/mp-lpr/lpr"
 /db_xref="taxon:10090"
 /cell_line="anti-Sm hybridoma 2E10"
 /cell_type="B-cell"
 /tissue_type="spleen"
 /dev_stage="adult"

BASE COUNT 82 a 87 c 103 g 79 t
 ORIGIN

Query Match 85.9%; Score 43.8; DB 10; Length 351;
 Best Local Similarity 95.7%; Pred. No. 1.1e-07;
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccactactatccagacactgtgcagggc 51
 |||||
 Db 152 TTAGTAGTGGTGGTGTAGCACCCTACTATCCAGACACTGTGAAGGC 198

RESULT 14
 A62623
 LOCUS 441 bp DNA linear PAT 12-MAR-1998
 DEFINITION Sequence 42 from Patent EP0781847.
 ACCESSION A62623
 VERSION A62623.1 GI:3716530
 KEYWORDS unidentified.
 SOURCE unidentified.
 ORGANISM unidentified.

REFERENCE 1 (bases 1 to 441)
 AUTHORS Bendig,M.D., Saldana,J.D. and Jones,T.D.
 TITLE Humanized monoclonal antibody
 JOURNAL Patent: EP 0781847-A 42 02-JUL-1997;
 COMMENT MERCK PATENT GMBH (DE)
 Other publication JP 9183799 19970715.
 FEATURES Location/Qualifiers
 1. .441
 /organism="unidentified"
 /db_xref="taxon:32644"

misc_signal 1. .11
 sig_peptide 12. .68
 CDS 12. .>428
 /function="FR'S, CDR'S"
 /codon_start=1
 /product="CHIMERIC MAB 15, HEAVY CHAIN VARIABLE REGION"
 /protein_id="CAA03670.1"
 /db_xref="GI:4530024"
 /translation="MNFGLSLIFLVLTLKGVKCEVQVVESSGGGLVKGPGSLKLSCAAS
 GFASFSDYDMSWVROTPEKRLWVAYLSRGSGSTYPDVKGRFTISRDNKKILFLQM
 TSLKSEDAAMYICARHGEEVPRWEDYQGLLVTVSA"

BASE COUNT 98 a 99 c 130 g 114 t
 ORIGIN

Query Match 85.9%; Score 43.8; DB 6; Length 441;
 Best Local Similarity 95.7%; Pred. No. 1.1e-07;
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccactactatccagacactgtgcagggc 51
 |||||
 Db 220 TTAGTAGAGGTGGTGTAGCACCCTACTATCCAGACACTGTGAAGGC 266

RESULT 15
 A62635
 LOCUS 445 bp DNA linear PAT 12-MAR-1998
 DEFINITION Sequence 54 from Patent EP0781847.
 ACCESSION A62635

VERSION A62635.1 GI:3716534
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 445)
AUTHORS Bendig, M.D., Saldana, J.D. and Jones, T.D.
TITLE Humanized monoclonal antibody
JOURNAL Patent: EP 0781847-A 54 02-JUL-1997;
MERCK PATENT GMBH (DE)
COMMENT Other publication JP 9183799 19970715.
FEATURES
source
1..445
/organism="unidentified"
/db_xref="taxon:32644"
misc_signal
1..15
sig_peptide
16..72
CDS
16..>432
/function="FR'S, CDR'S"
/codon_start=1
/product="RESHAPED MAB 15, HEAVY CHAIN VARIABLE REGION"
/protein_id="CAA03672.1"
/db_xref="GI:4530025"
/translation="MEFGSLWLELVAILKGVQCEVOLLESGGGLVQPGSLRLSCAAS
GETFSDYDMSWRQAPGKRLWYVLSRGGSTYYPTVKGRFTISKDNSKNTLYIQM
NSLRADTAVYTCARHGEVRPFWDYWGQGLTVSS"
BASE COUNT 91 a 108 c 141 g 105 t
ORIGIN

Query Match 85.9%; Score 43.8; DB 6; Length 445;
Best Local Similarity 95.7%; Pred. No. 1.1e-07;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 ttagtggtgtgtgtagcacctactatccagacactgtgcaggc 51
|||||
Db 224 TTAGTAGGTGGTGTAGCACCTACTATCCAGACACTGTGAGGGC 270
|||||

Search completed: August 21, 2002, 10:49:02
Job time: 9757 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 09:55:46 ; Search time 6260.2 Seconds
(without alignments)
109.956 Million cell updates/sec

Title: US-09-339-922a-103

Perfect score: 51

Sequence: 1 aaagttagtagtggtggtgg.....atccagacactgtgcagggc 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST : *
1: em_estba : *
2: em_esthum : *
3: em_estlin : *
4: em_estnu : *
5: em_estov : *
6: em_estpl : *
7: em_estro : *
8: em_htc : *
9: gb_estli : *
10: gb_estl2 : *
11: gb_htc : *
12: gb_gss : *
13: em_gss_hum : *
14: em_gss_inv : *
15: em_gss_pln : *
16: em_gss_vrt : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40.6	79.6	861	10	BI455668
2	39	76.5	650	10	BF579001
3	39	76.5	837	10	BG966355
4	38.4	75.3	662	10	BF163874
5	38.4	75.3	883	10	BI151077
6	38.4	75.3	908	10	BF161883
7	38.4	75.3	913	10	BF162056
8	38	74.5	877	10	BF144493
9	37.4	73.3	333	10	BI336517
10	37.4	73.3	424	10	BI337375
11	37.4	73.3	469	9	AI645111
12	37.4	73.3	823	9	AA170256
13	36.4	71.4	342	9	BB869694
14	36.4	71.4	494	10	BG145342
15	36.4	71.4	548	9	AW408295
16	35.8	70.2	758	10	BM083708
17	35.8	70.2	954	10	BG963956

18	35.2	69.0	898	10	BG757960
19	34.8	68.2	404	10	BF452207
20	34.8	68.2	406	9	AW403983
21	34.8	68.2	1559	10	BF138708
22	34.2	67.1	308	10	BF844139
23	34.2	67.1	330	10	F14516
24	34.2	67.1	332	10	BF153433
25	34.2	67.1	367	10	BI305075
26	34.2	67.1	372	9	AA581192
27	34.2	67.1	454	9	AW824857
28	34.2	67.1	648	10	BG340670
29	34.2	67.1	652	10	BG965201
30	34.2	67.1	689	10	BF579926
31	34.2	67.1	718	10	BF138279
32	34.2	67.1	735	10	BG745292
33	34.2	67.1	737	10	BF974929
34	34.2	67.1	862	10	BF143948
35	34.2	67.1	874	10	BF179541
36	34.2	67.1	875	10	BG340548
37	34.2	67.1	966	10	BG745389
38	34.2	67.1	1012	10	BF142302
39	33.4	65.5	672	12	AZ433093
40	33.2	65.1	624	12	BH021317
41	33.2	65.1	677	10	BE286624
42	33.2	65.1	1586	11	BC018461
43	32.6	63.9	294	9	AW606245
44	32.6	63.9	406	9	AW401971
45	32.6	63.9	412	9	AW800162

ALIGNMENTS

RESULT	1				
BI455668		861 bp	mrna	linear	EST 21-AUG-2001
LOCUS	603173862F1	NCL_CGAP_Mam5	Mus musculus	cdna clone	IMAGE:5253279 5',
DEFINITION	mRNA sequence.				
ACCESSION	BI455668				
VERSION	BI455668.1	GI:15246324			
KEYWORDS	EST.				
SOURCE	Mus musculus	house mouse.			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1	(bases 1 to 861)			
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11639 row: 1 column: 16 High quality sequence stop: 780. Location/Qualifiers 1. .861 /organism="Mus musculus" /strain="C57/B6" /db_xref="taxon:10090" /clone="IMAGE:5253279" /clone_lib="NCL_CGAP_Mam5" /tissue_type="tumor, gross tissue" /dev_stage="7 months" /lab_host="DH10B" /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators				
FEATURES	source				

```

providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 205 a 239 c 211 g 206 t
ORIGIN

Query Match 79.6%; Score 40.6; DB 10; Length 861;
Best Local Similarity 91.5%; Pred. No. 0.00021;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcaccattactatccagacactgtgcagggc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 279 TTAGTAATGTTGGTGGTAGCACCTATTATCCAGACACTGTGAAGGGC 325

RESULT 2
BF579001
LOCUS
DEFINITION 602096117F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4215844 5',
mRNA sequence.
ACCESSION BF579001
VERSION BF579001.1 GI:11652713
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 650)
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-NCI nih.gov/"
/note="National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)"
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9792 row: b column: 05
High quality sequence stop: 649.
Location/Qualifiers
1..650
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4215844"
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-NCI nih.gov/"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 154 a 177 c 165 g 154 t
ORIGIN

Query Match 76.5%; Score 39; DB 10; Length 650;
Best Local Similarity 89.4%; Pred. No. 0.00071;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcaccattactatccagacactgtgcagggc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 279 TTAATAGTAATGTTGGTAGCACCTACTATCCAGACACTGTGAAGGGC 325

RESULT 3
BG966355
LOCUS
DEFINITION 602832843F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4987379 5',
mRNA sequence.
ACCESSION BG966355

```

```

VERSTON BG966355.1 GI:14353992
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 837)
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-NCI nih.gov/"
/note="National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)"
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10998 row: e column: 12
High quality sequence stop: 692.
Location/Qualifiers
1..837
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4987379"
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-NCI nih.gov/"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 201 a 222 c 218 g 196 t
ORIGIN

Query Match 76.5%; Score 39; DB 10; Length 837;
Best Local Similarity 89.4%; Pred. No. 0.00078;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcaccattactatccagacactgtgcagggc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 286 TTAGTGGTGGTGGTAGCACCTACTATCCAGACACTGTGAAGGGC 332

RESULT 4
BF163874
LOCUS
DEFINITION 601772386F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3991460 5',
mRNA sequence.
ACCESSION BF163874
VERSION BF163874.1 GI:11044152
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 662)
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-NCI nih.gov/"
/note="National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)"
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9204 row: 1 column: 21
High quality sequence stop: 658.
Location/Qualifiers
1..662
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3991460"
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-NCI nih.gov/"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

```

[illegible]

```

REFERENCE
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE        NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9195 row: 1 column: 03
High quality sequence stop: 581.
Location/Qualifiers
1. .913
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT   218 a 248 c 260 g 187 t
ORIGIN

Query Match      75.3%; Score 38.4; DB 10; Length 913;
Best Local Similarity 87.5%; Pred. No. 0.0013;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 agttagtggtggtgtagcactactatccagacactgtgcagg 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 273 AGCCATTAGTAGTGGTGGTACCTACTATCCAGACAGTGTGAAGG 320

RESULT 8
BF144493
LOCUS      BF144493.1 NCI_CGAP_Lu30 877 bp mRNA linear EST 24-OCT-2000
DEFINITION 601790133F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4020753 5',
mRNA sequence.
ACCESSION  BF144493
VERSION     BF144493.1 GI:10983333
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 877)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9275 row: a column: 10
High quality sequence stop: 644.
Location/Qualifiers
1. .877
/organism="Mus musculus"

REFERENCE
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE        NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9195 row: 1 column: 03
High quality sequence stop: 581.
Location/Qualifiers
1. .913
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="spontaneous tumor, metastatic to mammary"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT   198 a 233 c 254 g 192 t
ORIGIN

Query Match      74.5%; Score 38; DB 10; Length 877;
Best Local Similarity 89.1%; Pred. No. 0.0018;
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcactactatccagacactgtgcagg 50
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 245 TTAGTAGTGGTGGTGGTACCTACTATCCAGACAGTGTGAAGG 290

RESULT 9
BF136517
LOCUS      BF136517.1 Porcine Spleen cDNA library Sus scrofa cDNA, mRNA
DEFINITION AR097807SPDD09S Porcine Spleen cDNA library Sus scrofa cDNA, mRNA
sequence.
ACCESSION  BF136517
VERSION     BF136517.1 GI:15417813
KEYWORDS   EST.
SOURCE     pig.
ORGANISM   Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 333)
Rink,A., Santschi,E.M. and Beattie,C.W.
Amplified, Normalized cDNA Libraries from a Porcine Model of
Orthopedic Implant Associated Staphylococcus aureus Infection
Unpublished (2001)
Contact: Rink A
Department of Animal Biotechnology
College of Agriculture, Biotechnology and Natural Resources,
University of Nevada, Reno
MS 202, FA 103, 1664 N Virginia St, Reno, NV 89557-0236, USA
Tel: 775 784 1705
Fax: 775 784 1375
Email: arink@cabnr.unr.edu
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGCACGAG'.
Location/Qualifiers
1. .333
/organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone_lib="Porcine Spleen cDNA library"
/tissue_type="Spleen"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/notes="vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGCACGAG'."
FEATURES
source

```


LOCUS AAL170256 823 bp mRNA linear EST 16-FEB-1997
 DEFINITION ms87g10.r1 Soares mouse 3NbMS Mus musculus CDNA clone IMAGE:618594
 5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION
 (HUMAN); gb:V00821 Mouse mRNA fragment for immunoglobulin mu
 encoding the C-terminus (MOUSE);, mRNA sequence.

ACCESSION AAL170256 GI:1748794
 VERSION AAL170256
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 823)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:379418
 Putative full length read
 vector to vector length is 867
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 492.

FEATURES
 source
 1..823
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:618594"
 /clone_lib="Soares mouse 3NbMS"
 /sex="male"
 /tissue_type="Spleen"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /note="vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(df) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. RNA
 provided by Dr. Bertrand Jordan. Library went through
 three rounds of normalization, and was constructed by
 Bento Soares and M.Fatima Bonaldo."
 200 a 208 c 202 g 213 t

BASE COUNT 200 a 208 c 202 g 213 t
 ORIGIN

Query Match 73.3%; Score 37.4; DB 9; Length 823;
 Best Local Similarity 87.2%; Pred. No. 0.0029;
 Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcactactatccagacactgtgcaggc 51
 |||||
 Db 269 TTAGTAGTGGTGGTATACATCTACATGCAGACACTGTGAAGGC 315

RESULT 13
 BB869694 342 bp mRNA linear EST 27-NOV-2001
 LOCUS BB869694 RIKEN full-length enriched, adult male accessory axillary
 DEFINITION lymph node Mus musculus CDNA clone G630015C08 5', mRNA sequence.

ACCESSION BB869694
 VERSION BB869694.1 GI:17115904
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 342)

AUTHORS Akimura,T., Arakawa,T., Carninci,P., Futuno,M., Hanagaki,T.,
 Hayatsu,T., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
 Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
 Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
 Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
 Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
 A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
 Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
 2001)

TITLE Unpublished (2001)
 JOURNAL Contact: Yoshihide Hayashizaki
 COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
 S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
 Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
 Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES
 source
 1..342
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="G630015C08"
 /clone_lib="RIKEN full-length enriched, adult male
 accessory axillary lymph node"
 /sex="male"
 /tissue_type="accessory axillary lymph node"
 /dev_stage="adult"

BASE COUNT 73 a 83 c 98 g 88 t
 ORIGIN

Query Match 71.4%; Score 36.4; DB 9; Length 342;
 Best Local Similarity 87.0%; Pred. No. 0.0048;
 Matches 40; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcactactatccagacactgtgcaggc 50
 |||||
 Db 291 TTAGTAGTGGTGGTATACCTACTATCCAGACACTGTGAAGGC 336

RESULT 14


```

BG145342
LOCUS      BG145342          494 bp      mRNA      linear      EST 01-FEB-2001
DEFINITION u072g05.y1 Soares_mouse_NMGB_bcell Mus musculus cDNA clone
IMAGE:3382089 5' similar to SW:HV58_MOUSE P18529 IG HEAVY CHAIN V
REGION 5-76 PRECURSOR. ;, mRNA sequence.
ACCESSION  BG145342
VERSION     BG145342.1 GI:12648749
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 494)
AUTHORS   NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Other_ESTs: u072g05.x1
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1087085
            Seq primer: -40RP from Gibco
            High quality sequence stop: 471.
FEATURES   Location/Qualifiers
            source          1..494
                        /organism="Mus musculus"
                        /db_xref="taxon:10090"
                        /clone="IMAGE:3382089"
                        /clone_lib="Soares_mouse_NMGB_bcell"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: germinal B-cell; Vector: pT73D-Pac
                        (Pharmacia) with a modified polylinker; Site_1: Not I;
                        Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                        oligo(dT) primer [5'
                        TGTTCACATCTGAAGTGGAGCGCGCGCTGTTTCTTTTCTTTTCTTTTCTTTT
                        T 3']; double-stranded cDNA was ligated to Eco RI
                        adaptors (Pharmacia), digested with Not I and cloned into
                        the Not I and Eco RI sites of the modified pT73 vector.
                        Library is normalized; constructed by Bento Soares and
                        M.Fatima Bonaldo."
BASE COUNT 115 a 136 c 131 g 112 t
ORIGIN

Query Match      71.4%; Score 36.4; DB 10; Length 494;
Best Local Similarity 87.0%; Pred. No. 0.0055;
Matches 40; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatccagacactgtgcaggg 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 178 TTAGTAGTGGTGTAGTTACACCTACTACTATCCAGACAGTGTGAAGGG 223

RESULT 15
AW408295
LOCUS      AW408295          548 bp      mRNA      linear      EST 16-FEB-2000
DEFINITION UI-HF-BK0-abj-d-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056327 5', mRNA sequence.
ACCESSION  AW408295
VERSION     AW408295.1 GI:6927352
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 548)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov

```

```

Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
            source          1..548
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:3056327"
                        /clone_lib="NIH_MGC_36"
                        /tissue_type="lymph"
                        /cell_type="germinal center B cells"
                        /cell_line="MGC85"
                        /lab_host="DH10B (LTI)"
                        /note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
                        Constructed from size fractionated cytoplasmic mRNA
                        (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                        M. Staudt, Ph.D. Library preparation by Maria de Fatima
                        Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 109 a 148 c 156 g 135 t
ORIGIN

Query Match      71.4%; Score 36.4; DB 9; Length 548;
Best Local Similarity 87.0%; Pred. No. 0.0057;
Matches 40; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatccagacactgtgcaggg 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 276 TTAGTGGGATGGTGGTAGCACCTACTATGCAGACTCTCTGTAAGGG 321

Search completed: August 21, 2002, 09:55:47
Job time: 9310 sec

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:27 ; Search time 754.01 Seconds
(without alignments)
116.129 Million cell updates/sec

Title: US-09-339-922A-103

Perfect score: 51

Sequence: 1 aaagttagtagtggtgtgg.....atccagacactgtgcagggc 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_032802.*
1: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA2001A.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-n-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	51	22	AAF28235
2	47.8	93.7	51	22	AAF28234
3	47.8	93.7	87	19	AAV49826
4	47.8	93.7	87	22	AAH74629
5	47.8	93.7	87	22	AAF28181
6	47.8	93.7	351	19	AAV49820
7	47.8	93.7	351	19	AAV49822
8	47.8	93.7	351	22	AAH74623
9	47.8	93.7	351	22	AAH74625

10	47.8	93.7	351	22	AAF28175	Vitaxin heavy chai
11	47.8	93.7	351	22	AAF28177	Antibody LM609 hea
12	43.8	85.9	85	18	AAH72258	Mouse Mab 15 heavy
13	43.8	85.9	369	19	AAV07642	anti-CD22 monoclon
14	43.8	85.9	441	18	AAH72269	Chimeric Mab 15 PC
15	43.8	85.9	445	18	AAH72237	Humanised reshaped
16	43.8	85.9	457	18	AAH72267	Mouse Mab 15 heavy
17	43.8	85.9	923	16	AAH51436	Murine Mab SK48-E2
18	42.2	82.7	482	11	AAQ05355	Sequence encoding
19	41.2	80.8	51	19	AAV44992	15D3 antibody heav
20	41.2	80.8	51	20	AAZ10944	15D3 VH chain CDR2
21	41.2	80.8	357	19	AAV44997	15D3 antibody heav
22	41.2	80.8	357	20	AAZ10957	15D3 VH chain codi
23	41.2	80.8	357	20	AAV08933	Antibody 15D3 heav
24	41.2	80.8	480	13	AAQ20070	MRK16-H chain. Ch
25	40.6	79.6	351	16	AAQ96282	Human IgE receptor
26	40.6	79.6	351	18	AAH90025	CDNA encoding heav
27	40.6	79.6	357	17	AAH28000	B5 immunoglobulin
28	40.6	79.6	360	17	AAH33445	EGF receptor chime
29	40.6	79.6	363	18	AAH75583	Monoclonal antibod
30	40.6	79.6	363	20	AAV81002	Murine 340 Vh DNA
31	40.6	79.6	363	24	AAH25246	Mouse monoclonal a
32	40.6	79.6	474	18	AAH70808	Mouse anti-idiotyp
33	40.6	79.6	474	18	AAH70810	Mouse anti-idiotyp
34	40.6	79.6	582	18	AAH90020	DNA encoding heav
35	40.6	79.6	761	20	AAH01214	Human antiFc epsil
36	40.6	79.6	770	20	AAH01216	Human antiFc epsil
37	39	76.5	80	24	AAH97073	Humanised TRA-8 he
38	39	76.5	354	14	AAQ48765	Monoclonal antibod
39	39	76.5	422	22	AAH90629	Plasmid gammalwt-t
40	39	76.5	747	22	AAH30725	Anti-FIX/FIXa anti
41	39	76.5	747	22	AAH30726	Anti-FIX/FIXa anti
42	39	76.5	783	16	AAH08490	Anti-C5 Mab N19/8
43	39	76.5	888	22	AAH87642	Single chain antib
44	38.8	76.1	3223	22	AAH11982	DNA encoding Human
45	38	74.5	125	19	AAV24267	Chimeric antibody

ALIGNMENTS

RESULT 1
AAF28235
ID AAF28235 standard; DNA; 51 BP.
XX
AC AAF28235;
XX
DT 03-APR-2001 (first entry)
XX
DE DNA encoding enhanced 2236-38/ 6H6LH heavy chain CDR2.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -
 XX Clam 14; Page 105; 132pp; English.
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX Sequence 51 BP; 13 A; 10 C; 16 G; 12 T; 0 other;
 SQ

Query Match 100.0%; Score 51; DB 22; Length 51;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacttactatccagacactgtgcaggc 51
 Db 1 aaagttagtagtggtggtgtagcacttactatccagacactgtgcaggc 51
 |||||

RESULT 2
 AAF28234
 ID AAF28234 standard; DNA; 51 BP.
 XX AAF28234;
 AC AAF28234;
 DT 03-APR-2001 (first entry)
 XX
 DE DNA encoding enhanced 5H6LH heavy chain CDR2.
 XX
 KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 XX Unidentified.
 OS
 XX WO200078915-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 23-JUN-2000; 2000WO-US17454.
 PF
 XX 24-JUN-1999; 99US-0339922.
 PR
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA
 XX Huse WD, Wu H;
 PI
 XX WPI; 2001-050110/06.
 DR
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 XX to alpha(V)beta3(3) integrin, useful in the diagnosis and treatment of
 XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 XX osteoporosis -
 XX
 XX Claim 16; Page 105; 132pp; English.
 PS
 XX The present invention relates to enhanced LM609 grafted antibodies
 XX exhibiting selective binding affinity to alphaVbeta3 integrin or
 XX their functional fragments. The antibodies or their functional
 XX fragments can be used in the diagnosis and treatment of
 XX alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 XX diseases (such as psoriasis and chronic articular rheumatism),
 XX disorders associated with inappropriate or inopportune invasion of
 XX vessels (such as diabetic retinopathy, neovascular glaucoma and
 XX cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX Sequence 51 BP; 13 A; 8 C; 16 G; 14 T; 0 other;
 SQ

Query Match 93.7%; Score 47.8; DB 22; Length 51;
 Best Local Similarity 96.1%; Pred. No. 3e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacttactatccagacactgtgcaggc 51
 Db 1 aaagttagtagtggtggtgtagcacttactatttagacactgtgcaggc 51
 |||||

RESULT 3
 AAV49826
 ID AAV49826 standard; DNA; 87 BP.
 XX AAV49826;
 AC AAV49826;
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody variable region oligonucleotide #3.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; ss.
 XX Synthetic.
 OS Mus sp.
 XX WO9833919-A2.
 PN
 XX 06-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX (IXSY-) IXSYS INC.
 PA
 XX Glaser SM, Huse WD;
 PI
 XX WPI; 1998-437472/37.
 DR
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Example 2; Page 65; 129pp; English.
 PS
 XX AAV49824-V49833 are oligonucleotides used in the construction of grafted
 CC LM609 monoclonal antibody heavy and light chain variable regions. LM609
 CC and the antibody vitaxin bind selectively to integrin alphavbeta3 and
 CC can be used to inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 XX Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;
 SQ

Query Match 93.7%; Score 47.8; DB 19; Length 87;
 Best Local Similarity 96.1%; Pred. No. 3.3e-09;

Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcactactatccagacactgtgcagggc 51
|||||
Db 10 aaagttagtagtggtggtgtagcactactattagacactgtgcagggc 60

RESULT 4

AAH74629
ID AAH74629 standard; DNA; 87 BP.

XX AC AAH74629;

XX DT 15-OCT-2001 (first entry)

XX DE PCR primer for heavy chain variable region of LM609 antibody.

XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW cancer; PCR primer; ss.

XX OS Mus sp.

XX PN US2001011125-A1.

XX PD 02-AUG-2001.

XX PF 30-JAN-1997; 97US-0790540.

XX PR 30-JAN-1997; 97US-0790540.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX PSI: 2001-496171/54.

XX PT New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer -

XX PS Example 2; Page 16; 25pp; English.

XX CC PCR primers AAH74627-31 were used to amplify DNA encoding fragments
CC of the heavy chain variable region of the monoclonal antibody LM609.
CC LM609 is a murine antibody which specifically recognises the integrin
CC alphavbeta3, and inhibits its functional activity. The specification
CC describes a LM609 grafted antibody which has the complementarity
CC determining regions (CDRs) substituted into a non-murine framework.
CC Nucleic acids encoding LM609 grafted heavy and light chain polypeptides
CC and fragments are useful in diagnostic and therapeutic purposes, such
CC as in the production of LM609 grafted antibodies and fragments having
CC binding specificity and inhibitory activity against the integrin
CC alphavbeta3. The antibody can be used for the diagnosis or treatment
CC of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic
CC articular rheumatism, psoriasis, disorders associated with inappropriate
CC or inappropriate invasion of vessels such as diabetic retinopathy,
CC neovascular glaucoma and capillary proliferation in atherosclerotic
CC plaques, or cancers), and to inhibit binding activity of alphavbeta3
CC that are necessary for progression of an alphavbeta3-mediated disease.

XX SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 93.7%; Score 47.8; DB 22; Length 87;

Best Local Similarity 96.1%; Pred. No. 3.3e-09;

Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcactactatccagacactgtgcagggc 51
|||||
Db 10 aaagttagtagtggtggtgtagcactactattagacactgtgcagggc 60

RESULT 5

AAF28181
ID AAF28181 standard; DNA; 87 BP.

XX AC AAF28181;

XX DT 03-APR-2001 (first entry)

XX DE Oligonucleotide #3.

XX KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX PSI: 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -

XX PS Example 2; Page 67; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 93.7%; Score 47.8; DB 22; Length 87;

Best Local Similarity 96.1%; Pred. No. 3.3e-09;

Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcactactatccagacactgtgcagggc 51
|||||
Db 10 aaagttagtagtggtggtgtagcactactattagacactgtgcagggc 60

RESULT 6

AAV49820
ID AAV49820 standard; DNA; 351 BP.

XX AC AAV49820;

XX DT 02-NOV-1998 (first entry)

XX DE Vitaxin antibody heavy chain variable region DNA.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; ss.
 OS Mus sp.

XX Key Location/Qualifiers
 FH 1..351
 FT /*tag= a
 FT /product= "vitaxin antibody heavy chain variable region"
 FT /note= "partial sequence, no start or stop codon given"
 XX

PN WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR P-PSDB; AAW76001.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 3; Fig 1a; 129pp; English.

XX This sequence encodes the vitaxin antibody variable heavy chain region.
 CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 93.7%; Score 47.8; DB 19; Length 351;
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacctactatccagacactgtgcaggcc 51
 |||||
 Db 148 aaagttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 198

RESULT 7

AAV49822

ID AAV49822 standard; DNA; 351 BP.

XX AAV49822;

XX 02-NOV-1998 (first entry)

DE LM609 antibody heavy chain variable region DNA fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; ss.

XX Mus sp.

XX Key Location/Qualifiers
 FH 1..351
 FT /*tag= a
 FT /product= "LM609 antibody heavy chain variable region"
 FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 37; Fig 2a; 129pp; English.

XX This sequence encodes the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

Query Match 93.7%; Score 47.8; DB 19; Length 351;
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacctactatccagacactgtgcaggcc 51
 |||||
 Db 148 aaagttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 198

RESULT 8

AAH74623

ID AAH74623 standard; DNA; 351 BP.

XX AAH74623;

XX 15-OCT-2001 (first entry)

DE DNA encoding heavy chain variable region of LM609 grafted antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer; ss.

OS Synthetic.

OS Mus sp.

XX

PN US2001011125-A1.
 XX 02-AUG-2001.
 XX 30-JAN-1997; 97US-0790540.
 XX 30-JAN-1997; 97US-0790540.
 XX (HUSE/) HUSE W D.
 XX Huse WD;
 XX WPI: 2001-496171/54.
 XX P-PSDB; AAG63587.
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX
 XX Claim 3; Fig 1A; 25pp; English.
 XX The present sequence encodes the heavy chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
 CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.
 XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;
 SQ

Query Match 93.7%; Score 47.8; DB 22; Length 351;
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcaccactatccagacactgtgcagggc 51
 |||||
 Db 148 aaagttagtagtggtggtgtagcaccactatccagacactgtgcagggc 198

RESULT 9
 AAH74625
 ID AAH74625 standard; DNA; 351 BP.
 XX
 AC AAH74625;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE DNA encoding heavy chain variable region of LM609 antibody.
 XX
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer; ss.
 XX
 OS Mus sp.
 XX
 PN US2001011125-A1.
 XX
 PD 02-AUG-2001.
 XX

PF 30-JAN-1997; 97US-0790540.
 XX
 PR 30-JAN-1997; 97US-0790540.
 XX
 PA (HUSE/) HUSE W D.
 XX
 PI Huse WD;
 XX
 DR WPI: 2001-496171/54.
 DR P-PSDB; AAG63589.
 XX
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 XX
 XX Disclosure; Fig 2A; 25pp; English.
 XX The present sequence encodes the heavy chain variable region of the
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.
 CC The specification describes a LM609 grafted antibody which has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.
 XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;
 SQ

Query Match 93.7%; Score 47.8; DB 22; Length 351;
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcaccactatccagacactgtgcagggc 51
 |||||
 Db 148 aaagttagtagtggtggtgtagcaccactatccagacactgtgcagggc 198

RESULT 10
 AAF28175
 ID AAF28175 standard; DNA; 351 BP.
 XX
 AC AAF28175;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Vitaxin heavy chain variable region DNA.
 XX
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 XX 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX

PI Huse WD, Wu H;
 DR WPI; 2001-050110/06.
 XX
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Fig 1; 132pp; English.
 XX
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;
 SQ

Query Match 93.7%; Score 47.8; DB 22; Length 351;
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtggtggtgtagcacctactatccagacactgtgcagggc 51
 |||||
 DB 148 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 198
 |||||

RESULT 11
 AAF28177
 ID AAF28177 standard; DNA; 351 BP.
 XX
 AC AAF28177;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Antibody LM609 heavy chain variable region DNA.
 XX
 KW LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
 XX
 OS Unidentified.
 XX
 XX WO200078815-A1.
 PN
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 XX WPI; 2001-050110/06.
 DR
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Fig 2; 132pp; English.
 XX
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta₃ integrin or

CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;
 SQ

Query Match 93.7%; Score 47.8; DB 22; Length 351;
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtggtggtgtagcacctactatccagacactgtgcagggc 51
 |||||
 DB 148 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 198
 |||||

RESULT 12
 AAT72258/C
 ID AAT72258 standard; DNA; 85 BP.
 XX
 AC AAT72258;
 XX
 DT 03-JAN-1998 (first entry)
 XX
 DE Mouse MAB 15 heavy chain backward PCR primer 4.
 XX
 KW Humanised antibody; monoclonal antibody; MAB 15; tumour;
 KW lung cancer; therapy; polymerase chain reaction; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 XX EF781847-A1.
 PN
 XX
 PD 02-JUL-1997.
 XX
 PF 25-OCT-1996; 96EP-0117154.
 XX
 PR 06-NOV-1995; 95EP-0117407.
 XX
 XX (MERE) MERCK PATENT GMBH.
 PA
 XX Bendig M, Jones T, Saldana J;
 PI
 XX WPI; 1997-334904/31.
 DR
 XX Humanised form of murine monoclonal antibody MAB 15 - useful for
 PT treating lung cancer
 PT
 XX Disclosure; Page 27; 71pp; English.
 PS
 XX This synthetic oligonucleotide comprises backward PCR primer 4
 CC that was used with other sense and antisense primers (AAT72255-60)
 CC to produce a sequence encoding a reshaped humanised monoclonal
 CC antibody (MAB) 15 heavy chain variable region VH sequence (see
 CC AAT72237). The full-length product was then amplified with external
 CC primers (see AAT72261-62) and subcloned into HCMV expression vector
 CC containing human heavy chain gamma-1 constant region. Humanised
 CC reshaped MAB 15 is claimed for use in the treatment of human
 CC tumours, especially lung cancer.
 XX
 XX Sequence 85 BP; 19 A; 23 C; 21 G; 22 T; 0 other;
 SQ

Query Match 85.9%; Score 43.8; DB 18; Length 85;
 Best Local Similarity 95.7%; Pred. No. 1.2e-07;
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

	AAT72237;
AC	XX
XX	DT
XX	DE
XX	KW
XX	KW
XX	OS
XX	OS
XX	OS
XX	XX
XX	FH
FT	sigs_peptide Location/Qualifiers 16..72
FT	/*tag= a
FT	73..432
FT	mat_peptide / *tag= b
FT	PX
PN	EP781847-A1.
XX	PD
XX	02-JUL-1997.
XX	25-OCT-1996; 96EP-0117154.
XX	06-NOV-1995; 95EP-0117407.
XX	(MERE) MERCK PATENT GMBH.
PA	Bendlig M, Jones T, Saldana J;
PI	WIPI; 1997-334904/31.
XX	P-PSDB; AAW21652.
DR	Humanised form of murine monoclonal antibody Mab 15 - useful for
PT	treating lung cancer
XX	Claim 2; Fig 12; 7ipp; English.
XX	This cDNA sequence encodes the heavy chain variable region VH
CC	(AAW21652) of humanised reshaped monoclonal antibody (Mab) 15
CC	comprising complementarity determining regions of murine Mab 15
CC	(DSM ACC211), and reshaped human 3DPl framework regions. It was
CC	prepared using PCR mutagenesis methods (see AAT72255-62). A
CC	claimed process for preparation of humanised reshaped Mab 15
CC	Involves: cloning and sequencing murine Mab 15 VL and VH regions
CC	(see AAT72238 and AAT72267); constructing, expressing and analysing
CC	chimeric Mab 15 antibody (see AAT72268-69); modelling the structure
CC	of murine Mab 15 variable regions; designing reshaped human Mab 15
CC	variable regions; preparing an oligonucleotide sequence which codes
CC	for the constant regions of the light and heavy chain of a human
CC	immunoglobulin; and constructing, expressing and analysing the
CC	complete reshaped human Mab 15. The humanised Mab can be used for
CC	treating tumours, especially lung cancer, and for the manufacture
CC	of a drug related to tumours, especially lung cancer.
XX	Sequence 445 BP; 91 A; 108 C; 141 G; 105 T; 0 other;
SQ	
<hr/>	
Query Match	85.9%; Score 43.8; DB 18; Length 445;
Best Local Similarity	95.7%; Pred. No. 1,7e-07;
Matches	45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	5 ttagatagtggtggctaggacacctactattccagacactgagtgcaggc 51
DG	
Db	224 ttgaataagtcggcggtaggacccttactattccagacactgctaagaqgc 270

GenCore version 4.5
Copyright (C) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:14 ; Search time 174.26 Seconds
(without alignments)
71.889 Million cell updates/sec

Title: US-09-339-922A-103

Perfect score: 51

Sequence: 1 aaagttagtggtggtgg.....atccagacactgtgcagggc 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43.8	85.9	923	5	PCT-US94-07659-1
2	41.2	80.8	51	1	US-08-475-000-2
3	41.2	80.8	51	2	US-08-483-199-2
4	41.2	80.8	51	2	US-08-484-508-2
5	41.2	80.8	357	1	US-08-475-000-15
6	41.2	80.8	357	2	US-08-483-199-15
7	41.2	80.8	357	2	US-08-484-508-15
8	40.6	79.6	357	1	US-08-331-398A-21
9	40.6	79.6	357	2	US-08-331-397B-21
10	40.6	79.6	357	2	US-08-759-804A-21
11	40.6	79.6	357	1	US-09-227-693-21
12	40.6	79.6	375	1	US-08-331-398A-59
13	40.6	79.6	375	2	US-08-331-397B-59
14	40.6	79.6	375	2	US-08-759-804A-58
15	40.6	79.6	474	2	US-08-653-402B-5
16	40.6	79.6	474	1	US-08-653-402B-9
17	39	76.5	354	1	US-08-326-362-1
18	39	76.5	783	4	US-08-487-283A-19
19	37.4	73.3	357	5	PCT-US94-07659-5
20	37.4	73.3	403	1	US-08-408-133-4
21	37.4	73.3	403	1	US-08-454-683-4
22	37.4	73.3	403	2	US-08-116-778B-20
23	37.4	73.3	403	2	US-08-454-680-4
24	37.4	73.3	403	2	US-08-438-562-20
25	37.4	73.3	403	2	US-08-483-528B-20
26	37.4	73.3	403	3	US-08-673-799C-20
27	37.2	72.9	51	5	PCT-US93-08435-17

Sequence 48, Appl
Sequence 9, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 19, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 9, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 30, Appl
Sequence 3, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 17, Appl

Sequence 102 5 PCT-US93-08435-48
Sequence 354 5 PCT-US93-08435-9
Sequence 389 5 PCT-US93-08435-11
Sequence 389 5 PCT-US93-08435-13
Sequence 405 4 US-08-579-378A-15
Sequence 405 4 US-08-579-378A-19
Sequence 519 1 US-08-339-582-1
Sequence 1329 5 PCT-US96-13152-3
Sequence 348 2 US-08-888-366-9
Sequence 348 2 US-08-888-366-11
Sequence 717 2 US-08-553-497A-17
Sequence 413 1 US-08-253-877C-56
Sequence 413 2 US-08-452-164A-56
Sequence 416 4 US-08-976-183A-30
Sequence 717 2 US-07-956-399-3
Sequence 721 2 US-08-224-591-15
Sequence 721 2 US-08-926-789-15
Sequence 733 2 US-08-224-591-17

ALIGNMENTS

RESULT 1
PCT-US94-07659-1
; Sequence 1, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; ADDRESSEE: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 923 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

```
; LOCATION: 169...909
PCT-US94-07659-1

Query Match      85.9%; Score 43.8; DB 5; Length 923;
Best Local Similarity 95.7%; Pred. No. 8.9e-09;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtgtggtgtagcaccattatccagacactgtgcaggc 51
|||||
Db 377 TTAGTAGTGTGTGGTGGCACCTACTATCCAGACACTGTGAAGGC 423

RESULT 2
US-08-475-000-2
; Sequence 2, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; NUMBER OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-475-000-2

Query Match      80.8%; Score 41.2; DB 1; Length 51;
Best Local Similarity 93.5%; Pred. No. 4.6e-08;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ttagtgtggtgtagcaccattatccagacactgtgcagg 50
|||||
Db 5 TTAGTAGTGTGTGGTGGTAACCTACTATCCAGACACTGTGAAGG 50

RESULT 3
US-08-483-199-2
; Sequence 2, Application US/08483199
; Patent No. 5849877
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; NUMBER OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,508
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-484-508-2

Query Match      80.8%; Score 41.2; DB 2; Length 51;
Best Local Similarity 93.5%; Pred. No. 4.6e-08;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ttagtgtggtgtagcaccattatccagacactgtgcagg 50
|||||
Db 5 TTAGTAGTGTGTGGTGGTAACCTACTATCCAGACACTGTGAAGG 50

RESULT 4
US-08-484-508-2
; Sequence 2, Application US/08484508
; Patent No. 5948647
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; NUMBER OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,508
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-483-199-2
```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-484-508-2

Query Match 80.8%; Score 41.2; DB 1; Length 51;
Best Local Similarity 93.5%; Pred. No. 4.6e-08;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttactagtgtggtgtagcacctactatccagacactgtgcaggg 50
|||||
Db 5 TTACTAGTGTGTTGGTGAACACCTACTACTATCCAGACAGTGTGAAGGG 50

RESULT 5

US-08-475-000-15
; Sequence 15, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..357
; US-08-475-000-15

Query Match 80.8%; Score 41.2; DB 1; Length 357;
Best Local Similarity 93.5%; Pred. No. 7.7e-08;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttactagtgtggtgtagcacctactatccagacactgtgcaggg 50
|||||
Db 152 TTACTAGTGTGTTGGTGAACACCTACTACTATCCAGACAGTGTGAAGGG 197

RESULT 6

US-08-483-199-15
; Sequence 15, Application US/08483199

; Patent No. 5849877
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/483,199
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..357
; US-08-483-199-15

Query Match 80.8%; Score 41.2; DB 2; Length 357;
Best Local Similarity 93.5%; Pred. No. 7.7e-08;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttactagtgtggtgtagcacctactatccagacactgtgcaggg 50
|||||
Db 152 TTACTAGTGTGTTGGTGAACACCTACTACTATCCAGACAGTGTGAAGGG 197

RESULT 7

US-08-484-508-15
; Sequence 15, Application US/08484508
; Patent No. 5948647
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/484,508

Query Match 80.8%; Score 41.2; DB 1; Length 357;
Best Local Similarity 93.5%; Pred. No. 7.7e-08;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttactagtgtggtgtagcacctactatccagacactgtgcaggg 50
|||||
Db 152 TTACTAGTGTGTTGGTGAACACCTACTACTATCCAGACAGTGTGAAGGG 197

RESULT 6

US-08-483-199-15
; Sequence 15, Application US/08483199

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 357 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;     NAME/KEY: -
;     LOCATION: 1..357
;     OTHER INFORMATION: /note= "B5 Variable Heavy Chain (V-H)"
US-08-331-398A-21

Query Match          79.6%; Score 40.6; DB 1; Length 357;
Best Local Similarity 91.5%; Pred. No. 1.3e-07;
Matches 43; Conservative 0; Mismatches 4; Indels

Qy 5 ttagtagtggtgggtgagcacttactatccagacactgtgcagggc 51
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 152 TTAGTAATGGTGGGTAGCACCATTATCCAGACACTGTAAGGGC 198

RESULT 9
US-08-331-397B-21
; Sequence 21, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
;   APPLICANT: Pastan, Ira
;   APPLICANT: Benhar, Itai
;   TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tu
;   TITLE OF INVENTION: Specific Antibody Fragments, Fusion Pro
;   TITLE OF INVENTION: Thereof
;   NUMBER OF SEQUENCES: 68
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew
;   STREET: One Market Plaza, Stewart Street Plaza
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105-1492
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/331,397B
;   FILING DATE: 28-OCT-1994
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/767,331
;   FILING DATE: 30-SEP-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/596,289
;   FILING DATE: 12-OCT-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Hunter, Tom
;   REGISTRATION NUMBER: 38,498
;   REFERENCE/DOCKET NUMBER: 015280-126120US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 543-9600
;   TELEFAX: (415) 543-5043
;   INFORMATION FOR SEQ ID NO: 21:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 357 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA
;     FEATURE:
;       NAME/KEY: -
;       LOCATION: 1..357
;       OTHER INFORMATION: /note= "B5 Variable Heavy Chain (V-H)"

```

US-08-331-397B-21

Query Match 79.6%; Score 40.6; DB 2; Length 357;
Best Local Similarity 91.5%; Pred. No. 1.3e-07;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatccagacactgtgcaggcc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 152 TTAGTAATGGTGGTGTAGCACCTATTATCCAGACACTGTAAAGGC 198

RESULT 10

US-08-759-804A-21
; Sequence 21, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..357
; OTHER INFORMATION: /note= "B5 Variable Heavy chain (V-H)"
US-08-759-804A-21

Query Match 79.6%; Score 40.6; DB 2; Length 357;
Best Local Similarity 91.5%; Pred. No. 1.3e-07;

Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatccagacactgtgcaggcc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 152 TTAGTAATGGTGGTGTAGCACCTATTATCCAGACACTGTAAAGGC 198

RESULT 11

US-09-227-693-21
; Sequence 21, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..357
; OTHER INFORMATION: /standard_name= "B5
; OTHER INFORMATION: variable heavy chain"
US-09-227-693-21

Query Match 79.6%; Score 40.6; DB 4; Length 357;
Best Local Similarity 91.5%; Pred. No. 1.3e-07;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatccagacactgtgcaggcc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 152 TTAGTAATGGTGGTGTAGCACCTATTATCCAGACACTGTAAAGGC 198

RESULT 12
 US-08-331-398A-59
 Sequence 59, Application US/08331398A
 Patent No. 5608039
 GENERAL INFORMATION:
 APPLICANT: Pastan, Ira
 APPLICANT: Willingham, Mark
 APPLICANT: FitzGerald, David
 APPLICANT: Brinkmann, Ulrich
 APPLICANT: Pai, Lee
 TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
 TITLE OF INVENTION: and Their Uses (as amended)
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew
 STREET: One Market Plaza, Steuart Street Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/331,398A
 FILING DATE: 28-OCT-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 015280-1261100S
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 375 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..375
 OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
 OTHER INFORMATION: Heavy chain region"
 US-08-331-398A-59

	Query Match	79.5%	Score 40.6	DB 1	Length 375
	Best Local Similarity	91.5%	Pred. No. 1.4e-07		
	Matches 43	Conservative	0	Mismatches 4	Indels
QY	5	ttagttagtgggtggtagcacctactatccagacactgtgcagggc	51		
Db	152	TTAGTAATGGTGGGTAGCACCTATTATCCAGACACTGTAAGGGC	198		

RESULT 13
US-08-331-397B-59
; Sequence 59, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:

```

> APPLICANT: Pastan, Ira
> APPLICANT: Benhar, Itai
> TITLE OF INVENTION: Chmeric and Mutationally Stabilized Tumor-
> SPECIFIC ANTIBODY FRAGMENTS, FUSION PROTEINS, AND USES
> THEREOF
> TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
> THEREOF
> NUMBER OF SEQUENCES: 68
> CORRESPONDENCE ADDRESS:
> ADDRESSEE: Townsend and Townsend and Crew
> STREET: One Market Plaza, Steuart Street Plaza
> CITY: San Francisco
> STATE: California
> COUNTRY: USA
> ZIP: 94105-1492
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Floppy disk
> COMPUTER: IBM PC compatible
> OPERATING SYSTEM: PC-DOS/MS-DOS
> SOFTWARE: PatentIn Release #1.0, Version #1.30
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/08/331,397B
> FILING DATE: 28-OCT-1994
> CLASSIFICATION: 435
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 07/767,331
> FILING DATE: 30-SEP-1991
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 07/596,289
> FILING DATE: 12-OCT-1990
> ATTORNEY/AGENT INFORMATION:
> NAME: Hunter, Tom
> REGISTRATION NUMBER: 38,498
> REFERENCE/DOCKET NUMBER: 015280-1261200US
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (415) 543-9600
> TELEFAX: (415) 543-5043
> INFORMATION FOR SEQ ID NO: 59:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 375 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: DNA
> FEATURE:
> NAME/KEY: -
> LOCATION: 1..375
> OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
> OTHER INFORMATION: Heavy chain region"
>
> US-08-331-397B-59

```

```

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..375
; OTHER INFORMATION: /note= "Mouse monoclonal an
; OTHER INFORMATION: Heavy chain region"
; US-08-759-804A-58

Query Match 79.6%; Score 40.6; DB 2;
Best Local Similarity 91.5%; Pred. No. 1.4e-07;
Matches 43; Conservative 0; Mismatches 4;

QY 5 ttagtgtgtgtgtgtagcacctactatccagacactgtgcag
||||| ||||||| ||||||| ||||||| ||||||| ||
Db 152 TTAGTATGTTGGTGTAGCACCTATTATCCAGACACTGTAAGG

RESULT 15
US-08-653-402B-5
; Sequence 5, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEB, Jaume
; APPLICANT: PIOLATIS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies wh
; TITLE OF INVENTION: immune response against epid
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia

```


GenCore version 4.5
Copyright (C) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:49:02 ; Search time 2408.76 Seconds
(without alignments)
208.504 Million cell updates/sec

Title: US-09-339-922A-105

Perfect score: 24

Sequence: 1 catcttcattggcagttttgtctct 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pi.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sv.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_hgt_hum.*

31: em_hgt_inv.*

32: em_hgt_other.*

33: em_hgtgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

RESULT 1

AX060884

LOCUS

DEFINITION

AX060884

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

AX060884

Sequence 105 from Patent WO0078815.

AX060884.1

GI:12406262

synthetic construct.

synthetic construct.

artificial sequence.

1 (bases 1 to 24)

Huse, W. D. and Wu, H.

Anti-g(a) v2.g(b)3? recombinant human antibodies, nucleic acids

encoding same and methods of use

Patent: WO 0078815-A 105 28-DEC-2000;

Applied Molecular Evolution (US)

Location/Qualifiers

1..24

/organism="synthetic construct"

/db_xref="taxon:32630"

<1..>24

/note="Mutated complementarity determining region (CDR)"

/codon_start=1

ALIGNMENTS

AX060884

Sequence 105 from Patent WO0078815.

AX060884.1

GI:12406262

synthetic construct.

synthetic construct.

artificial sequence.

1 (bases 1 to 24)

Huse, W. D. and Wu, H.

Anti-g(a) v2.g(b)3? recombinant human antibodies, nucleic acids

encoding same and methods of use

Patent: WO 0078815-A 105 28-DEC-2000;

Applied Molecular Evolution (US)

Location/Qualifiers

1..24

/organism="synthetic construct"

/db_xref="taxon:32630"

<1..>24

/note="Mutated complementarity determining region (CDR)"

/codon_start=1

```

/transl_table=11
/protein_id="CAC24928.1"
/db_xref="GI:12406263"
/translation="HLGFSFAS" 11 t
BASE COUNT      3 a      6 c      4 g
ORIGIN
Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 catcttcaggcaggttttgccttc 24
|||||
Db 1 CATCTTCATGGCAGTTTGTCTTC 24

RESULT 2
AP003776      AP003776      152948 bp      DNA      linear      HTG 23-JUN-2001
LOCUS      Homo sapiens chromosome 11 clone RP11-209L12 map 11q, WORKING DRAFT
DEFINITION      SEQUENCE, 11 unordered pieces.
ACCESSION      AP003776
VERSION      AP003776.1 GI:145330688
KEYWORDS      HTG; HNGS_PHASE1; HTGS_DRAFT
SOURCE      Homo sapiens DNA, clone:RP11-209L12.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 152948)
AUTHORS      Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL
COMMENT
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-209L12
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 148988 bases at least Q40
Consensus quality: 151056 bases at least Q30
Consensus quality: 151725 bases at least Q20
Insert size: 151948; sum-of-contigs
Quality coverage: 5.98x in Q20 bases; sum-of-contigs
-----
NOTE: This is a 'working draft' sequence. It currently consists of
11 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 35942 contig of 35942 bp in length
36043 64596 contig of 28554 bp in length
64697 88056 contig of 23360 bp in length
88157 108127 contig of 19971 bp in length
121652 121753 contig of 11150 bp in length
132903 132902 contig of 100 bp
133003 139176 contig of 6174 bp in length
139177 139276 contig of 100 bp
144518 144517 contig of 5241 bp in length
144618 147983 contig of 3366 bp in length
147984 148084 contig of 4204 bp in length
152288 152387 contig of 100 bp
152388 152948 contig of 561 bp in length.
FEATURES
source
1..152948
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-209L12"
misc_feature
1..35942
/note="assembly_fragment"
36043..64596
/note="assembly_fragment"
64697..88056
/note="assembly_fragment"
88157..108127
/note="assembly_fragment"
108228..121652
/note="assembly_fragment"
121753..132902
/note="assembly_fragment"
133003..139176
/note="assembly_fragment"
139277..144517
/note="assembly_fragment"
144618..147983
/note="assembly_fragment"
148084..152287
/note="assembly_fragment"
152388..152948
/note="assembly_fragment"
BASE COUNT 42013 a 33863 c 34632 g 41440 t 1000 others
ORIGIN
Query Match 87.5%; Score 21; DB 2; Length 152948;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tcttcaggcaggttttgccttc 23
|||||
Db 134726 TCITCATGGCAGTTTGTCTTC 134746

RESULT 3

```

```

152388 152948 contig of 561 bp in length.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 35942: contig of 35942 bp in length
35943 36042: gap of 100 bp
36043 64596: contig of 28554 bp in length
64597 88056: contig of 23360 bp in length
88057 88156: gap of 100 bp
88157 108127: contig of 19971 bp in length
108128 108227: gap of 100 bp
108228 121652: contig of 13425 bp in length
121653 121752: gap of 100 bp
121753 132902: contig of 11150 bp in length
132903 133002: gap of 100 bp
133003 139176: contig of 6174 bp in length
139177 139276: gap of 100 bp
139277 144517: contig of 5241 bp in length
144518 144617: gap of 100 bp
144618 147983: contig of 3366 bp in length
147984 148083: gap of 100 bp
148084 152287: contig of 4204 bp in length
152288 152387: gap of 100 bp
152388 152948: contig of 561 bp in length.
FEATURES
Location/Qualifiers
1..152948
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-209L12"
misc_feature
1..35942
/note="assembly_fragment"
36043..64596
/note="assembly_fragment"
64697..88056
/note="assembly_fragment"
88157..108127
/note="assembly_fragment"
108228..121652
/note="assembly_fragment"
121753..132902
/note="assembly_fragment"
133003..139176
/note="assembly_fragment"
139277..144517
/note="assembly_fragment"
144618..147983
/note="assembly_fragment"
148084..152287
/note="assembly_fragment"
152388..152948
/note="assembly_fragment"
BASE COUNT 42013 a 33863 c 34632 g 41440 t 1000 others
ORIGIN

```

```

AC015518/1
LOCUS       AC015518
DEFINITION  Homo sapiens clone RP11-22P3, DNA linear HTG 26-NOV-2000
ACCESSION   AC015518
VERSION     AC015518.3 GI:11345004
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 73992)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-22P3
Unpublished
2 (bases 1 to 73992)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Balwin,J., Barna,N., Beckerly,R., Bogustavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Gatagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,K., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 26, 2000 this sequence version replaced gi:9124480.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4159
Center clone name: 22_P_3
-----
* NOTE: This record contains 92 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 680: contig of 680 bp in length
781 780: gap of 100 bp
1450 1449: contig of 669 bp in length
1550 2241: contig of 692 bp in length
2242 2341: gap of 100 bp
2342 3051: contig of 710 bp in length
3052 3151: gap of 100 bp
3152 3863: contig of 712 bp in length
3864 3963: gap of 100 bp
3964 4678: contig of 715 bp in length
4679 4778: gap of 100 bp
4779 5508: contig of 730 bp in length
5509 5608: gap of 100 bp
5609 6332: contig of 724 bp in length
6333 6432: gap of 100 bp
6433 7152: contig of 720 bp in length
7153 7252: gap of 100 bp
7253 7933: contig of 681 bp in length
7934 8033: gap of 100 bp
8034 8713: contig of 680 bp in length
8714 8813: gap of 100 bp
8814 9508: contig of 695 bp in length
9509 9608: gap of 100 bp
9609 10316: contig of 708 bp in length
10317 10416: gap of 100 bp
10417 11114: contig of 698 bp in length
11115 11214: gap of 100 bp
11215 11924: contig of 710 bp in length
11925 12024: gap of 100 bp
12025 12730: contig of 706 bp in length
12731 12830: gap of 100 bp
12831 13540: contig of 710 bp in length
13541 13640: gap of 100 bp
13641 14353: contig of 713 bp in length
14354 14453: gap of 100 bp
14454 15168: contig of 715 bp in length
15169 15268: gap of 100 bp
15269 15977: contig of 709 bp in length
15978 16077: gap of 100 bp
16078 16801: contig of 724 bp in length
16802 16901: gap of 100 bp
16902 17590: contig of 689 bp in length
17591 17690: gap of 100 bp
17691 18374: contig of 684 bp in length
18375 18474: gap of 100 bp
18475 19166: contig of 692 bp in length
19167 19266: gap of 100 bp
19267 19980: contig of 714 bp in length
19981 20080: gap of 100 bp
20081 20764: contig of 684 bp in length
20765 20864: gap of 100 bp
20865 21550: contig of 686 bp in length
21551 21650: gap of 100 bp
21651 22359: contig of 709 bp in length
22360 22459: gap of 100 bp
22460 23193: contig of 734 bp in length
23194 23293: gap of 100 bp
23294 24016: contig of 723 bp in length
24017 24116: gap of 100 bp
24117 24823: contig of 707 bp in length
24824 24923: gap of 100 bp
24924 25640: contig of 717 bp in length
25641 25740: gap of 100 bp
25741 26460: contig of 720 bp in length
26461 26560: gap of 100 bp
26561 27245: contig of 685 bp in length
27246 27345: gap of 100 bp
27346 27980: contig of 635 bp in length
27981 28080: gap of 100 bp
28081 28764: contig of 684 bp in length
28765 28864: gap of 100 bp
28865 29574: contig of 710 bp in length
29575 29674: gap of 100 bp
29675 30372: contig of 698 bp in length
30373 30472: gap of 100 bp
30473 31177: contig of 705 bp in length
31178 31277: gap of 100 bp
31278 32026: contig of 749 bp in length
32027 32126: gap of 100 bp
32127 32848: contig of 722 bp in length
32849 32948: gap of 100 bp
32949 33667: contig of 719 bp in length
33668 33767: gap of 100 bp
33768 34468: contig of 701 bp in length
34469 34568: gap of 100 bp
34569 35293: contig of 725 bp in length
35294 35393: gap of 100 bp
35394 36079: contig of 686 bp in length
36080 36179: gap of 100 bp

```

* 36180 36879: contig of 700 bp in length
* 36880 36979: gap of 100 bp
* 37680 37686: contig of 707 bp in length
* 37687 37786: gap of 100 bp
* 37787 38495: contig of 709 bp in length
* 38496 38595: gap of 100 bp
* 38596 39302: contig of 707 bp in length
* 39303 39402: gap of 100 bp
* 39403 40094: contig of 692 bp in length
* 40095 40194: gap of 100 bp
* 40195 40891: contig of 697 bp in length
* 40892 40991: gap of 100 bp
* 40992 41697: contig of 706 bp in length
* 41698 41797: gap of 100 bp
* 41798 42509: contig of 712 bp in length
* 42510 42609: gap of 100 bp
* 42610 43323: contig of 714 bp in length
* 43324 43423: gap of 100 bp
* 43424 44141: contig of 718 bp in length
* 44142 44241: gap of 100 bp
* 44242 44957: contig of 716 bp in length
* 44958 45057: gap of 100 bp
* 45058 45748: contig of 691 bp in length
* 45749 45848: gap of 100 bp
* 45849 46554: contig of 706 bp in length
* 46555 46654: gap of 100 bp
* 46655 47354: contig of 700 bp in length
* 47355 47454: gap of 100 bp
* 47455 48154: contig of 700 bp in length
* 48155 48254: gap of 100 bp
* 48255 48958: contig of 704 bp in length
* 48959 49058: gap of 100 bp
* 49059 49762: contig of 704 bp in length
* 49763 49862: gap of 100 bp
* 49863 50580: contig of 718 bp in length
* 50581 50680: gap of 100 bp
* 50681 51403: contig of 723 bp in length
* 51404 51503: gap of 100 bp
* 51504 52212: contig of 709 bp in length
* 52213 52312: gap of 100 bp
* 52313 53008: contig of 696 bp in length
* 53009 53108: gap of 100 bp
* 53109 53795: contig of 687 bp in length
* 53796 53895: gap of 100 bp
* 53896 54588: contig of 693 bp in length
* 54589 54688: gap of 100 bp
* 54689 55392: contig of 704 bp in length
* 55393 55492: gap of 100 bp
* 55493 56201: contig of 709 bp in length
* 56202 56301: gap of 100 bp
* 56302 57009: contig of 708 bp in length
* 57010 57109: gap of 100 bp
* 57110 57801: contig of 692 bp in length
* 57802 57901: gap of 100 bp
* 57902 58603: contig of 702 bp in length

Query Match 82.5%; Score 19.8; DB 2; Length 73992;

Best Local Similarity 91.3%; Pred. No. 72;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcattgacgagtttcttct 24
|||||
Db 32608 ATCTTCATGGCACCTTTCCTCT 32586

RESULT 4

AC008464

LOCUS

DEFINITION

AC008464

21 unordered pieces.

ACCESSION

AC008464.5

VERSION

HTG; HTGS_PHASE1; HTGS_DRAFT.

124758 bp DNA linear HTG 21-JUN-2000
Homo sapiens chromosome 5 clone CTC-353G13, WORKING DRAFT SEQUENCE,
HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 124758)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
DOE Joint Genome Institute.
2 (bases 1 to 124758)
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 21, 2000 this sequence version replaced gi:7708881.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 320887, H318
Center clone name: CIT-HSPC_353G13

Summary Statistics
Consensus quality: 95334 bases at least Q40
Consensus quality: 111998 bases at least Q30
Consensus quality: 116380 bases at least Q20
Estimated insert size: 139000; pulse field gel estimation
Estimated insert size: 129758; sum-of-contigs estimation
Quality coverage: 3.95 in Q20 bases; pulse field gel estimation.
Quality coverage: 4.48 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1255: contig of 1255 bp in length
1256: gap of unknown length
1356: contig of 1095 bp in length
2451: gap of unknown length
2551: contig of 1209 bp in length
3760: gap of unknown length
3860: contig of 1194 bp in length
5054: gap of unknown length
5154: contig of 1282 bp in length
6436: gap of unknown length
6536: contig of 2386 bp in length
8921: gap of unknown length
9022: contig of 2768 bp in length
11789: gap of unknown length
11890: contig of 3213 bp in length
15103: gap of unknown length
15203: contig of 3354 bp in length
18557: gap of unknown length
18657: contig of 4263 bp in length
22920: gap of unknown length
23020: contig of 3316 bp in length
26336: gap of unknown length
26436: contig of 6950 bp in length
33386: gap of unknown length
33486: contig of 7543 bp in length
41029: gap of unknown length
41129: contig of 5898 bp in length
47027: gap of unknown length
47127: contig of 6309 bp in length
53436: gap of unknown length
53536: contig of 2352 bp in length
55888: gap of unknown length
55988: contig of 15592 bp in length
71580: gap of unknown length


```

repeat_region /note="<30 qual SNGL region"
repeat_region /rpt_family="AT_rich"
repeat_region /rpt_family="L2"
repeat_region complement(16789..16908)
repeat_region /rpt_family="L2"
repeat_region 17386..18185
repeat_region /rpt_family="MER63C"
repeat_region 18446..18980
repeat_region /rpt_family="MLT1D"
repeat_region 19332..20129
repeat_region /rpt_family="MIR"
repeat_region complement(20187..20307)
repeat_region /rpt_family="MIR"
repeat_region 20318..20460
repeat_region /rpt_family="MER5A"
repeat_region 21019..21144
repeat_region /rpt_family="MIR"
repeat_region complement(21154..21364)
repeat_region /rpt_family="MER58A"
repeat_region complement(21723..21982)
repeat_region /rpt_family="MIR"
repeat_region 22720..22753
repeat_region /rpt_family="(CA)n"
repeat_region 22843..22869
repeat_region /rpt_family="(GAAA)n"
repeat_region complement(22910..22958)
repeat_region /rpt_family="MIR"
repeat_region complement(23319..23697)
repeat_region /rpt_family="MLT1B"
repeat_region complement(23705..23865)
repeat_region /rpt_family="MIR"
repeat_region 24597..25037
repeat_region /rpt_family="L1ME4A"
repeat_region 25227..25269
repeat_region /rpt_family="AT_rich"
repeat_region complement(26596..26745)
repeat_region /rpt_family="MER117"
repeat_region 27214..27236
repeat_region /rpt_family="(GA)n"
repeat_region 27297..27478
repeat_region /rpt_family="MIR"
repeat_region complement(28096..28255)
repeat_region /rpt_family="MER5B"
repeat_region complement(29315..29490)
repeat_region /rpt_family="MER53"
repeat_region 29632..29677
repeat_region /rpt_family="L2"
repeat_region 30128..30165
repeat_region /rpt_family="(CA)n"
repeat_region complement(30506..30579)
repeat_region /rpt_family="MIR"
repeat_region 31588..31677
repeat_region /rpt_family="MIR"
repeat_region 32021..32177
repeat_region /rpt_family="MIR"
repeat_region 32178..32538
repeat_region /rpt_family="THE1B"
repeat_region 32539..32657
repeat_region /rpt_family="MIR"
repeat_region complement(32663..32809)
repeat_region /rpt_family="L2"
repeat_region complement(33697..34051)
repeat_region /rpt_family="THE1B"
repeat_region complement(35133..35383)
repeat_region /rpt_family="MLT1A1"
repeat_region 35384..35672
repeat_region /rpt_family="AluX"
repeat_region 35672..35676
repeat_region /note="<30 qual SNGL region"
repeat_region complement(35673..35796)
repeat_region /rpt_family="MLT1A1"

```

```

repeat_region complement(35812..36064)
repeat_region /rpt_family="AluY"
repeat_region 36547..36683
repeat_region /rpt_family="MIR"
repeat_region complement(37757..37841)
repeat_region /rpt_family="MIR"
repeat_region complement(37864..37923)
repeat_region /rpt_family="MIR3"
repeat_region complement(38144..38429)
repeat_region /rpt_family="AluX"

Query Match      82.5%; Score 19.8; DB 9; Length 140009;
Best Local Similarity 91.3%; Pred No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcattggcagttttgtctct 24
|||||
Db 26629 ATCTTCATGGCACATTTCTCTCT 26651

RESULT 6
AC008705/c
LOCUS AC008705 159709 bp DNA linear PRI 18-DEC-2001
DEFINITION Homo sapiens chromosome 5 clone CTB-77H17, complete sequence.
ACCESSION AC008705
VERSION AC008705.6 GI:17921194
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 159709)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159709)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 159709)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 159709)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 18, 2001 this sequence version replaced gi:15799574.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.

FEATURES
source
1..159709
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTB-77H17"

BASE COUNT 46361 a 34053 c 32796 g 46499 t
ORIGIN

Query Match      82.5%; Score 19.8; DB 9; Length 159709;
Best Local Similarity 91.3%; Pred No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcattggcagttttgtctct 24
|||||

```

Db 151639 ATGTTTCATGCAGGTTTGCTTCT 151617

RESULT 7

AC026321

LOCUS

DEFINITION

AC026321 163283 bp DNA linear HTG 05-OCT-2001
Homo sapiens chromosome 3 clone RP11-26K1, WORKING DRAFT SEQUENCE,
12 unordered pieces.

ACCESSION

AC026321.8 GI:15741283

VERSION

HTG; HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 163283)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaralunga, H.C., Are, J.R., Banks, T., Barbaria, J.,

Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J.,

Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,

Burck, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,

Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,

Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,

Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,

Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,

Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,

Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,

Elhaj, C., Escoto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,

Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,

Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,

Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,

Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,

Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,

Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,

Joudah, S., Kratison, E., Kelly, S., Khan, U., King, L., Korvah, J.,

Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,

Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,

Loulsegh, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,

Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,

Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,

Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,

Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,

Nguyen, A., Nguyen, S., Nguyen, N., Nickerson, E., Nwokweto, S.,

Ogih, M., Okuwonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,

Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,

Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M.,

Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N.,

Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,

Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,

Tang, H., Tansey, J., Taylor, C., Taylor, P., Telford, B., Thomas, N.,

Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R.,

Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,

Watlington, S., Williams, G., Williamson, A., Wleczky, R., Wooden, S.,

Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,

Weinstock, G. and Gibbs, R.

Direct Submission

Unpublished

2 (bases 1 to 163283)

Worley, K.C.

Direct Submission

Submitted (22-MAR-2000) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Sep 25, 2001 this sequence version replaced gi:9966567.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: hgsc-help@bcm.tmc.edu

----- project information

Center project name: HAPR

Center clone name: RP11-26K1

----- Summary Statistics

Sequencing vector: M13: L08821
Chemistry: Dye-terminator Big Dye: 83% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 145707 bases at least Q40
Consensus quality: 155746 bases at least Q30
Consensus quality: 159150 bases at least Q20
Estimated insert size: 160720; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 4.2x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1 35745: contig of 35745 bp in length
* 35746 35845: gap of unknown length
* 35846 61648: contig of 25803 bp in length
* 61649 61748: gap of unknown length
* 61749 88812: contig of 27064 bp in length
* 88813 88912: gap of unknown length
* 88913 103528: contig of 14616 bp in length
* 103529 103628: gap of unknown length
* 103629 118839: contig of 15211 bp in length
* 118840 118939: gap of unknown length
* 118940 130598: contig of 11659 bp in length
* 130599 130698: gap of unknown length
* 130699 141004: contig of 10306 bp in length
* 141005 141104: gap of unknown length
* 141105 147790: contig of 6686 bp in length
* 147791 147890: gap of unknown length
* 147891 152770: contig of 4780 bp in length
* 152771 152770: gap of unknown length
* 152771 157138: contig of 4368 bp in length
* 157139 157238: gap of unknown length
* 157239 160268: contig of 3030 bp in length
* 160269 160368: gap of unknown length
* 160369 163283: contig of 2915 bp in length.

FEATURES
source

1..163283
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"

BASE COUNT 50282 a 31786 c 32976 g 47106 t 1133 others
ORIGIN

Query Match 82.5%; Score 19.8; DB 2; Length 163283;
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catcttcagtcagctttgtcttc 23

||||| ||||||| ||||||| |||||||

Db 75829 CATCATCGGCAGTTCCTTC 75851

RESULT 8

AC008134

LOCUS

DEFINITION

AC008134 AC008134 175132 bp DNA linear PRI 01-DEC-2001
Homo sapiens 3q26.2-27 BAC RPC11-263C16 (Roswell Park Cancer

Institute Human BAC Library) complete sequence.

ACCESSION

AC008134

VERSION

AC008134.3 GI:5801655

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175132)
Muzny,D.M., Adams,C., Aronson,A., Bailey,M., Barbara,J., Buhay,C., Blankenburg,K., Bodota,B., Bouck,J., Bowie,S., Brooks,A., Chacko,J., Chen,Z., Bunac,C., Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C., David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N., Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Frantz,P., Ganesh,R., Garcia,D.K., Gorrell,J.H., Gorrell,L.L., Guevara,W., Harris,K., He,X., Hernandez,J., Hodgson,A., Hoques,M., Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O., Lu,J., Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Meli,G., Moore,S., Moorish,T., Morgan,M., Morris,S., Nash,S., Nelson,A., Nguyen,B., Nguyen,N., Nguyen,S., Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L., Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S., Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sugang,R., Tabot,P., Taylor,T., Vasquez,L., Vinson,R., Vo,O., Wabwah,M., Watlington,S., Weinstein,G., Weinstein,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Naylor,S.L. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 175132)
Worley,K.C.
Direct Submission
Submitted (25-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 175132)
Worley,K.C.
Direct Submission
Submitted (28-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 175132)
Worley,K.C.
Direct Submission
Submitted (01-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 175132)
Worley,K.C.
Direct Submission
Submitted (01-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Aug 28, 1999 this sequence version replaced gi:5764701.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished,) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

----- Summary Statistics -----
Contig length: 175132
Phrap values in estimate: 172880
Average error rate (BCM-Phrap estimate): 0.000229977
Fraction of Phrap values less than 40 : 0.0260585
Number of consensus changing edits: 15
Number of N's in consensus : 0

----- Consensus changing edits -----
Position Original+Context Edited+Context
43389 gtctaattga(n)actttgtacc gtctaattga(a)actttgtacc
47062 gatctgccg(n)ctcgcccttc gatctgccg(c)ctcgcccttc
64597 atctcgtac(a)aatcaacccc atctcgtac(c)aaagcaaccc
64700 tccgtacaaa(t)gcacccctgt tccgtacaaa(a)gcacccctgt
76432 tcaataatt(n)atttttaagt tcaataatt(t)atttttaagt
89673 aatgtctatt(n)tcaaaaagcc aatgtctatt(t)tcaaaaagcc
89706 gggtgtttat(n)taagatgcaa gggtgtttat(t)taagatgcaa
96986 ttgaccttt(n)atacctgttt ttgaccttt(t)atacctgttt
11902 taaaaaaaa(n)aaaaaaggaa taaaaaaaa(a)aaaaaaggaa
141888 aaagaataa(n)aagaatacaaa aaagaataa(a)aagaatacaaa
149374 aattacta(n)attggctgctt aattacta(c)attggctgctt
151541 gttaacttc(n)tttttttttt gttaacttc(c)tttttttttt
152439 tcagttcttc(c)ccattaaagta tcagttcttc(a)ccattaaagta
153782 aaaaaaaa(n)gatacactta aaaaaaaa(a)gatacactta
153786 aaaaaangat(n)cacttacata aaaaaangat(a)cacttacata

----- Distribution of Quality < 40 Bases -----
1000| * * * * *
900| * * * * *
800| * * * * *
700| * * * * *
600| * * * * *
500| * * * * *
400| * * * * *
300| * * * * *
200| * * * * *
100| * * * * *
0| * * * * *
5 10 15 20 25 30 35 40
Phrap Value Range

Version: 1.01 qxfo.
FEATURES
source Location/Qualifiers
1..175132
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3q26.2-27"
/clones="RPC111-263C16"
complement(1..2014)
misc_feature
/note="overlaps bases 1..2014 of clone AC092919"
/function="clone overlap"


```

repeat_region complement(187..492)
repeat_region /rpt_family="AluJo"
665..829
/rpt_family="MIR"
repeat_region 1042..1189
/rpt_family="L1MB4"
repeat_region complement(1190..1475)
1476..1547
/rpt_family="AluJb"
repeat_region /rpt_family="L1MB4"
1769..1817
/rpt_family="(TA)n"
repeat_region complement(2108..2753)
/rpt_family="L2"
repeat_region complement(2820..3551)
3626..3650
/rpt_family="L2"
repeat_region /rpt_family="AT-rich"
3874..4094
/rpt_family="L1MC4"
repeat_region 4111..4245
/rpt_family="MER20"
repeat_region 4250..4616
/rpt_family="MSTA"
repeat_region 4624..4710
/rpt_family="MER20"
repeat_region complement(5062..5109)
/rpt_family="MIR"
repeat_region complement(5187..5498)
/rpt_family="AluSp"
repeat_region complement(5530..5663)
/rpt_family="L2"
repeat_region complement(5972..6147)
/rpt_family="MER5A"
repeat_region 6997..7133
/rpt_family="FLAM_C"
repeat_region 7463..7500
/rpt_family="(TCTA)n"
repeat_region complement(9036..9342)
/rpt_family="AluSp"
repeat_region complement(9464..9695)
/rpt_family="MIR"
repeat_region complement(11255..11314)
/rpt_family="MER5B"
repeat_region 11653..11682
/rpt_family="(TA)n"

Query Match 82.5% Score 19.8; DB 9; Length 175132;
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catcttcagtcagtttgcctc 23
|||||
Db 111192 CATCATCATGGCAGTTTCGCTTC 111214

RESULT 9
AC019265
LOCUS Homo sapiens clone RP11-6N20, WORKING DRAFT SEQUENCE, 2 ordered
DEFINITION pieces
AC019265
VERSION AC019265.4 GI:11079354
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 178328)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-6N20
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 178328)

AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Domino,M., Doyle,M., Fenesstor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneses,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT
Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141 USA
On Nov 3, 2000 this sequence version replaced gl:7239535.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBK
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2911
Center clone name: 6_N_20
----- Summary Statistics
Sequencing vector: M13; M7815; 45% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 177609 bases at least Q40
Consensus quality: 177915 bases at least Q30
Consensus quality: 178053 bases at least Q20
Insert size: 165000; agarose-fp
Insert size: 178228; sum-of-contigs
Quality coverage: 11.2 in Q20 bases; agarose-fp
Quality coverage: 10.4 in Q20 b.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 96718: contig of 96718 bp in length
* 96719 96818: gap of 100 bp
* 96819 178328: contig of 81510 bp in length.
FEATURES
source
1..178328
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-6N20"
/clone_lib="RPCI-11 Human Male BAC"
1..96718
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
96819..178328
/note="assembly_fragment"
clone_end:T7
vector_side:right"
misc_feature
54890 a 35740 c 33735 g 53863 t 100 others
BASE COUNT
ORIGIN

```

```

Query Match      82.5%; Score 19.8; DB 2; Length 178328;
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catcttcaggcaggttttgccttc 23
||||| ||||||| ||||||| |||||||
Db 55871 CATCATCGGCAGTTCGCTTC 55893

RESULT 10
AC092971 AC092971 179375 bp DNA linear HTG 09-AUG-2001
LOCUS Homo sapiens chromosome 3q clone RP11-6N20, WORKING DRAFT SEQUENCE,
DEFINITION 3 unordered pieces.
ACCESSION AC092971 GI:15136598
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 179375)
AUTHORS Muray,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Blinage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowtie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhey,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Ieal,B., Lewis,L.C.,
Lewis,B., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,B., Liu,W.,
Louisgied,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogulu,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoostari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,R., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 179375)
Worley,K.C.
Direct Submission
Submitted (09-AUG-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM

```

```

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HDCT
Center clone name: RP11-6N20
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 179232 bases at least Q40
Consensus quality: 180406 bases at least Q30
Consensus quality: 181319 bases at least Q20
Estimated insert size: 178906; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved
*
* 1 81511: contig of 81511 bp in length
* 81512 81611: gap of unknown length
* 81612 149467: contig of 67856 bp in length
* 149468 149567: gap of unknown length
* 149568 179375: contig of 29808 bp in length.
FEATURES             Location/Qualifiers
     source            1..179375
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="3q"
                     /clone="RP11-6N20"
BASE COUNT  55185 a 35941 c 33923 g 54126 t 200 others
ORIGIN
Query Match      82.5%; Score 19.8; DB 2; Length 179375;
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catcttcaggcaggttttgccttc 23
||||| ||||||| ||||||| |||||||
Db 108605 CATCATCGGCAGTTCGCTTC 108627

RESULT 11
AL589696
LOCUS Mus musculus chromosome 15 clone RP23-454M13, *** SEQUENCING IN
DEFINITION PROGRESS ***, in ordered pieces.
ACCESSION AL589696
VERSION AL589696.8 GI:18375812
KEYWORDS HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Dunn,M.
Direct Submission
Submitted (17-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 25, 2002 this sequence version replaced gi:16944949.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information

```

Center project name: bm454M13
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 207161 bases at least Q40
Consensus quality: 207332 bases at least Q30
Consensus quality: 207385 bases at least Q20
Insert size: 207415; sum-of-ctnigs
Insert size: 201201; 5.9% error; agarose-fp
Quality coverage: 12.54% in Q20 bases; sum-of-ctnigs Quality
coverage: 12.99% in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
1..207415
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="15"
/clone="RP23-454M13"
/clone_lib="RPCI-23"
misc_feature
1..207415
/note="assembly_fragment:04323
clone_end:SP6
vector_side:right
clone_end:T7
vector_side:left"
BASE COUNT 65722 a 42071 c 39838 g 59784 t
ORIGIN

Query Match 82.5%; Score 19.8; DB 2; Length 207415;
Best Local Similarity 91.3%; Pred. No. 69;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcagtcagcttttgccttc 24
||||| ||||||| |||||
Db 106803 ATCTTCATGTCAGCTTTTCCCTCT 106825

RESULT 12
AC109337
LOCUS AC109337 64742 bp DNA linear HTG 03-FEB-2002
DEFINITION Homo sapiens chromosome 15 clone RP11-62303 map 15, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC109337
VERSION AC109337.1 GI:18482270
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 64742)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Unpublished
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 64742)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepl,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T.,

Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Reta.R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L24566
Center clone name: 623_O_3

* NOTE: This record contains 81 individual
* sequencing reads that have not been assembled into
* ctnigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1
* 704 803: contig of 703 bp in length
* 804 1511: contig of 708 bp in length
* 1512 1611: gap of 100 bp
* 1612 2320: contig of 709 bp in length
* 2321 2420: gap of 100 bp
* 2421 3113: contig of 693 bp in length
* 3114 3213: gap of 100 bp
* 3214 3991: contig of 778 bp in length
* 3992 4091: gap of 100 bp
* 4092 4811: contig of 720 bp in length
* 4812 4911: gap of 100 bp
* 4912 5609: contig of 698 bp in length
* 5610 5709: gap of 100 bp
* 5710 6395: contig of 686 bp in length
* 6396 6495: gap of 100 bp
* 6496 7198: contig of 703 bp in length
* 7199 7298: gap of 100 bp
* 7299 8006: contig of 708 bp in length
* 8007 8106: gap of 100 bp
* 8107 8799: contig of 693 bp in length
* 8800 8899: gap of 100 bp
* 8900 9606: contig of 707 bp in length
* 9607 9706: gap of 100 bp
* 9707 10407: contig of 701 bp in length
* 10408 10507: gap of 100 bp
* 10508 11207: contig of 700 bp in length
* 11208 11307: gap of 100 bp
* 11308 12001: contig of 694 bp in length
* 12002 12101: gap of 100 bp
* 12102 12789: contig of 688 bp in length
* 12790 12889: gap of 100 bp
* 12890 13594: contig of 705 bp in length
* 13595 13694: gap of 100 bp
* 13695 14372: contig of 678 bp in length
* 14373 14472: gap of 100 bp
* 14473 15167: contig of 695 bp in length

```
* 15168 15267: gap of 100 bp
* 15268 15954: contig of 687 bp in length
* 15955 16054: gap of 100 bp
* 16055 16736: contig of 682 bp in length
* 16737 16836: gap of 100 bp
* 16837 17534: contig of 698 bp in length
* 17535 17634: gap of 100 bp
* 17635 18342: contig of 708 bp in length
* 18343 18442: gap of 100 bp
* 18443 19148: contig of 706 bp in length
* 19149 19248: gap of 100 bp
* 19249 19958: contig of 710 bp in length
* 19959 20058: gap of 100 bp
* 20059 20796: contig of 738 bp in length
* 20797 20896: gap of 100 bp
* 20897 21594: contig of 698 bp in length
* 21595 21694: gap of 100 bp
* 21695 22406: contig of 712 bp in length
* 22407 22506: gap of 100 bp
* 22507 23207: contig of 701 bp in length
* 23208 23307: gap of 100 bp
* 23308 24003: contig of 696 bp in length
* 24004 24103: gap of 100 bp
* 24104 24814: contig of 711 bp in length
* 24815 24914: gap of 100 bp
* 24915 25614: contig of 700 bp in length
* 25615 25714: gap of 100 bp
* 25715 26426: contig of 712 bp in length
* 26427 26526: gap of 100 bp
* 26527 27230: contig of 704 bp in length
* 27231 27330: gap of 100 bp
* 27331 28027: contig of 697 bp in length
* 28028 28127: gap of 100 bp
* 28128 28819: contig of 692 bp in length
* 28820 28919: gap of 100 bp
* 28920 29614: contig of 695 bp in length
* 29615 29714: gap of 100 bp
* 29715 30403: contig of 689 bp in length
* 30404 30503: gap of 100 bp
* 30504 31201: contig of 698 bp in length
* 31202 31301: gap of 100 bp
* 31302 31983: contig of 682 bp in length
* 31984 32083: gap of 100 bp
* 32084 32772: contig of 689 bp in length
* 32773 32872: gap of 100 bp
* 32873 33575: contig of 703 bp in length
* 33576 33675: gap of 100 bp
* 33676 34394: contig of 719 bp in length
* 34395 34494: gap of 100 bp
* 34495 35200: contig of 706 bp in length
* 35201 35300: gap of 100 bp
* 35301 36015: contig of 715 bp in length
* 36016 36115: gap of 100 bp
* 36116 36819: contig of 704 bp in length
* 36820 36919: gap of 100 bp
* 36920 37544: contig of 625 bp in length
* 37545 37644: gap of 100 bp
* 37645 38295: contig of 651 bp in length
* 38296 38395: gap of 100 bp
* 38396 39095: contig of 700 bp in length
* 39096 39195: gap of 100 bp
* 39196 39964: contig of 769 bp in length
* 39965 40064: gap of 100 bp
* 40065 40766: contig of 702 bp in length
* 40767 40866: gap of 100 bp
* 40867 41570: contig of 704 bp in length
* 41571 41670: gap of 100 bp
* 41671 42376: contig of 706 bp in length
* 42377 42476: gap of 100 bp
* 42477 43184: contig of 708 bp in length
* 43185 43284: gap of 100 bp
* 43285 43992: contig of 708 bp in length
* 43993 44092: gap of 100 bp
```

```
* 44093 44797: contig of 705 bp in length
* 44798 44897: gap of 100 bp
* 44898 45604: contig of 707 bp in length
* 45605 45704: gap of 100 bp
* 45705 46384: contig of 680 bp in length
* 46385 46484: gap of 100 bp
* 46485 47193: contig of 709 bp in length
* 47194 47293: gap of 100 bp
* 47294 47950: contig of 657 bp in length
* 47951 48050: gap of 100 bp
* 48051 48759: contig of 709 bp in length
* 48760 48859: gap of 100 bp
* 48860 49544: contig of 685 bp in length
* 49545 49644: gap of 100 bp
* 49645 50348: contig of 704 bp in length
* 50349 50448: gap of 100 bp
* 50449 51140: contig of 692 bp in length
* 51141 51240: gap of 100 bp
* 51241 51943: contig of 703 bp in length
* 51944 52043: gap of 100 bp
* 52044 52726: contig of 683 bp in length
* 52727 52826: gap of 100 bp
* 52827 53534: contig of 708 bp in length
* 53535 53634: gap of 100 bp
* 53635 54347: contig of 713 bp in length
* 54348 54447: gap of 100 bp
* 54448 55156: contig of 709 bp in length

Query Match      80.8%  Score 19.4;  DB 2;  Length 64742;
Best Local Similarity 95.2%  Pred. No. 1.1e+02;
Matches 20;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
```

```
QY 3 tcttcattggcagtttcttc 23
|||
Db 30754 TCATCATGGCAGTTTGCTTC 30774
```

```
RESULT 13
AC092306
```

```
LOCUS Homo sapiens chromosome 19 clone LLNLR-231D4, WORKING DRAFT
DEFINITION AC092306 72628 bp DNA linear HTG 03-JUL-2001
SEQUENCE, 29 unordered pieces.
```

```
ACCESSION AC092306
VERSION AC092306.1 GI:14589495
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFTN.
SOURCE human.
ORGANISM Homo sapiens
```

```
REFERENCE 1 (bases 1 to 72628)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 19
JOURNAL Unpublished
```

```
REFERENCE 2 (bases 1 to 72628)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
```

```
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 22390, R27120
Center clone name: LLNL-R_231D4
-----
Summary Statistics
Consensus quality: 50309 bases at least Q40
Consensus quality: 61253 bases at least Q30
Consensus quality: 63234 bases at least Q20
Estimated insert size: 40040; agarose-fp estimation
Estimated insert size: 69828; sum-of-contigs estimation
```


repeat_region /note="L1M1 repeat: matches 1389. .1590 of consensus"
repeat_region /note="L1M1 repeat: matches 1868. .2541 of consensus"
repeat_region /note="L1PA4 repeat: matches 5862. .6146 of consensus"
repeat_region /note="L1M1 repeat: matches 958. .1869 of consensus"
misc_feature /note="match: GSS: Em:AQ767211"
misc_feature complement(12619. .13196)
misc_feature /note="match: GSS: Em:B69623"
misc_feature complement(12739. .13190)
misc_feature /note="match: GSS: Em:AQ270964"
misc_feature complement(13127. .13629)
misc_feature /note="match: GSS: Em:AQ187800"
misc_feature /note="match: GSS: Em:AQ420261"
misc_feature 13637. .14075
misc_feature /note="match: GSS: Em:AQ407983"
misc_feature 13652. .14060
misc_feature /note="match: GSS: Em:AQ403809"
misc_feature complement(15664. .16024)
misc_feature /note="match: GSS: Em:AQ043704"
misc_feature complement(16006. .16524)
misc_feature /note="match: GSS: Em:AQ695438"
misc_feature complement(16090. .16493)
misc_feature /note="match: GSS: Em:AQ776673"
repeat_region 16833. .17237
repeat_region /note="L1M2 repeat: matches 5555. .5934 of consensus"
repeat_region 17546. .19508
misc_feature /note="L1M2 repeat: matches 3547. .5555 of consensus"
misc_feature complement(19331. .19799)
repeat_region /note="match: GSS: Em:AQ695800"
repeat_region 19680. .19934
repeat_region /note="L1M5 repeat: matches 7273. .7523 of consensus"
repeat_region 19935. .20246
repeat_region /note="L1M5 repeat: matches 1. .309 of consensus"
repeat_region 20247. .20623
repeat_region /note="L1M5 repeat: matches 7523. .7913 of consensus"
repeat_region 20638. .20804
misc_feature /note="FRAM repeat: matches 1. .162 of consensus"
misc_feature complement(21615. .22036)
misc_feature /note="match: GSS: Em:AQ423530"
misc_feature 22090. .22639
misc_feature /note="match: GSS: Em:AQ382070"
repeat_region 22099. .22507
repeat_region /note="match: GSS: Em:AQ412213"
repeat_region 22201. .22288
repeat_region /note="44 copies 2 mer aa 63% conserved"
repeat_region 22616. .24206
repeat_region /note="L1PA7 repeat: matches 4544. .6145 of consensus"
repeat_region 24383. .24695
repeat_region /note="L1M6 repeat: matches 5174. .5480 of consensus"
repeat_region 24701. .24738
repeat_region /note="19 copies 2 mer tg 100% conserved"
repeat_region 24796. .24958
misc_feature /note="MER63 repeat: matches 1. .789 of consensus"
misc_feature 26026. .26451
misc_feature /note="match: GSS: Em:AQ312975"
misc_feature 26047. .26517
repeat_region /note="match: GSS: Em:AQ428497"
repeat_region 30300. .30347
repeat_region /note="L1M6 repeat: matches 1. .46 of consensus"
repeat_region 30723. .30815
repeat_region /note="MER89 repeat: matches 5. .98 of consensus"
repeat_region 31055. .31155
repeat_region /note="MER89 repeat: matches 388. .490 of consensus"
repeat_region 31716. .31791
misc_feature /note="MER89 repeat: matches 474. .559 of consensus"
misc_feature complement(34341. .34846)
repeat_region /note="match: GSS: Em:AQ423311"
repeat_region 35950. .35985
repeat_region /note="18 copies 2 mer tc 94% conserved"

repeat_region 37953. .39151
repeat_region /note="L1M3 repeat: matches 6507. .7735 of consensus"
repeat_region 41925. .42085
repeat_region /note="L1PA16 repeat: matches 5999. .6157 of consensus"
repeat_region 42390. .42516
repeat_region /note="L1PA16 repeat: matches 5872. .5999 of consensus"
repeat_region 42534. .42713
misc_feature /note="Alus9/x repeat: matches 123. .302 of consensus"
misc_feature 43671. .44128
misc_feature /note="match: GSS: Em:AQ005776"
misc_feature 43703. .43840
repeat_region /note="match: GSS: Em:B34641"
repeat_region 43938. .44717
repeat_region /note="L1PA2 repeat: matches 2. .776 of consensus"
repeat_region 44713. .49953
repeat_region /note="L1PA2 repeat: matches 900. .6146 of consensus"
repeat_region 50213. .50462
repeat_region /note="MSTA repeat: matches 192. .426 of consensus"
repeat_region 50769. .50955
repeat_region /note="MSTA repeat: matches 1. .192 of consensus"
repeat_region 51555. .51626
repeat_region /note="MSTB repeat: matches 355. .426 of consensus"
repeat_region 52001. .52354
repeat_region /note="MSTB repeat: matches 1. .370 of consensus"
repeat_region 53067. .53239
repeat_region /note="MER5B repeat: matches 1. .178 of consensus"
repeat_region 54514. .54736
repeat_region /note="L1R16C repeat: matches 166. .387 of consensus"
repeat_region 56342. .56429
misc_feature /note="L1M1J repeat: matches 46. .182 of consensus"
repeat_region 57323. .57994
repeat_region /note="match: GSS: Em:AQ560111"
misc_feature 59147. .59180
misc_feature /note="17 copies 2 mer aa 94% conserved"
misc_feature 59847. .60120
misc_feature /note="match: GSS: Em:AQ040668"
repeat_region 60897. .61171
repeat_region /note="match: STS: Em:HSPF11E9"
repeat_region 61139. .61336
repeat_region /note="L1PB3 repeat: matches 5949. .6146 of consensus"
repeat_region 61856. .62275
repeat_region /note="L1M6 repeat: matches 5317. .5752 of consensus"
repeat_region 62742. .63019
misc_feature /note="L1M6 repeat: matches 5532. .5818 of consensus"
misc_feature complement(62900. .63417)
repeat_region /note="match: GSS: Em:AQ167031"
repeat_region 63136. .63432
repeat_region /note="L1M6 repeat: matches 5072. .5380 of consensus"
repeat_region 64545. .64712
misc_feature /note="84 copies 2 mer ta 58% conserved"
misc_feature complement(65036. .65356)
repeat_region /note="match: STS: Em:G08057"
repeat_region 65145. .65196
repeat_region /note="26 copies 2 mer ag 75% conserved"
repeat_region 65200. .65411
repeat_region /note="MLT2D repeat: matches 295. .514 of consensus"
repeat_region 65421. .65475
repeat_region /note="MERVL repeat: matches 3416. .3471 of consensus"
repeat_region 65461. .67498
repeat_region /note="HERVL repeat: matches 1375. .3438 of consensus"
repeat_region 68860. .68997
misc_feature /note="69 copies 2 mer tt 59% conserved"
misc_feature complement(69498. .69643)
repeat_region /note="match: GSS: Em:AQ678423"
repeat_region 70239. .70400
repeat_region /note="L1R16C repeat: matches 70. .235 of consensus"
repeat_region 70439. .70577
repeat_region /note="L1MB8 repeat: matches 6030. .6171 of consensus"
repeat_region 71763. .71936
repeat_region /note="MER5B repeat: matches 13. .177 of consensus"

Query Match 80.8%; Score 19.4; DB 9; Length 125698;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;

Matches' 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ttttcattggcagttttgcttc 23
|| |||||
Db 84877 TCATCATGGCAGTTTGTCTTC 84897

RESULT 15

AC024600 147876 bp DNA linear PRI 24-AUG-2000
LOCUS Homo sapiens chromosome 10 clone RP11-179K3, complete sequence.
DEFINITION AC024600
ACCESSION AC024600
VERSION AC024600.4 GI:9887597
KEYWORDS HTG.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 147876)
AUTHORS Smith,D.R.

TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 147876)
AUTHORS Smith,D.R.

TITLE Direct Submission
JOURNAL Submitted (01-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
REFERENCE 3 (bases 1 to 147876)
AUTHORS Smith,D.R.

TITLE Direct Submission
JOURNAL Submitted (24-AUG-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
COMMENT On Aug 24, 2000 this sequence version replaced gi:8569065.

FEATURES
source
1. 147876
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-179K3"
/clone_lib="RPCI-11"
BASE COUNT 46967 a 25749 c 26005 g 49155 t
ORIGIN

Query Match 80.8%; Score 19.4; DB 9; Length 147876;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ttttcattggcagttttgcttc 23
|| |||||
Db 71619 TCATCATGGCAGTTTGTCTTC 71639

Search completed: August 21, 2002, 10:49:56
Job time: 9811 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 09:55:47 ; Search time 6260.2 Seconds
(without alignments) updates/sec
51.744 Million cell

Title: US-09-339-922A-105

Perfect score: 24

Sequence: 1 catcttcagtcagtttgcttct 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estl:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.4	85.0	855	12	CNS02E0S
2	19.8	82.5	313	9	AW256968
3	19.8	82.5	471	10	C84597
4	19.8	82.5	582	9	BE154166
5	19.8	82.5	597	9	AW686308
6	19.8	82.5	617	9	BE204884
7	19.8	82.5	626	10	BE999842
8	19.8	82.5	633	9	AW559550
9	19.8	82.5	645	10	BF642179
10	19.8	82.5	656	9	AW695027
11	19.8	82.5	663	9	AW692889
12	19.8	82.5	682	10	BG452255
13	19.2	80.0	241	10	BF378810
14	19.2	80.0	491	9	AW786151
15	19.2	80.0	536	10	BF191434
16	19.2	80.0	538	10	BF193498
17	19.2	80.0	610	12	AQ744319

18	19.2	80.0	653	12	AG073249
19	19.2	80.0	776	10	BG747830
20	19.2	80.0	1037	10	BM478125
21	18.8	78.3	452	10	BI820101
22	18.8	78.3	568	9	AW850973
23	18.8	78.3	587	12	AQ944218
24	18.8	78.3	600	12	AQ660116
25	18.8	78.3	716	12	AZ213382
26	18.8	78.3	722	12	AQ645036
27	18.8	78.3	724	10	BG426971
28	18.8	78.3	764	9	AL554662
29	18.8	78.3	813	10	BG707577
30	18.4	76.7	770	12	AG167827
31	18.2	75.8	153	12	AZ986091
32	18.2	75.8	198	10	BG508089
33	18.2	75.8	221	10	BF963803
34	18.2	75.8	407	12	AQ989925
35	18.2	75.8	442	10	BI797255
36	18.2	75.8	459	9	AU162173
37	18.2	75.8	465	10	BF425397
38	18.2	75.8	475	12	AQ246544
39	18.2	75.8	501	10	BF598453
40	18.2	75.8	517	12	BH340494
41	18.2	75.8	524	12	AQ322747
42	18.2	75.8	524	12	AQ348649
43	18.2	75.8	536	10	BI893110
44	18.2	75.8	536	10	BM178753
45	18.2	75.8	548	10	BM086100

ALIGNMENTS

RESULT 1

CNS02E0S

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CNS02E0S 855 bp DNA linear GSS 13-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
261K20 of library G from Tetraodon nigroviridis, genomic survey
sequence.

AL193141
AL193141.1 GI:7831245
GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases 1 to 855)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.

Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

Unpublished
2 (bases 1 to 855)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence

Unpublished
3 (bases 1 to 855)

Genoscope.
Direct Submission

Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.

Location/Qualifiers
1..855
/organism="Tetraodon nigroviridis"


```

/db_xref="taxon:99883"
/clone_lib="261K20"
/notes="Genoscope sequence ID : COAG261BF10SP1-end :
PUC-ori"
BASE COUNT 185 a 200 c 213 g 253 t 4 others
ORIGIN

Query Match
Best Local Similarity 85.0%; Score 20.4; DB 12; Length 855;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 tcttcattgcagtttgccttct 24
||||| ||||| ||||| ||||| |||||
Db 784 TCTTCATGCGAGTTTGCCTTT 805

RESULT 2
AW256968
LOCUS AW256968 313 bp mRNA linear EST 20-DEC-1999
DEFINITION EST305105 KV2 Medicago truncatula cDNA clone KV2-6B17, mRNA
sequence.
ACCESSION AW256968
VERSION AW256968.1 GI:6605225
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 313)
AUTHORS VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
TITLE ESTs from roots of Medicago truncatula after Rhizobium inoculation
JOURNAL Unpublished (1999)
COMMENT Contact: VandenBosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: kate@mail.bio.tamu.edu
Texas A&M EST name: T115673e
TIGR sequence name: MTAAK09TK
More information is available at: (and for clone ordering info)
http://chrystie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
FEATURES
source
Location/Qualifiers
1..313
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone_lib="KV2"
/tissue_type="KV2"
/dev_stage="2 days post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK-; Site1: EcoRI; Site2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-zap phage using
Ex-assist helper phage and propagated in SOLR cells."
BASE COUNT 88 a 62 c 70 g 93 t
ORIGIN

Query Match
82.5%; Score 19.8; DB 9; Length 313;

```

```

Best Local Similarity 91.3%; Pred. No. 2.5e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcattgcagtttgccttct 24
||||| ||||| ||||| ||||| |||||
Db 139 ATCTTCATGCGTGTTCCTTCT 161

RESULT 3
C84597/c
LOCUS C84597 471 bp mRNA linear EST 26-MAR-1999
DEFINITION C84597 osteoclast subtracted library Oryctolagus cuniculus cDNA,
mRNA sequence.
ACCESSION C84597
VERSION C84597.1 GI:4527857
KEYWORDS EST.
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 471)
AUTHORS Kobori,M., Ikeda,Y., Nara,H., Kato,M., Kumegawa,M., Nojima,H. and
Kawashima,H.
TITLE Large scale isolation of osteoclast-specific genes by an improved
method involving the preparation of a subtracted cDNA library
JOURNAL Genes Cells 3 (7), 459-475 (1998)
MEDLINE 98424349
COMMENT Contact: Kobori M
Molecular Medicine Laboratories
Institute for Drug Discovery Research, Yamanouchi Pharmaceutica
21, Miyukigaoka, Tsukuba, Ibaraki 305, Japan
Email: kobori@yamanouchi.co.jp
PROJECT = 'OSG'.
FEATURES
source
Location/Qualifiers
1..471
/organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
/clone_lib="osteoclast subtracted library"
/tissue_type="long bone"
/cell_type="osteoclast"
/cell_line="primary"
/dev_stage="5 day-old"
BASE COUNT 73 a 141 c 140 g 108 t 9 others
ORIGIN

Query Match
82.5%; Score 19.8; DB 10; Length 471;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catcttcattgcagtttgccttc 23
||||| ||||| ||||| ||||| |||||
Db 200 CTCTTCATGCGAGTTTGCCTTC 178

RESULT 4
BE154166
LOCUS BE154166 582 bp mRNA linear EST 21-JUN-2000
DEFINITION PM1-HT0340-201299-004-h02 HT0340 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE154166
VERSION BE154166.1 GI:8616887
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

```

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20022663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-PM1-HT0340-201
299-004-h02st3-1999-12-20et4-1)
Seq primer: puc 18 forward
High quality sequence stop: 582.

FEATURES

source
1. .582
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0340"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

192 a 130 c 107 g 153 t

BASE COUNT

ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 582;
Best Local Similarity 91.3%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcaggcagtttgccttct 24

|||||

Db 517 ATGTCATGCGAGTTTGCTTCT 539

RESULT 5

AW686308
LOCUS NF036D09NR1F1000 Nodulated root Medicago truncatula cDNA clone
DEFINITION NF036D09NR 5', mRNA sequence.

AW686308 597 bp mRNA linear EST 20-DEC-2000

AW686308 2 GI:11930962

VERSION EST.

KEYWORDS barrel medic.

SOURCE Medicago truncatula

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE 1 (bases 1 to 597)

AUTHORS Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May
,G.D. and Paiva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula nodulated root library
Unpublished (2000)

On Apr 14, 2000 this sequence version replaced gi:7561044.

CONTACT: Paiva NL

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7317

Fax: 580 221 7380

Email: nlpaiva@noble.org

Insert Length: 667 Std Error: 0.00
Plate: 036 row: D column: 09
Seq primer: TCACACAGAAACACCTATGAC.

FEATURES

source

1. .597
Location/Qualifiers

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF036D09NR"

/clone_lib="Nodulated root"

/tissue_type="root"

/dev_stage="Pooled developmental"

/note="Vector: Lambda Zap; Four-week old Rhizobium

meliloti-inoculated Medicago truncatula roots, containing

a mixture of young and old roots and nodules."

159 a 123 c 133 g 182 t

BASE COUNT

ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 597;

Best Local Similarity 91.3%; Pred. No. 3e+02;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcaggcagtttgccttct 24

|||||

Db 215 ATCTTCATCGCTGTGTGCTTCT 237

RESULT 6

BE204884

LOCUS EST397624 KV0 Medicago truncatula cDNA clone pKV0-18J18, mRNA

DEFINITION BE204884 617 bp mRNA linear EST 05-SEP-2000

ACCESSION BE204884

VERSION BE204884.1 GI:8748241

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

REFERENCE 1 (bases 1 to 617)

AUTHORS VandenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,

Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and

Fraser,C.M.

ESTs from uninoculated seedling roots of Medicago truncatula

Unpublished (1999)

Contact: VandenBosch K

Department of Biology

Texas A&M University

College Station, TX 77843-3258, USA

Tel: 409 845 7707

Fax: 409 845 2891

Email: kate@mail.bio.tamu.edu

Texas A&M University name:T264720e

TIGR sequence name:MTGBF57TK

More information is available at .

http://chrysis.tamu.edu/medicago

Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

Location/Qualifiers

1. .617

/organism="Medicago truncatula"

/cultivar="genotype A17"

/db_xref="taxon:3880"

/clone="pKV0-18J18"

/clone_lib="KV0"

/tissue_type="Seedling roots"

/dev_stage="Immediately prior to inoculation with

Sinorhizobium meliloti (0 hour)"

/lab_host="E.coli strain XL0LR"

/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:

XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA

was directionally ligated into the Unizap XR vector from

Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

BASE COUNT 187 a 144 c 125 g 161 t
ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 617;
Best Local Similarity 91.3%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcaggcagtttgccttct 24
||||||| || |||||||||
Db 417 ATCTTCATCGCTGTTTGTCTCT 439

RESULT 7
BE999842
LOCUS BE999842 626 bp mRNA linear EST 06-OCT-2000
DEFINITION EST431565 GVSN Medicago truncatula cDNA clone pGVSN-24B2, mRNA
sequence.
ACCESSION BE999842
VERSION BE999842.1 GI:10700118
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE 1 (bases 1 to 626)
AUTHORS Fedorova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P., Town
,C.D., Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M.
ESTs from senescent nodules of Medicago truncatula
Unpublished (2000)
CONTACT: Carroll P. Vance
DEPARTMENT OF AGRONOMY AND PLANT GENETICS
UNIVERSITY OF MINNESOTA
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058

Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M273820e TIGR sequence name:
MTKBJ010TK More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: Skmod (CTA gAA CTA gTg gAT CC).

Location/Qualifiers

FEATURES source

1. .626
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVSN-24B2"
/clone_lib="GVSN"
/tissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from the
mixture of effective nodules of 40 day old plants
harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage. The
cDNA was directionally ligated into the Uni-ZAP XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts were
excised from the recombinant lambda-ZAP phage using
Ex-Assist helper phage and propagated in SOLR cells."

BASE COUNT 183 a 153 c 122 g 168 t
ORIGIN

Query Match 82.5%; Score 19.8; DB 10; Length 626;
Best Local Similarity 91.3%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcaggcagtttgccttct 24
||||||| || |||||||||
Db 455 ATCTTCATCGCTGTTTGTCTCT 477

RESULT 8
AW559550
LOCUS AW559550 633 bp mRNA linear EST 07-SEP-2000
DEFINITION EST314598 DSIR Medicago truncatula cDNA clone pDSIR-24A9, mRNA
sequence.
ACCESSION AW559550
VERSION AW559550.1 GI:7204976
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE 1 (bases 1 to 633)
AUTHORS Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,J.S., Peng
,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
Holt,I.E. and Fraser,C.M.
ESTs from roots of Medicago truncatula after inoculation with
Phytophthora medicaginis
Unpublished (1999)
CONTACT: Carroll P. Vance
DEPARTMENT OF AGRONOMY AND PLANT GENETICS
UNIVERSITY OF MINNESOTA
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058

Email: vance004@maroon.tc.umn.edu
Minnesota Est name:M250836e ; TIGR sequence name:MTBAM05TK ; More
information, including clone ordering, is available at:
'http://chrysie.tamu.edu/medicago'
Seq primer: Skmod (CTA gAA CTA gTg gAT CC).

Location/Qualifiers

FEATURES source

1. .633
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSIR-24A9"
/clone_lib="DSIR"
/tissue_type="roots infected with Phytophthora
medicaginis"
/dev_stage="roots harvested at 10 days post inoculation
with Phytophthora medicaginis"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10 days post inoculation with
Phytophthora medicaginis. The cDNA was directionally
ligated into the Uni-ZAP XR vector from Stratagene and
packaged using Gigapack III Gold packaging extracts.
Plasmids containing cDNA inserts were excised from the
recombinant lambda-ZAP phage using Ex-Assist helper phage
and propagated in XL0LR cells. Note: EST may be of fungal
origin."

BASE COUNT 183 a 142 c 140 g 168 t
ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 633;
Best Local Similarity 91.3%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcaggcagtttgccttct 24
||||||| || |||||||||

Db 342 ATCTTCATCGCTGTTTGCTTCT 364

RESULT 9

BF642179 645 bp mRNA linear EST 19-DEC-2000
 LOCUS NF061E08IN1F1066 Insect herbivory Medicago truncatula cDNA clone
 DEFINITION NF061E08IN 5', mRNA sequence.
 ACCESSION BF642179
 VERSION BF642179.1 GI:11906337
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 645)
 AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
 H.R., Inman,J.T., Weller,J.W. and May,G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula insect herbivory library
 COMMENT Unpublished (2000)
 Contact: Korth K
 Dept. of Plant Pathology
 University of Arkansas
 217 Plant Science Building, Fayetteville, AR 72701, USA
 Tel: 501 575 5191
 Fax: 501 575 7601
 Email: korth@comp.uark.edu

Insert Length: 645 Std Error: 0.00
 Plate: 061 row: E column: 08
 Seq primer: TCACACAGGAACAGCTATGAC.
 Location/Qualifiers
 1..645

FEATURES

source

/organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF061E08IN"
 /clone_lib="Insect herbivory"
 /tissue_type="local and systemic leaves"
 /dev_stage="mature"
 /note="Vector: Lambda Zap; Library was produced from fully
 expanded M. truncatula leaves of plants fed upon by
 Spodoptera exigua (beet armyworm) for 24 hours. Systemic
 (undamaged leaves from injured plants) and wounded leaves
 were harvested and pooled."
 BASE COUNT 194 a 146 c 136 g 169 t
 ORIGIN

Query Match 82.5%; Score 19.8; DB 10; Length 645;
 Best Local Similarity 91.3%; Pred. No. 3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcaggcagtttgccttct 24

||||||| || |||||||||

Db 405 ATCTTCATCGCTGTTTGCTTCT 427

RESULT 10

AW695027 656 bp mRNA linear EST 15-JUN-2000
 LOCUS NF082F07ST1F1062 Developing stem Medicago truncatula cDNA clone
 DEFINITION NF082F07ST 5', mRNA sequence.

ACCESSION AW695027
 VERSION AW695027.1 GI:7569789
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 656)
 AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
 C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
 R.A.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula stem library
 COMMENT Unpublished (2000)
 Contact: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380
 Email: radixon@noble.org

Insert Length: 656 Std Error: 0.00
 Plate: 082 row: F column: 07
 Seq primer: TCACACAGGAACAGCTATGAC.
 Location/Qualifiers
 1..656

FEATURES source

/organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF082F07St"
 /clone_lib="Developing stem"
 /tissue_type="stem"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda Zap; Contains a mixture of
 internodal stem segments"
 BASE COUNT 192 a 159 c 125 g 180 t
 ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 656;
 Best Local Similarity 91.3%; Pred. No. 3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcaggcagtttgccttct 24

||||||| || |||||||||

Db 459 ATCTTCATCGCTGTTTGCTTCT 481

RESULT 11

AW692889 663 bp mRNA linear EST 15-JUN-2000
 LOCUS NF056G09ST1F1000 Developing stem Medicago truncatula cDNA clone
 DEFINITION NF056G09ST 5', mRNA sequence.

ACCESSION AW692889
 VERSION AW692889.1 GI:7567625
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 663)
 AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
 C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
 R.A.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula stem library
 COMMENT Unpublished (2000)
 Contact: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380
 Email: radixon@noble.org

Insert Length: 663 Std Error: 0.00
 Plate: 056 row: G column: 09
 Seq primer: TCACACAGGAACAGCTATGAC.
 Location/Qualifiers
 1..663

FEATURES

source

/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_lib="NF056G09St"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
Internodal stem segments"
194 a 162 c 126 g 181 t

BASE COUNT

ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 663;
Best Local Similarity 91.3%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcaggcaggtttgcttct 24
||||||| ||||| ||||| ||||| |||||

Db 464 ATCTTCATCGCTGTTTGCTTCT 486

RESULT 12

LOCUS BG452255 682 bp mRNA linear EST 16-MAR-2001
DEFINITION NF085D04LF1042 Developing leaf Medicago truncatula cDNA clone
ACCESSION NF085D04LF 5', mRNA sequence.
VERSION BG452255
KEYWORDS BG452255.1 GI:13371049
SOURCE EST.
barrel medic.
Medicago truncatula

REFERENCE

1 (bases 1 to 682)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula leaf library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 682 Std Error: 0.00
Plate: 085 row: D column: 04
Seq primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers
1. .682

FEATURES

source
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_lib="NF085D04LF"
/clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
202 a 162 c 134 g 181 t 3 others

BASE COUNT

ORIGIN

Query Match 82.5%; Score 19.8; DB 10; Length 682;
Best Local Similarity 91.3%; Pred. No. 3.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcaggcaggtttgcttct 24
||||||| ||||| ||||| ||||| |||||

Db 452 ATCTTCATCGCTGTTTGCTTCT 474

RESULT 13

BF378810 241 bp mRNA linear EST 27-NOV-2000
LOCUS IL2-UM0081-300500-091-D10 UM0081 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF378810
ACCESSION BF378810
VERSION BF378810.1 GI:11367935
KEYWORDS EST.
SOURCE human.
Homo sapiens
ORGANISM human

REFERENCE

1 (bases 1 to 241)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-UM0081-
300500-091-D10&t3=2000-05-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 241.
Location/Qualifiers
1. .241
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UM0081"
/dev_stage="Adult"

TITLE

JOURNAL
MEDLINE
COMMENT
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-UM0081-
300500-091-D10&t3=2000-05-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 241.
Location/Qualifiers
1. .241
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UM0081"
/dev_stage="Adult"

FEATURES

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UM0081"
/dev_stage="Adult"

BASE COUNT

ORIGIN

Query Match 80.0%; Score 19.2; DB 10; Length 241;
Best Local Similarity 87.5%; Pred. No. 4.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 catcttcaggcaggtttgcttct 24
||||||| ||||| ||||| ||||| |||||

Db 75 CCTCTTCAAGACAGTTTGCTTCT 98

RESULT 14

AW786151/c 491 bp mRNA linear EST 09-JUL-2000
LOCUS AW786151
DEFINITION 118657 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AW786151
VERSION AW786151.1 GI:7842927
KEYWORDS EST.
SOURCE pig.
Sus scrofa
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 491)
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
        Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
        Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
        and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
        EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
        USDA, ARS, US Meat Animal Research Center
        PO Box 166, Clay Center, NE 68933-0166, USA
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smith@email.marc.usda.gov
        Single pass sequencing. Bases called and alt_trimmed with phred
        v0.980904.e. Vector identified by cross_match with the -minscore 18
        and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCGAGTCACGACG
Plate: 41 row: P column: 10
Seq primer: ATTAGTGACACTATAG.
FEATURES
        source
        Location/Qualifiers
            1..491
            /organism="Sus scrofa"
            /db_xref="taxon:9823"
            /clone_lib="MARC 1P1G"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
            Library made from pooled tissue from day 11, 13, 15, 20,
            and 30 embryos."
BASE COUNT 135 a 120 c 117 g 119 t
ORIGIN

Query Match 80.0%; Score 19.2; DB 9; Length 491;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catcttcaggcagttgtctct 24
||||||| || ||||| |||||
Db 393 CATCTTCAAGGAAGTTTCTCTCT 370

RESULT 15
BF191434/c
LOCUS 536 bp mRNA linear EST 02-NOV-2000
DEFINITION 239021 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BF191434
VERSION BF191434.1 GI:11074803
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 536)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
        EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
        USDA, ARS, US Meat Animal Research Center
        PO Box 166, Clay Center, NE 68933-0166, USA
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smith@email.marc.usda.gov
        Single pass sequencing. Bases called and alt_trimmed with phred
        v0.980904.e. Vector identified by cross_match with the -minscore 18
        and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCGAGTCACGACG
Plate: 72 row: N column: 23
Seq primer: ATTAGTGACACTATAG.
FEATURES
        source
        Location/Qualifiers
            1..536
            /organism="Sus scrofa"
            /db_xref="taxon:9823"
            /clone_lib="MARC 2P1G"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
            Library made from pooled tissue from testis, ovary,
            endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 129 a 118 c 136 g 153 t
ORIGIN

Query Match 80.0%; Score 19.2; DB 10; Length 536;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catcttcaggcagttgtctct 24
||||||| || ||||| |||||
Db 128 CATCTTCAAGGAAGTTTCTCTCT 105

Search completed: August 21, 2002, 09:55:54
Job time: 9317 sec

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:28 ; Search time 754.01 Seconds
(without alignments)
54.849 Million cell updates/sec

Title: US-09-339-922A-105

Perfect score: 24

Sequence: 1 catcttcattgcagttttgcttct 24

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

1:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	AAF28236	DNA encoding enhan
2	19.2	80.0	30	AAV49874	LM609 grafted anti
3	19.2	80.0	30	AAF28230	DNA encoding multi
C 4	17.6	73.3	5681	AAK68974	Human immune/haema
C 5	17.6	73.3	7576	AAAS36813	Human cardiovasecul
C 6	17.6	73.3	11626	AAV0607	Sindbis-like virus
C 7	17.6	73.3	27048	AAAS02354	Porcine Gal alpha(
C 8	17.6	73.3	269223	AAAF28554	Genomic fragment #
C 9	17.4	72.5	1698	AAAS03895	Human secreted pro

10	17.2	71.7	30	19	AAV49857	LM609 grafted anti
11	17.2	71.7	30	22	AAF28213	DNA encoding mutan
C 12	17.2	71.7	259	21	AAC32907	Human secreted pro
C 13	17.2	71.7	301	21	AAC50555	Human secreted pro
C 14	17.2	71.7	885	17	AAAT18832	Mouse survival mot
15	17.2	71.7	2312	22	AAK70886	Human immune/haema
16	17.2	71.7	6742	22	AAK66424	Human immune/haema
17	17.2	71.7	8033	23	ABL19178	Drosophila melanog
18	17.2	71.7	10772	22	AAK66425	Human immune/haema
19	17.2	71.7	12788	23	ABL10968	Drosophila melanog
C 20	17.2	71.7	31169	22	AAAS41761	Genomic sequence #
C 21	17.2	71.7	31169	22	AAK75191	Human immune/haema
C 22	16.8	70.0	359	22	AAK10607	Human breast cance
C 23	16.8	70.0	483	22	ABA55876	Human foetal liver
24	16.8	70.0	483	22	AAK40494	Human brain expres
25	16.8	70.0	483	22	AAK29575	Human bone marrow
26	16.8	70.0	483	22	AAI14150	Probe #4083 for ge
27	16.8	70.0	483	22	AAI03997	Probe #3988 used t
C 28	16.8	70.0	1584	16	AAO86997	Aminopeptidase 012
C 29	16.8	70.0	1770	21	AAA14243	Camel male-specifi
C 30	16.8	70.0	3170	21	AAA42444	Camel male-specifi
C 31	16.8	70.0	12595	22	AAAS42100	Genomic sequence #
C 32	16.6	69.2	223	23	AAAS0244	Staphylococcus aur
C 33	16.6	69.2	386	22	AAK65658	Human immune/haema
C 34	16.6	69.2	386	22	AAK65659	Human immune/haema
C 35	16.6	69.2	386	22	AAK79606	Human immune/haema
C 36	16.6	69.2	386	22	AAK79607	Human immune/haema
37	16.6	69.2	404	21	AAH30269	Human colon cancer
38	16.6	69.2	498	21	AAAC44428	Arabidopsis thalia
39	16.6	69.2	500	21	AAC36178	Arabidopsis thalia
40	16.6	69.2	637	22	AAH19204	Human secreted pro
C 41	16.6	69.2	700	22	AAH92715	Human inflammatory
C 42	16.6	69.2	1008	21	AAC35990	Arabidopsis thalia
43	16.6	69.2	1305	22	AAK64639	Human immune/haema
44	16.6	69.2	1485	21	AAC41125	Arabidopsis thalia
45	16.6	69.2	1622	22	AAK83087	Human immune/haema

ALIGNMENTS

RESULT 1

AAF28236

ID AAF28236 standard; DNA; 24 BP.

XX AAF28236;

XX AC

XX 03-APR-2001 (first entry)

DT

DE DNA encoding enhanced 5H6LH heavy chain CDR3.

XX

XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX

OS Unidentified.

XX

XX WO200078815-A1.

XX

XX 28-DEC-2000.

XX

XX 23-JUN-2000; 2000WO-US17454.

XX

XX 24-JUN-1999; 99US-0339922.

XX

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX

XX Huse WD, Wu H;

XX

XX WPI; 2001-050110/06.

XX

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -
PS Claim 14; Page 105; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
XX osteoporosis.
SQ Sequence 24 BP; 3 A; 6 C; 4 G; 11 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catcttcagcgagtttgcctct 24
Db 1 catcttcagcgagtttgcctct 24

RESULT 2
AAV49874
ID AAV49874 standard; DNA; 30 BP.
XX
AC AAV49874;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 DNA fragment #13.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region; ss.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
XX 06-AUG-1998.
PD
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
PI
XX
DR WPI; 1998-437472/37.
DR P-PSDB; AA76037.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Disclosure; Page 43; 129pp; English.
PS
XX
XX AAV49844-V49877 are nucleotide fragments of the grafted monoclonal
CC antibody LM609 heavy and light chain variable region. LM609 and the
CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used
CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
XX greater than that of parent the parent antibody.
SQ Sequence 30 BP; 8 A; 7 C; 6 G; 9 T; 0 other;

Query Match 80.0%; Score 19.2; DB 19; Length 30;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catcttcagcgagtttgcctct 24
Db 7 cataaccatggcagtttgcctct 30

RESULT 3
AAF28230
ID AAF28230 standard; DNA; 30 BP.
XX
AC AAF28230;
XX
DT 03-APR-2001 (first entry)
XX
DE DNA encoding multiple mutant VH CDR3 #1.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX inflammatory; cancer; retina; restenosis; osteoporosis; ss.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
XX 28-DEC-2000.
PD
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
PI
XX WPI; 2001-050110/06.
DR
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
PS
XX Disclosure; Page 43; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
XX osteoporosis.
SQ Sequence 30 BP; 8 A; 7 C; 6 G; 9 T; 0 other;

Query Match 80.0%; Score 19.2; DB 22; Length 30;

Best Local Similarity 87.5%; Pred. No. 15;	
Matches	21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 catcttcacggcagttttgtctt 24
Db	7 cataaccatggcagttttgtctt 30
RESULT 4	
AAK68974/c	
ID	AAK68974 standard; DNA; 5681 BP.
XX	
AC	AAK68974;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23786.
XX	
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW	cytostatic; gene therapy; vaccine; metastasis; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200157182-A2.
XX	
PD	09-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US01354.
XX	
PR	31-JAN-2000; 2000US-0179065.
PR	04-FEB-2000; 2000US-0180628.
PR	24-FEB-2000; 2000US-0184664.
PR	02-MAR-2000; 2000US-0186350.
PR	16-MAR-2000; 2000US-0189874.
PR	17-MAR-2000; 2000US-0190076.
PR	18-APR-2000; 2000US-0198123.
PR	19-MAY-2000; 2000US-0205515.
PR	07-JUN-2000; 2000US-0209467.
PR	28-JUN-2000; 2000US-0214886.
PR	30-JUN-2000; 2000US-0215135.
PR	07-JUL-2000; 2000US-0216647.
PR	07-JUL-2000; 2000US-0216880.
PR	11-JUL-2000; 2000US-0217487.
PR	11-JUL-2000; 2000US-0217496.
PR	14-JUL-2000; 2000US-0218290.
PR	26-JUL-2000; 2000US-0220963.
PR	26-JUL-2000; 2000US-0220964.
PR	14-AUG-2000; 2000US-0224518.
PR	14-AUG-2000; 2000US-0224519.
PR	14-AUG-2000; 2000US-0225213.
PR	14-AUG-2000; 2000US-0225214.
PR	14-AUG-2000; 2000US-0225266.
PR	14-AUG-2000; 2000US-0225267.
PR	14-AUG-2000; 2000US-0225268.
PR	14-AUG-2000; 2000US-0225270.
PR	14-AUG-2000; 2000US-0225271.
PR	14-AUG-2000; 2000US-0225447.
PR	14-AUG-2000; 2000US-0225757.
PR	14-AUG-2000; 2000US-0225758.
PR	14-AUG-2000; 2000US-0225759.
PR	18-AUG-2000; 2000US-0226279.
PR	22-AUG-2000; 2000US-0226681.
PR	22-AUG-2000; 2000US-0226686.
PR	22-AUG-2000; 2000US-0227182.
PR	23-AUG-2000; 2000US-0227009.
PR	30-AUG-2000; 2000US-0228924.
PR	01-SEP-2000; 2000US-0229287.
PR	01-SEP-2000; 2000US-0229343.
PR	01-SEP-2000; 2000US-0229344.
PR	01-SEP-2000; 2000US-0229345.
PR	05-SEP-2000; 2000US-0229509.
PR	05-SEP-2000; 2000US-0229513.
PR	06-SEP-2000; 2000US-0230437.
PR	06-SEP-2000; 2000US-0230438.

PR	08-SEP-2000; 2000US-0231242.
PR	08-SEP-2000; 2000US-0231243.
PR	08-SEP-2000; 2000US-0231244.
PR	08-SEP-2000; 2000US-0231413.
PR	08-SEP-2000; 2000US-0231414.
PR	08-SEP-2000; 2000US-0232080.
PR	08-SEP-2000; 2000US-0232081.
PR	12-SEP-2000; 2000US-0231968.
PR	14-SEP-2000; 2000US-0232397.
PR	14-SEP-2000; 2000US-0232398.
PR	14-SEP-2000; 2000US-0232399.
PR	14-SEP-2000; 2000US-0232400.
PR	14-SEP-2000; 2000US-0232401.
PR	14-SEP-2000; 2000US-0233063.
PR	14-SEP-2000; 2000US-0233064.
PR	21-SEP-2000; 2000US-0234223.
PR	21-SEP-2000; 2000US-0234274.
PR	25-SEP-2000; 2000US-0234997.
PR	25-SEP-2000; 2000US-0234998.
PR	26-SEP-2000; 2000US-0235484.
PR	27-SEP-2000; 2000US-0235834.
PR	27-SEP-2000; 2000US-0235836.
PR	29-SEP-2000; 2000US-0236327.
PR	29-SEP-2000; 2000US-0236367.
PR	29-SEP-2000; 2000US-0236368.
PR	29-SEP-2000; 2000US-0236369.
PR	29-SEP-2000; 2000US-0236370.
PR	02-OCT-2000; 2000US-0236802.
PR	02-OCT-2000; 2000US-0237037.
PR	02-OCT-2000; 2000US-0237038.
PR	02-OCT-2000; 2000US-0237039.
PR	13-OCT-2000; 2000US-0237040.
PR	13-OCT-2000; 2000US-0239935.
PR	13-OCT-2000; 2000US-0239937.
PR	20-OCT-2000; 2000US-0240960.
PR	20-OCT-2000; 2000US-0241221.
PR	20-OCT-2000; 2000US-0241785.
PR	20-OCT-2000; 2000US-0241786.
PR	20-OCT-2000; 2000US-0241787.
PR	20-OCT-2000; 2000US-0241808.
PR	20-OCT-2000; 2000US-0241809.
PR	20-OCT-2000; 2000US-0241826.
PR	01-NOV-2000; 2000US-0244617.
PR	08-NOV-2000; 2000US-0246475.
PR	08-NOV-2000; 2000US-0246476.
PR	08-NOV-2000; 2000US-0246477.
PR	08-NOV-2000; 2000US-0246478.
PR	08-NOV-2000; 2000US-0246523.
PR	08-NOV-2000; 2000US-0246524.
PR	08-NOV-2000; 2000US-0246525.
PR	08-NOV-2000; 2000US-0246526.
PR	08-NOV-2000; 2000US-0246527.
PR	08-NOV-2000; 2000US-0246528.
PR	08-NOV-2000; 2000US-0246532.
PR	08-NOV-2000; 2000US-0246609.
PR	08-NOV-2000; 2000US-0246610.
PR	08-NOV-2000; 2000US-0246611.
PR	08-NOV-2000; 2000US-0246613.
PR	17-NOV-2000; 2000US-0249207.
PR	17-NOV-2000; 2000US-0249208.
PR	17-NOV-2000; 2000US-0249209.
PR	17-NOV-2000; 2000US-0249210.
PR	17-NOV-2000; 2000US-0249211.
PR	17-NOV-2000; 2000US-0249212.
PR	17-NOV-2000; 2000US-0249213.
PR	17-NOV-2000; 2000US-0249214.
PR	17-NOV-2000; 2000US-0249215.
PR	17-NOV-2000; 2000US-0249216.
PR	17-NOV-2000; 2000US-0249217.
PR	17-NOV-2000; 2000US-0249218.
PR	17-NOV-2000; 2000US-0249244.

PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-451930/48.
XX New cardiovascular system related polynucleotides and polypeptides,
XX useful for diagnosing, treating and/or preventing disorders of the
XX cardiovascular system -
XX Claim 1; SEQ ID No 2313; 674pp; English.
XX Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode
XX the cardiovascular system antigen polypeptides of the invention.
XX Cardiovascular system antigens and their associated polynucleotides are
XX useful in the diagnosis, treatment and prevention of various types of
XX disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
XX chickens or sheep. A pathological condition can be determined by
XX detecting the presence or absence of a mutation in a cardiovascular
XX system antigen polynucleotide. The treatable disorders include autoimmune
XX diseases such as rheumatoid arthritis, hyperproliferative disorders such
XX as neoplasms of the breast or liver, cardiovascular disorders such as
XX cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,
XX nervous system disorders such as Alzheimer's disease, infections caused
XX by bacteria, viruses and fungi, ocular disorders such as corneal
XX infection, endocrine disorders such as premature labour and infertility,
XX gastrointestinal disorders such as Crohn's disease, renal disorders such
XX as glomerulonephritis and respiratory disorders such as asthma and
XX pleurisy. The polypeptides can also be used to aid wound healing, to
XX prevent skin aging due to sunburn, to maintain organs before
XX transplantation, to regenerate tissues and in chemotaxis.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

Query Match 73.3%; Score 17.6; DB 22; Length 7576;
Best Local Similarity 83.3%; Pred No. 2, 1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 catcttcagcgagtttgcttct 24
||| ||| ||||| ||| |||
Db 460 CATTTTCCTGCGAGTTTTCGTCT 437

RESULT 6
AAA70607/c

ID AAA70607 standard; cDNA; 11626 BP.

XX AAA70607;

XX 06-DEC-2000 (first entry)

XX Sindbis-like virus strain XJ-160 complete genome sequence.

DE Genome; Sindbis-like virus strain XJ-160; primer: RT-PCR; vaccine;
KW epidemic; Sindbis encephalitis; evolution; epidemiology; ds.

XX Sindbis-like virus strain XJ-160.

OS CNI252444-A.

XX 10-MAY-2000.

XX 27-OCT-1998; 98CN-0120692.
 XX 27-OCT-1998; 98CN-0120692.
 XX (VIRO-) INST VIROLOGY CHINESE ACAD PREVENTIVE ME.
 XX Liang G, Li L, Zhou G;
 XX WPI; 2000-443225/39.
 XX Whole genome sequence of Sindbis virus strain and its cloning method -
 XX Claim 1; Page 2-5; 17pp; Chinese.
 XX This sequence represents the complete genome of the Sindbis-like virus
 CC strain XJ-160. The genome was cloned as 15 fragments using the PCR
 CC primers AAA70608-A70635 into the plasmid pGEM-T. The invention relates
 CC to the isolation and method of cloning the complete genome for the
 CC Sindbis-like virus strain XJ-160 by a RT-PCR process. The XJ-160
 CC strain virus appears to be the optimal candidate for a vaccine to
 CC prevent epidemics of Sindbis encephalitis. The sequence of this
 CC strain's genome shows the difference between this viral strain and
 CC other epidemic Sindbis virus strains at the molecular level and is
 CC useful for understanding the source, evolution and molecular
 CC epidemiology of Sindbis viruses.
 XX
 SQ Sequence 11626 BP; 3283 A; 2770 C; 2850 G; 2723 T; 0 other;
 Query Match 73.3%; Score 17.6; DB 21; Length 11626;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 1 catcttcacggcagtttctct 24
 || ||||| ||||| |||||
 Db 2331 CAATTTCACGGCAGTTTCTCT 2308
 RESULT 7
 ID AAS02354
 XX AAS02354 standard; DNA; 27048 BP.
 AC AAS02354;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Porcine Gal alpha(1,3) galactosyl transferase gene introns 3-8.
 XX
 KW Pig; Gal alpha(1,3) galactosyl transferase; intron 3-8; gene targeting;
 KW transgenic animal; transplant rejection; immunomodulation;
 KW systemic lupus erythematosus; immune-haemolytic anaemia;
 KW rheumatoid arthritis; ds.
 XX
 OS Sus scrofa.
 XX
 FH Key Location/Qualifiers
 FT Intron 1..4851
 FT /*tag= a
 FT /number= 3
 FT primer_bind 10..23
 FT /*tag= b
 FT primer_bind complement (3998..4020)
 FT /*tag= c
 FT exon 4852..4937
 FT /*tag= d
 FT /number= 4
 FT /note= "The exon sequence is represented by dashes
 FT in the sequence presented in figure 1 in the
 FT specification and have been replaced with N's to
 FT maintain the sequence numbering"
 FT 4938..11715
 FT /*tag= d
 FT

FT /number= 4
 FT /note= "This sequence is specifically claimed in
 FT claim 14"
 FT 11521..11537
 FT /*tag= e
 FT primer_bind complement (11688..11716)
 FT /*tag= f
 FT exon 11716..11752
 FT /*tag= g
 FT /number= 5
 FT /note= "The exon sequence is represented by dashes
 FT in the sequence presented in figure 1 in the
 FT specification and have been replaced with N's to
 FT maintain the sequence numbering"
 FT 11753..13747
 FT /*tag= h
 FT /number= 5
 FT exon 13748..13810
 FT /*tag= i
 FT /number= 6
 FT /note= "The exon sequence is represented by dashes
 FT in the sequence presented in figure 1 in the
 FT specification and have been replaced with N's to
 FT maintain the sequence numbering"
 FT 13811..14358
 FT /*tag= j
 FT /number= 6
 FT exon 14359..14463
 FT /*tag= k
 FT /number= 7
 FT /note= "The exon sequence is represented by dashes
 FT in the sequence presented in figure 1 in the
 FT specification and have been replaced with N's to
 FT maintain the sequence numbering"
 FT 14464..21627
 FT /*tag= l
 FT /number= 7
 FT /note= "This sequence is specifically claimed in
 FT claim 16"
 FT exon 21628..21705
 FT /*tag= m
 FT /number= 8
 FT /note= "The exon sequence is represented by dashes
 FT in the sequence presented in figure 1 in the
 FT specification and have been replaced with N's to
 FT maintain the sequence numbering"
 FT 21766..27048
 FT /*tag= n
 FT /number= 8
 FT /note= "This sequence is specifically claimed in
 FT claim 42"
 FT
 PN WO200123541-A2.
 XX
 XX 05-APR-2001.
 XX
 XX 02-OCT-2000; 2000WO-US27065.
 XX
 XX 30-SEP-1999; 99US-0156953.
 XX
 XX (ALEX-) ALEXION PHARM INC.
 XX
 XX Fodor WL, Ramsoondar JJ;
 XX WPI; 2001-266147/27.
 XX
 XX Modulating the expression of a eukaryotic gene in a cell, involves
 XX transfecting the cell with a nucleic acid construct that disrupts at
 XX least a portion of the DNA sequence of the gene to be modulated -
 XX Example 1; Fig 1; 86pp; English.
 XX
 CC The sequence represents Porcine Gal alpha(1,3) galactosyl transferase

CC infection and life-threatening, systemic diseases including endocarditis
CC and meningitis.
XX
SQ Sequence 269223 BP; 77067 A; 56596 C; 57380 G; 78180 T; 0 other;

Query Match 73.3%; Score 17.6; DB 22; Length 269223;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 catcttcacggcagtttgcttct 24
||||| ||||||||| |||
Db 267189 CATCTTTTGGCAGTTTGGTGT 267166

RESULT 9
AAS03895/C
ID AAS03895 standard; cDNA; 1698 BP.
XX AC
XX AAS03895;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human secreted protein gene #14.
XX
KW Human secreted protein; autoimmune disorder; hyperproliferative disorder;
KW cardiovascular disorder; cerebrovascular disorder; angiogenesis;
KW nervous system disorder; bacterial infection; viral infection; ss;
KW fungal infection; ocular disorder; wound healing; tissue regeneration;
KW epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
XX
OS Homo sapiens.
XX
XX WO200123598-A1.
XX
XX 05-APR-2001.
PD
PF 26-SEP-2000; 2000WO-US26324.
XX
PR 27-SEP-1999; 99US-0155807.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Komatsoulis G, Ruben SM, Rosen CA;
XX
XX WPI: 2001-281684/29.
DR
DR P-PSDB; AAU01939.
XX
PT Forty one nucleic acid molecules encoding human secreted proteins, useful
PT in the prevention, treatment and diagnosis of cancer, immune disorders,
PT cardiovascular disorders and neurological diseases -
XX
PS Disclosure; Page 454; 518pp; English.
XX
XX Sequences AAS03873-AAS03922 represent isolated nucleic acid molecules and
CC PCR primers of the invention, acid of the invention. Secreted proteins
CC and their related nucleic acids can be used in the diagnosis of or
CC susceptibility to a pathological condition by determining the presence or
CC absence of a mutation in a nucleic acid or the presence or amount of
CC expression of a secreted protein. The sequences are used to prevent,
CC treat or ameliorate a medical condition in e.g. humans, mice, rabbits,
CC goats, horses, cats, dogs, chickens or sheep. The antibodies to the
CC polypeptides can also be used in alleviating symptoms associated with
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
CC linked immunosorbent assays (ELISA). The disorders include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.
CC The peptides can also be used to aid wound healing and epithelial cell
CC proliferation, to help prevent skin ageing due to sunburn, to maintain
CC organs before transplantation, to regenerate tissues, in chemotaxis and

```
CC as a food additive or preservative to alter storage capabilities.
XX Sequence 1698 BP; 464 A; 380 C; 339 G; 487 T; 28 other;
SQ

Query Match 72.5%; Score 17.4; DB 22; Length 1698;
Best Local Similarity 78.3%; Pred. No. 2e+02;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 atcttcagcgagtttgcttct 24
Db 1630 AGCTTTAAGTCAGYTTTGCTTCT 1608
|||||:|||||

RESULT 10
AAV49857
ID AAV49857 standard; DNA; 30 BP.
XX
AC AAV49857;
XX
XX 02-NOV-1998 (first entry)
DT
DE LM609 grafted antibody V-H region CDR3 DNA fragment #2.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-H region; CDR;
XX complementarity determining region; ss.
XX
OS Mus sp.
XX
XX WO9833919-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 30-JAN-1998; 98WO-US01826.
PF
XX
XX 30-JAN-1997; 97US-0791391.
PR
XX
XX (IXSY-) IXSYS INC.
PA
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI; 1998-437472/37.
DR
XX
XX P-PSDB; AAW76020.
DR
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Disclosure; Page 42; 129pp; English.
XX
XX AAV49844-V49877 are nucleotide fragments of the grafted monoclonal
XX antibody LM609 heavy and light chain variable region. LM609 and the
XX antibody vitaxin bind selectively to integrin alphavbeta3 and can be used
XX to inhibit binding of alphavbeta3 to a ligand and thus block
XX integrin-mediated signal transduction. This is useful in the treatment,
XX prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
XX rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
XX antibodies contain non-murine framework regions so are suitable for use
XX in humans. Enhanced types of LM609 have affinity more than 90 times
XX greater than that of parent the parent antibody.
XX
XX Sequence 30 BP; 9 A; 7 C; 6 G; 8 T; 0 other;
SQ

Query Match 71.7%; Score 17.2; DB 19; Length 30;
Best Local Similarity 86.4%; Pred. No. 1.3e+02;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 atcttcagcgagtttgcttct 24
Db 1630 AGCTTTAAGTCAGYTTTGCTTCT 1608
|||||:|||||

RESULT 12
AAC22907/c
ID AAC22907 standard; cDNA; 259 BP.
XX
XX
AC AAC22907;
XX
```

```
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catcttcagcgagtttgctt 22
Db 7 cataaccatgcagtttgctt 28
|||||:|||||

RESULT 11
AAF28213
ID AAF28213 standard; DNA; 30 BP.
XX
AC AAF28213;
XX
XX 03-APR-2001 (first entry)
DT
DE DNA encoding mutant VH CDR3 peptide #1.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
XX inflammatory; cancer; retina; restenosis; osteoporosis; ss.
XX
XX Unidentified.
OS
XX
XX WO200078815-A1.
PN
XX
XX 28-DEC-2000.
PD
XX
XX 23-JUN-2000; 2000WO-US17454.
PF
XX
XX 24-JUN-1999; 99US-0339922.
PR
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX
XX Huse WD, Wu H;
PI
XX
XX WPI; 2001-050110/06.
DR
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX osteoporosis -
XX
XX Disclosure; Page 42; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
XX exhibiting selective binding affinity to alphavbeta_3 integrin or
XX their functional fragments. The antibodies or their functional
XX fragments can be used in the diagnosis and treatment of
XX alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX diseases (such as psoriasis and chronic articular rheumatism),
XX disorders associated with inappropriate or inopportune invasion of
XX vessels (such as diabetic retinopathy, neovascular glaucoma and
XX cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX
XX Sequence 30 BP; 9 A; 7 C; 6 G; 8 T; 0 other;
SQ

Query Match 71.7%; Score 17.2; DB 22; Length 30;
Best Local Similarity 86.4%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catcttcagcgagtttgctt 22
Db 7 cataaccatgcagtttgctt 28
|||||:|||||

RESULT 12
AAC22907/c
ID AAC22907 standard; cDNA; 259 BP.
XX
XX
AC AAC22907;
XX
```

DT 06-OCT-2000 (first entry)
 XX Human secreted protein 5' EST, SEQ ID NO: 26982.
 DE
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 XX 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 XX 26-FEB-1999; 99US-0122487.
 XX (GEST) GENSET.
 PA Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-500381/45.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 PS Claim 1; SEQ ID 26982; 71pp + CD-ROM; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 SQ Sequence 259 BP; 73 A; 54 C; 55 G; 74 T; 3 other;
 XX
 Query Match 71.7%; Score 17.2; DB 21; Length 259;
 Best Local Similarity 79.2%; Pred. No. 1.8e+02;
 Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 XX
 QY 1 catcttcagtcaggtttgtcttct 24
 DB 245 CATTTCTCGCAGTTTWTCTGCT 222
 XX
 RESULT 13
 AAC05655/c
 ID AAC05655 standard; cDNA; 301 BP.
 XX
 AC AAC05655;
 XX
 XX 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 9730.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX

PD 06-SEP-2000.
 XX 21-FEB-2000; 2000EP-0200610.
 XX
 XX 26-FEB-1999; 99US-0122487.
 XX (GEST) GENSET.
 PA Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-500381/45.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1; SEQ ID 9730; 71pp + CD-ROM; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 SQ Sequence 301 BP; 53 A; 76 C; 77 G; 95 T; 0 other;
 XX
 Query Match 71.7%; Score 17.2; DB 21; Length 301;
 Best Local Similarity 86.4%; Pred. No. 1.9e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 tcttcacgcagtttgccttct 24
 DB 57 TCTTCATTCAGCATTCCTCT 36
 XX
 RESULT 14
 AAT18832/c
 ID AAT18832 standard; cDNA; 885 BP.
 XX
 AC AAT18832;
 XX
 DT 02-OCT-1996 (first entry)
 XX
 DE Mouse survival motor neuron homologue cDNA.
 XX
 KW Survival motor neuron gene; SMN gene; spinal muscular atrophy;
 KW transgenic mouse; animal model; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 18..884
 FT /*tag= a
 XX
 PN EP11833-A2.
 XX
 PD 15-MAY-1996.
 XX
 PF 19-OCT-1995; 95EP-0402335.
 XX
 PR 19-OCT-1994; 94EP-0402353.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

```
XX Melki J, Munnich A;
XX WPI; 1996-232098/24.
DR P-PSDB; AAR94966.
XX
XX Human survival motor neuron gene T-BCD541, variant C-BCD541 and
PT murine equiv. - useful to develop primers and probes for in vitro
PT detection of motor neuron diseases e.g. spinal muscular atrophy
XX
XX Claim 11; Fig 12; 47pp; English.
XX
XX A cDNA clone (AAT18832) was identified as the mouse homologue of
CC the human survival motor neuron (SMN) gene, T-BCD541 (AAT18868).
CC It was isolated by screening a mouse foetal cDNA library using
CC human SMN cDNA (AAT18828) as a probe. The encoded protein (AAR94966)
CC shows 83% homology to the human SMN protein (AAR94963). A transgenic
CC mouse model is presented that hyperexpresses all or part of the SMN
CC gene, and a transgenic mouse that by homologous recombination
CC with a mutated mouse SMN gene produces abnormalities in the
CC SMN gene.
XX
XX Sequence 885 BP; 257 A; 235 C; 207 G; 186 T; 0 other;
SQ
Query Match 71.7%; Score 17.2; DB 17; Length 885;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 tcttcattggcaggtttgtctct 24
DB 240 TCCTCTGGCAGGTTTCTTCT 219
RESULT 15
AAK70886
ID AAK70886 standard; DNA; 2312 BP.
AC AAK70886;
XX
XX 06-NOV-2001 (first entry)
DT
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25698.
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX
XX WO200157182-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216847.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
```


PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 25698; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 2312 BP; 643 A; 482 C; 564 G; 623 T; 0 other;

Query Match 71.7%; Score 17.2; DB 22; Length 2312;
Best Local Similarity 86.4%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ttttcattggcagtttgcctct 24
||||| ||| |||||||||
Db 1216 ttttcattggtagtttgcctct 1237

Search completed: August 21, 2002, 10:08:39
Job time: 10057 sec

GenCore version 4.5
Copyright (C) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:14 ; Search time 174.26 Seconds
(without alignments)
33.830 Million cell updates/sec

Title: US-09-339-922A-105
Perfect score: 24
Sequence: 1 catcttcagtcagtttgccttct 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents,NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.2	71.7	885	3	Sequence 20, Appl
C 2	16.6	69.2	2622	4	Sequence 170, App
C 3	16.2	67.5	72928	3	Sequence 1, Appli
C 4	16	66.7	671	1	Sequence 18, Appl
C 5	16	66.7	671	2	Sequence 18, Appl
C 6	16	66.7	2037	1	Sequence 4, Appli
C 7	16	66.7	2037	1	Sequence 4, Appli
C 8	16	66.7	2037	1	Sequence 4, Appli
C 9	16	66.7	2037	1	Sequence 4, Appli
C 10	16	66.7	2037	1	Sequence 4, Appli
C 11	16	66.7	2037	1	Sequence 4, Appli
C 12	16	66.7	2811	4	Sequence 3, Appli
C 13	16	66.7	2813	2	Sequence 99, Appl
C 14	16	66.7	2813	4	Sequence 99, Appl
C 15	16	66.7	3080	4	Sequence 4, Appli
C 16	16	66.7	3258	2	Sequence 2, Appli
C 17	16	66.7	5141	1	Sequence 9, Appli
C 18	16	66.7	5141	2	Sequence 9, Appli
C 19	16	66.7	5141	2	Sequence 9, Appli
C 20	16	66.7	5141	4	Sequence 9, Appli
C 21	16	66.7	5639	3	Sequence 1, Appli
C 22	16	66.7	6285	1	Sequence 49, Appl
C 23	16	66.7	6285	1	Sequence 49, Appl
C 24	16	66.7	6285	1	Sequence 49, Appl
C 25	16	66.7	6285	1	Sequence 49, Appl
C 26	16	66.7	6285	3	Sequence 49, Appl
C 27	16	66.7	6285	5	Sequence 49, Appl

C 28	16	66.7	6306	5	PCT-US94-00658-1	Sequence 1, Appli
C 29	16	66.7	6367	1	US-08-470-299-1	Sequence 1, Appli
C 30	16	66.7	6367	3	US-08-776-511-3	Sequence 3, Appli
C 31	16	66.7	6557	1	US-08-286-740-3	Sequence 3, Appli
C 32	16	66.7	6557	5	PCT-US95-09576-3	Sequence 3, Appli
C 33	16	66.7	6889	1	US-08-286-740-2	Sequence 2, Appli
C 34	16	66.7	6889	5	PCT-US95-09576-2	Sequence 2, Appli
C 35	16	66.7	6926	1	US-08-470-299-2	Sequence 2, Appli
C 36	16	66.7	7360	1	US-08-286-740-1	Sequence 1, Appli
C 37	16	66.7	7360	5	PCT-US95-09576-1	Sequence 1, Appli
C 38	16	66.7	7892	2	US-07-916-098A-40	Sequence 68, Appl
C 39	16	66.7	8120	3	US-09-027-449-68	Sequence 68, Appl
C 40	16	66.7	8120	3	US-09-026-985-68	Sequence 2, Appli
C 41	16	66.7	8540	1	US-08-149-099C-2	Sequence 2, Appli
C 42	16	66.7	8540	2	US-08-478-967A-2	Sequence 1, Appli
C 43	16	66.7	8541	1	US-08-476-275-1	Sequence 5, Appli
C 44	16	66.7	8614	4	US-09-247-352-5	Sequence 5, Appli
C 45	16	66.7	8858	4	US-09-247-352-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-545-196B-20/C
; Sequence 20, Application US/08545196B
; Patent No. 6080577
; GENERAL INFORMATION:
; APPLICANT: MELKI, JUDITH
; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
; TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,196B
; FILING DATE: 19-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FARACI, C. J.
; REGISTRATION NUMBER: 32,350
; REFERENCE/DOCKET NUMBER: 2121-110P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 885 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 18..881
US-08-545-196B-20

Query Match 71.7%; Score 17.2; DB 3; Length 885;
Best Local Similarity 86.4%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tcttcagcagcttttgcctct 24
||||| ||||| ||| |||||
Db 240 TCTCTTGGCAGGTTTCTTCT 219

RESULT 2

US-09-130-616-170
; Sequence 170, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 170
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-130-616-170

Query Match 69.2%; Score 16.6; DB 4; Length 2622;
Best Local Similarity 82.6%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 atcttcagcagcttttgcctct 24
||||| ||||| ||||| |||||
Db 1676 atcttcaggtagcttgcctct 1698

RESULT 3

US-09-009-913-1
; Sequence 1, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axys Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231

TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72928 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-009-913-1

Query Match 67.5%; Score 16.2; DB 3; Length 72928;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catcttcagcagcttttgcct 21
||||| ||||| ||||| ||
Db 27567 CCTCTCATGACAGTTTCT 27587

RESULT 4

US-08-644-664B-18/c
; Sequence 18, Application US/08644664B
; Patent No. 5776746
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Gene Amplification Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,664B
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: GENITOPE-00912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 671 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..573
US-08-644-664B-18

Query Match 66.7%; Score 16; DB 1; Length 671;
Best Local Similarity 79.2%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 catcttcagcagcttttgcctct 24
||||| ||||| ||||| |||||
Db 586 CATCTCTGTAGTCTTCTTCT 563

```

: COUNTRY: USA
: ZIP: 07148
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/143,497
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: KELLEY, ROBIN D
: REGISTRATION NUMBER: 34,637
: REFERENCE/DOCKET NUMBER: CRP084
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/248-7000
: TELEFAX: 617/248-7100
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2037 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1..2037
: OTHER INFORMATION: /note= "adeval"
:
: US-08-143-497-4
:
Query Match 66.7%; Score 16; DB 1; Length 2037;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0;

Qy 1 catcttcatgcagcttgcctct 24
||||| || ||| || ||||
Db 1962 CATCTCTCTGTTAGTCTTCTCT 1939

RESULT 7
US-08-461-666-4/c
: Sequence 4, Application US/08461666
: Patent No. 5614385
: GENERAL INFORMATION:
: APPLICANT: OPPERMANN, HERMANN
: APPLICANT: DORAI, HAIMANTI
: APPLICANT: KAPLAN, PAUL
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
: TITLE OF INVENTION: PRODUCTION FROM RECOMBINANT DNA
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
: STREET: 45 SOUTH STREET
: CITY: HOPKINTON
: STATE: MA
: COUNTRY: USA
: ZIP: 07148
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/461,666
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/143,497
: FILING DATE: 25-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: KELLEY, ROBIN D

```



```
RESULT 10
US-08-757-300-4/C
; Sequence 4, Application US/08757300
; Patent No. 5712119
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: DORAI, HAIMANTI
; APPLICANT: KAPLAN, PAUL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM RECOMBINANT DNA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08757,300
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/143,497
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2037
; OTHER INFORMATION: /note= "adeval"
US-08-757-300-4

Query Match 66.7%; Score 16; DB 1; Length 2037;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catcttcaggcagttgtctct 24
||||| || ||| ||| ||| |||
Db 1962 CATCTTCCTGTTAGTCTTCTCT 1939

RESULT 11
US-08-464-589-4/C
; Sequence 4, Application US/08464589
; Patent No. 5733782
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: DORAI, HAIMANTI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
```

```
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,589
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,498
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2037
; OTHER INFORMATION: /note= "adeval"
US-08-464-589-4

Query Match 66.7%; Score 16; DB 1; Length 2037;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catcttcaggcagttgtctct 24
||||| || ||| ||| ||| |||
Db 1962 CATCTTCCTGTTAGTCTTCTCT 1939

RESULT 12
US-08-482-073-3/C
; Sequence 3, Application US/08482073
; Patent No. 6307025
; GENERAL INFORMATION:
; APPLICANT: Hession, Catherine A.
; APPLICANT: Lobb, Roy R.
; APPLICANT: Goelz, Susan E.
; APPLICANT: Osborn, Laurelee
; APPLICANT: Benjamin, Christopher D.
; APPLICANT: Rosa, Margaret D.
; TITLE OF INVENTION: ENDOTHELIAL CELL-LEUKOCYTE ADHESION
; TITLE OF INVENTION: MOLECULES (ELAMS) AND MOLECULES INVOLVED IN LEUKOCYTE
; TITLE OF INVENTION: ADHESION (MILAS)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,073
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,336
; FILING DATE:
; APPLICATION NUMBER: US 07/608298
; FILING DATE: 31-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 90/02357
; FILING DATE: 27-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/452675
; FILING DATE: 18-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/359516
; FILING DATE: 01-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/354151
; FILING DATE: 28-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B124CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2811 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-482-073-3

Query Match 66.7%; Score 16; DB 4; Length 2811;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 catcttcaggcagtttgcttct 24
||||| ||||||| ||||
Db 2259 CATCTTGATGCGACTTACTGTCT 2236

RESULT 13
US-08-344-155C-99/c
; Sequence 99, Application US/08344155C
; Patent No. 5883082
; GENERAL INFORMATION:
; APPLICANT: Bennett and Stepkowski
; TITLE OF INVENTION: Compositions and Methods for Preventing
; TITLE OF INVENTION: and Treating Allograft Rejection
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodland Falls Corporate Park
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,155C
; FILING DATE: No. 5883082ember 23, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 939,855
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05209
; FILING DATE: July 23, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063,167
; FILING DATE: 5/17/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/007,997
; FILING DATE: 1/21/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,855
; FILING DATE: 9/2/92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,286
; FILING DATE: 8/14/90
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0098
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2813
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-344-155C-99

Query Match 66.7%; Score 16; DB 2; Length 2813;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 catcttcaggcagtttgcttct 24
||||| ||||||| ||||
Db 2259 CATCTTGATGCGACTTACTGTCT 2236

RESULT 14
US-09-009-490A-90/c
; Sequence 90, Application US/09009490A
; Patent No. 6300491
; GENERAL INFORMATION:
; APPLICANT: Bennett and Mirabelli
; TITLE OF INVENTION: Oligonucleotide Modulation
; TITLE OF INVENTION: of Cell Adhesion
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,490A
; FILING DATE: January 20, 1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,740
; FILING DATE: May 12, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 063,167

; FILING DATE: May 17, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 969,151
; FILING DATE: February 10, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 007,997
; FILING DATE: January 20, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 939,855
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 567,286
; FILING DATE: August 14, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2813
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-09-009-490A-90

Query Match 66.7%; Score 16; DB 4; Length 2813;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catcttcattggcagtttgcctct 24
||||| ||||| ||||| |||||
Db 2259 CATCTTGATGGCAGTTACTGTCT 2236

RESULT 15
US-08-482-073-4/c
; Sequence 4, Application US/08482073
; Patent No. 6307025
; GENERAL INFORMATION:
; APPLICANT: Hession, Catherine A.
; APPLICANT: Lobb, Roy R.
; APPLICANT: Goelz, Susan E.
; APPLICANT: Osborn, Laurelee
; APPLICANT: Benjamin, Christopher D.
; APPLICANT: Rosa, Margaret D.
; TITLE OF INVENTION: ENDOTHELIAL CELL-LEUKOCYTE ADHESION
; TITLE OF INVENTION: MOLECULES (ELAMS) AND MOLECULES INVOLVED IN LEUKOCYTE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1231 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,073
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,336
; FILING DATE:

; APPLICATION NUMBER: US 07/608298
; FILING DATE: 31-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 90/02357
; FILING DATE: 27-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/452675
; FILING DATE: 18-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/359516
; FILING DATE: 01-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/354151
; FILING DATE: 28-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B124CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-482-073-4

Query Match 66.7%; Score 16; DB 4; Length 3080;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catcttcattggcagtttgcctct 24
||||| ||||| ||||| |||||
Db 2528 CATCTTGATGGCAGTTACTGTCT 2505

Search completed: August 21, 2002, 10:52:19
Job time: 9659 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: August 21, 2002, 10:49:56 ; Search time 2408.76 Seconds
(without alignments)
286.693 Million cell updates/sec

Title: US-09-339-922A-107
Perfect score: 33
Sequence: 1 caggccagccaaagtattagcaaccactacac 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.:

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

RESULT	1	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
DEFINITION	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
ACCESSION	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
VERSION	AX060886.1	GI:12406264	33 bp	DNA	linear	PAT 22-JAN-2001	
KEYWORDS	AX060886.1	GI:12406264	33 bp	DNA	linear	PAT 22-JAN-2001	
SOURCE	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
ORGANISM	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
REFERENCE	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
AUTHORS	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
TITLE	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
JOURNAL	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
FEATURES	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
source	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	
CDS	AX060886	Sequence 107 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001	

AX060886 Sequence
AX060820 Sequence
AX060782 Sequence
AX060786 Sequence
AX060810 Sequence
AX060794 Sequence
AX060803 Sequence
AX060888 Sequence
AX060867 Sequence
I31962 Sequence 91
I78574 Sequence 91
I78629 Sequence 91
U19309 Mus musculus
AF139842 Mus muscu
AF139843 Mus muscu
AF137617 Mus muscu
M34528 Mouse Ig ka
S60864 Ab2 kappa c
X59211 Mouse immu
X02555 Mouse mRNA
X02556 Mouse mRNA
X02234 Mouse mRNA
AF087030 Mus muscu
AF163757 Mus muscu
X90901 M.musculus
AJ277215 Mus muscu
M95943 Mouse mRNA
M95945 Mouse mRNA
L08211 Mouse anti-
AF087031 Mus muscu
AF139844 Mus muscu
AF139847 Mus muscu
U60469 Mus musculus
L78684 Mus musculus
Y16070 Mus musculus
M93959 Mouse Ig ac
AR136864 Sequence
E07933 cDNA encodi
I31959 Sequence 82
I78571 Sequence 82
I78626 Sequence 82
AF045514 Mus muscu
M24100 Mouse Ig un
X14625 Murine nonf
M16162 Mouse Ig ka

ALIGNMENTS

```

/translation="QASQSIHNLH"
BASE COUNT      12 a  12 c  5 g  4 t
ORIGIN

Query Match      100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaaccacctacac 33
|||||
Db 1 CAGCCAGCCAAAGTATTAGCAACCACCTACAC 33

RESULT 2
AX060820
LOCUS      AX060820          39 bp      DNA          linear          PAT 22-JAN-2001
DEFINITION Sequence 41 from Patent WO0078815.
ACCESSION  AX060820
VERSION     AX060820.1 GI:12406198
KEYWORDS   house mouse.
SOURCE      Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  Huse, W.D. and Wu, H.
AUTHORS    Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
TITLE      encoding same and methods of use
JOURNAL    Patent: WO 0078815-A 41 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES   Location/Qualifiers
source     1..39
/organism="Mus musculus"
/db_xref="taxon:10090"
<1..>39
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAC24896.1"
/db_xref="GI:12406199"
/translation="QASQSIHNLHWY"
BASE COUNT      13 a  12 c  7 g  7 t
ORIGIN

Query Match      100.0%; Score 33; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaaccacctacac 33
|||||
Db 1 CAGCCAGCCAAAGTATTAGCAACCACCTACAC 33

RESULT 3
AX060782
LOCUS      AX060782          321 bp      DNA          linear          PAT 22-JAN-2001
DEFINITION Sequence 3 from Patent WO0078815.
ACCESSION  AX060782
VERSION     AX060782.1 GI:12406162
KEYWORDS   synthetic construct.
SOURCE      synthetic construct.
ORGANISM   artificial sequence.
REFERENCE  Huse, W.D. and Wu, H.
AUTHORS    Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
TITLE      encoding same and methods of use
JOURNAL    Patent: WO 0078815-A 3 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES   Location/Qualifiers
source     1..321
/organism="Mus musculus"
/db_xref="taxon:10090"
<1..>321
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAC24891.1"
/db_xref="GI:12406167"
/translation="DIVLTQSPATLSVTPGDSVLSQASQSIHNLHWHYQKSHESP
RLLIKYRSQISIGIPARFSGSGSDTFTLTISLLEPEDFAVYICQQSGSWPHTFGGT
KLEIK"
BASE COUNT      83 a  83 c  77 g  78 t
ORIGIN

/translation="QASQSIHNLH"
BASE COUNT      12 a  12 c  5 g  4 t
ORIGIN

Query Match      100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaaccacctacac 33
|||||
Db 70 CAGCCAGCCAAAGTATTAGCAACCACCTACAC 102

RESULT 4
AX060786
LOCUS      AX060786          321 bp      DNA          linear          PAT 22-JAN-2001
DEFINITION Sequence 7 from Patent WO0078815.
ACCESSION  AX060786
VERSION     AX060786.1 GI:12406166
KEYWORDS   house mouse.
SOURCE      Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  Huse, W.D. and Wu, H.
AUTHORS    Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
TITLE      encoding same and methods of use
JOURNAL    Patent: WO 0078815-A 7 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES   Location/Qualifiers
source     1..321
/organism="Mus musculus"
/db_xref="taxon:10090"
<1..>321
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAC24891.1"
/db_xref="GI:12406167"
/translation="DIVLTQSPATLSVTPGDSVLSQASQSIHNLHWHYQKSHESP
RLLIKYRSQISIGIPARFSGSGSDTFTLTISLLEPEDFAVYICQQSGSWPHTFGGT
KLEIK"
BASE COUNT      83 a  83 c  77 g  78 t
ORIGIN

Query Match      100.0%; Score 33; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaaccacctacac 33
|||||
Db 70 CAGCCAGCCAAAGTATTAGCAACCACCTACAC 102

RESULT 5
AX060810
LOCUS      AX060810          321 bp      DNA          linear          PAT 22-JAN-2001
DEFINITION Sequence 31 from Patent WO0078815.
ACCESSION  AX060810

```

```

VERSION      AX060810.1 GI:12406189
KEYWORDS
SOURCE       synthetic construct.
ORGANISM     synthetic construct.
REFERENCE    1 (bases 1 to 321)
AUTHORS      Huse,W.D. and Wu,H.
TITLE        Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL      Patent: WO 0078815-A 31 28-DEC-2000;
              Applied Molecular Evolution (US)
FEATURES     Location/Qualifiers
              source
              1..321
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="grafted antibody variable region"
              145..147
              /note="NNN-CGT OR ATG"
              76 a 93 c 78 g 71 t 3 others
BASE COUNT   76 a 93 c 78 g 71 t 3 others
ORIGIN
variation
Query Match 100.0%; Score 33; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaaccacctacac 33
|||||
Db 70 CAGGCCAGCCAAAGTATTAGCAACCACCTACAC 102

RESULT 6
AX060794/c
LOCUS       AX060794 72 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 15 from Patent WO0078815.
ACCESSION  AX060794
VERSION     AX060794.1 GI:12406174
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE    1 (bases 1 to 72)
AUTHORS      Huse,W.D. and Wu,H.
TITLE        Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL      Patent: WO 0078815-A 15 28-DEC-2000;
              Applied Molecular Evolution (US)
FEATURES     Location/Qualifiers
              source
              1..72
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="oligonucleotide"
              13 a 13 c 24 g 22 t
BASE COUNT   13 a 13 c 24 g 22 t
ORIGIN
Query Match 90.9%; Score 30; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 gccagccaaagtattagcaaccacctacac 33
|||||
Db 72 GCCAGCCAAAGTATTAGCAACCACCTACAC 43

RESULT 7
AX060803/c
LOCUS       AX060803 75 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 24 from Patent WO0078815.
ACCESSION  AX060803
VERSION     AX060803.1 GI:12406183
KEYWORDS
SOURCE      synthetic construct.

```

```

ORGANISM     synthetic construct.
REFERENCE    1 (bases 1 to 75)
AUTHORS      Huse,W.D. and Wu,H.
TITLE        Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL      Patent: WO 0078815-A 24 28-DEC-2000;
              Applied Molecular Evolution (US)
FEATURES     Location/Qualifiers
              source
              1..75
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="oligonucleotide"
              14 a 13 c 24 g 24 t
BASE COUNT   14 a 13 c 24 g 24 t
ORIGIN
Query Match 90.9%; Score 30; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 gccagccaaagtattagcaaccacctacac 33
|||||
Db 75 GCCAGCCAAAGTATTAGCAACCACCTACAC 46

RESULT 8
AX060888
LOCUS       AX060888 33 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 109 from Patent WO0078815.
ACCESSION  AX060888
VERSION     AX060888.1 GI:12406266
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE    1 (bases 1 to 33)
AUTHORS      Huse,W.D. and Wu,H.
TITLE        Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL      Patent: WO 0078815-A 109 28-DEC-2000;
              Applied Molecular Evolution (US)
FEATURES     Location/Qualifiers
              source
              1..33
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              <1..>33
              /note="Mutated complementarity determining region (CDR)"
              /codon_start=1
              /transl_table=11
              /protein_id="CAC24930.1"
              /db_xref="GI:12406267"
              /translation="QASQISINFLH"
              11 a 11 c 5 g 6 t
BASE COUNT   11 a 11 c 5 g 6 t
ORIGIN
Query Match 90.3%; Score 29.8; DB 6; Length 33;
Best Local Similarity 93.9%; Pred. No. 0.0063;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaaccacctacac 33
|||||
Db 1 CAGGCCAGCCAAAGTATTAGCAACCTTCCTACAC 33

RESULT 9
AR126867/c
LOCUS       AR126867 128 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 91 from patent US 6180370.
ACCESSION  AR126867
VERSION     AR126867.1 GI:14113460
KEYWORDS

```

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 128)
AUTHORS Queen,C.L. and Selick,H.E.
TITLE Humanized immunoglobulins and methods of making the same
JOURNAL Patent: US 6180370-A 91 30-JAN-2001;
FEATURES Location/Qualifiers
source
1. .128
BASE COUNT 26 a 25 c 36 g 41 t
ORIGIN

Query Match 89.1%; Score 29.4; DB 6; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.0095;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gccagccaaagtattagcaaccactacac 33
Db 95 GCCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 10
LOCUS I31962/c 128 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 91 from patent US 5585089.
ACCESSION I31962
VERSION I31962.1 GI:1822753
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 128)
AUTHORS Queen,C.L. and Selick,H.E.
TITLE Humanized immunoglobulins
JOURNAL Patent: US 5585089-A 91 17-DEC-1996;
FEATURES Location/Qualifiers
source
1. .128
BASE COUNT 26 a 25 c 36 g 41 t
ORIGIN

Query Match 89.1%; Score 29.4; DB 6; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.0095;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gccagccaaagtattagcaaccactacac 33
Db 95 GCCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 11
LOCUS I78574/c 128 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 91 from patent US 5693761.
ACCESSION I78574
VERSION I78574.1 GI:3014728
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 128)
AUTHORS Queen,C.L., Schneider,W.P. and Selick,H.E.
TITLE Polynucleotides encoding improved humanized immunoglobulins
JOURNAL Patent: US 5693761-A 91 02-DEC-1997;
FEATURES Location/Qualifiers
source
1. .128
BASE COUNT 26 a 25 c 36 g 41 t
ORIGIN

Query Match 89.1%; Score 29.4; DB 6; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.0095;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gccagccaaagtattagcaaccactacac 33
Db 95 GCCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 12
LOCUS I78629/c 128 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 91 from patent US 5693762.
ACCESSION I78629
VERSION I78629.1 GI:3014783
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 128)
AUTHORS Queen,C.L., Co,M.Sung., Schneider,W.P., Landolfi,N.F.,
Coelmingh,K.L. and Selick,H.E.
TITLE Humanized immunoglobulins
JOURNAL Patent: US 5693762-A 91 02-DEC-1997;
FEATURES Location/Qualifiers
source
1. .128
BASE COUNT 26 a 25 c 36 g 41 t
ORIGIN

Query Match 89.1%; Score 29.4; DB 6; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.0095;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gccagccaaagtattagcaaccactacac 33
Db 95 GCCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 13
LOCUS MMU19309 243 bp mRNA linear ROD 21-JUN-1995
DEFINITION Mus musculus immunoglobulin kappa light chain variable region mRNA,
clone MRL1-17, partial cds.
ACCESSION U19309
VERSION U19309.1 GI:619954
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 243)
AUTHORS Roark,J.H., Kuntz,C.L., Nguyen,K.A., Caton,A.J. and Erikson,J.
TITLE Breakdown of B cell tolerance in a mouse model of systemic lupus
erythematosus
J Exp. Med. 181 (3), 1157-1167 (1995)
MEDLINE 95173583
REFERENCE 2 (bases 1 to 243)
AUTHORS Roark,J.H.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-1995) Jessica H. Roark, Wistar Institute, 3601
Spruce St., Philadelphia, PA 19104, USA
FEATURES Location/Qualifiers
source
1. .243
/organism="Mus musculus"
/strain="MRL-lpr/lpr"
/db_xref="taxon:10090"
/clone="MRL1-17"
/cell_type="splenic B cell hybridoma"
/tissue_type="spleen"
/dev_stage="adult"

```

CDS
<1..>243
/codon_start=1
/product="immunoglobulin kappa light chain variable
region"
/protein_id="AAA68563.1"
/db_xref="GI:619955"
/translation="ACRASQISNYLHWYQKSHESPRLLIKYASQISGIPSRFSQS
GSGDTLTSINSVETEDFGMYFCQSNWPHFGSGT"
BASE COUNT    65 a    62 c    56 g    60 t
ORIGIN
|||||
1

Query Match      89.1%; Score 29.4; DB 10; Length 243;
Best Local Similarity 96.8%; Pred. No. 0.0093;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3 ggcagccaaagtattagcaaccactacac 33
      |||||||
Db   9 GGCAGCCAAAGTATTAGCAACTACTACAC 39

RESULT 14
AF139842
LOCUS      285 bp    DNA    linear    ROD 04-NOV-1999
DEFINITION Mus musculus clone GL1 immunoglobulin kappa light chain variable
region Vk23 (Ig) gene, partial cds.
ACCESSION  AF139842
VERSION     AF139842.1 GI:4732148
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 285)
AUTHORS   Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE     Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
JOURNAL   J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE   99406777
PUBMED    10477553
REFERENCE  2 (bases 1 to 285)
AUTHORS   Brard,F. and Weigert,M.
TITLE     Direct Submission
JOURNAL   Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES   source
            location/qualifiers
            1..>285
            /organism="Mus musculus"
            /strain="MRL/Mp-lpr/lpr"
            /db_xref="taxon:10090"
            /chromosome="6"
            /clone="GL1"
            /tissue_type="tail"
            /germline
            <1..>285
            /gene="Ig"
            /note="variable region"
            <1..>285
            /codon_start=1
            /product="immunoglobulin kappa light chain variable region
Vk23"
            /protein_id="AAD28629.1"
            /db_xref="GI:4732149"
            /translation="DIVLTQSPATLSVTPGDRVSLSCRASQISNLYLHWYQKSHESP
RLLIKVASQISGIPSRFSGSGTDTLSINSVETEDFGMYFCQSNWSP"
            /misc_feature 70..105
            /gene="Ig"
            /note="CDR1; complementarity determining region 1"
            148..168
            /gene="Ig"
            /note="CDR2; complementarity determining region 2"
            75 a    73 c    63 g    74 t

BASE COUNT    75 a    73 c    63 g    74 t

Query Match      89.1%; Score 29.4; DB 10; Length 286;
Best Local Similarity 96.8%; Pred. No. 0.0093;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3 ggcagccaaagtattagcaaccactacac 33
      |||||||
Db   72 GGCAGCCAAAGTATTAGCAACTACTACAC 102

RESULT 15
AF139843
LOCUS      286 bp    DNA    linear    ROD 04-NOV-1999
DEFINITION Mus musculus clone GL2 immunoglobulin kappa light chain variable
region Vk23 (Ig) gene, partial cds.
ACCESSION  AF139843
VERSION     AF139843.1 GI:4732150
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 286)
AUTHORS   Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE     Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
JOURNAL   J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE   99406777
PUBMED    10477553
REFERENCE  2 (bases 1 to 286)
AUTHORS   Brard,F. and Weigert,M.
TITLE     Direct Submission
JOURNAL   Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES   source
            location/qualifiers
            1..>286
            /organism="Mus musculus"
            /strain="MRL/Mp-lpr/lpr"
            /db_xref="taxon:10090"
            /chromosome="6"
            /clone="GL2"
            /tissue_type="tail"
            /germline
            <1..>286
            /gene="Ig"
            /note="variable region"
            <1..>286
            /codon_start=1
            /product="immunoglobulin kappa light chain variable region
Vk23"
            /protein_id="AAD28630.1"
            /db_xref="GI:4732151"
            /translation="DIVLTQSPATLSVTPGDSVSLSCRASQISNNLHWYQKSHESP
RLLIKVASQISGIPSRFSGSGTDTLSINSVETEDFGMYFCQSNWSP"
            /misc_feature 70..105
            /gene="Ig"
            /note="CDR1; complementarity determining region 1"
            148..168
            /gene="Ig"
            /note="CDR2; complementarity determining region 2"
            75 a    75 c    62 g    74 t

BASE COUNT    75 a    75 c    62 g    74 t

Query Match      89.1%; Score 29.4; DB 10; Length 286;
Best Local Similarity 96.8%; Pred. No. 0.0093;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3 ggcagccaaagtattagcaaccactacac 33
      |||||||
Db   72 GGCAGCCAAAGTATTAGCAACTACTACAC 102

```

Db 72 GGCCAGCCAAAGTATTAGCAACAACCTACAC 102

Search completed: August 21, 2002, 10:49:57
Job time: 9812 sec

Result No.	Score	Query Match	Length	DB	ID	Description	
1	29.4	89.1	202	10	BG144658	ut73a01.y	
C	2	29.4	89.1	517	12	AG2846516	2M0146517
	3	29.4	89.1	738	10	BF582153	602099743
	4	29.4	89.1	772	10	BI105452	B105452
5	29.4	89.1	833	10	BG966582	602834412	
6	29.4	89.1	835	10	BI083006	B1083006	
7	29.4	89.1	835	10	BF579007	602874524	
8	23	69.7	849	10	BF583521	602096124	
C	9	22.2	67.3	517	12	A2928596	479.dfl1
	10	21.8	66.1	569	12	A2653355	1M0527C04
	11	21.8	66.1	619	10	BE251590	601110617
C	12	21.8	66.1	878	10	BF786148	602110427
	13	21.6	65.5	239	10	BF756995	MR0-CT045
	14	21.6	65.5	290	10	BG058466	nah17907.
15	21.6	65.5	740	10	BG397970	602439490	
16	21.4	64.8	414	10	BG225085	kp64a02.y	
17	21.4	64.8	613	12	BH504364	BOGNB20TR	

the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 53 a 61 c 45 g 43 t
ORIGIN

Query Match 89.1%; Score 29.4; DB 10; Length 202;
Best Local Similarity 96.8%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 1;

QY 3 ggcagcgaagatttagcaaccacccctacac 33
|||||
Db 40 GGCACGCCAAGTATTAGCAACACCTACAC 70

RESULT 2
AZ846516/c 517 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0146D17R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION clone UUGC2M0146D17 R, DNA sequence.

ACCESSION AZ846516
VERSION AZ846516.1 GI:13016424
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 517)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: D column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 517.
Location/Qualifiers
1..517

FEATURES
source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0146D17"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 159 a 99 c 118 g 141 t
ORIGIN

Query Match 89.1%; Score 29.4; DB 12; Length 517;
Best Local Similarity 96.8%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 1;

QY 3 ggcagcgaagatttagcaaccacccctacac 33
|||||
Db 370 GGCACGCCAAGTATTAGCAACACCTACAC 340

RESULT 3
BF582153 738 bp mRNA linear EST 12-DEC-2000
LOCUS 602099743F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219402 5',
DEFINITION mRNA sequence.

ACCESSION BF582153
VERSION BF582153.1 GI:11655865
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 738)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM9801 row: f column: 11
High quality sequence stop: 714.
Location/Qualifiers
1..738
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4219402"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source
1..738

Query Match 89.1%; Score 29.4; DB 10; Length 738;
Best Local Similarity 96.8%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 1;

QY 3 ggcagcgaagatttagcaaccacccctacac 33
|||||
Db 144 GGCACGCCAAGTATTAGCAACACCTACAC 174

RESULT 4
BI105452 772 bp mRNA linear EST 26-JUN-2001
LOCUS 602891971F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5037137 5',
DEFINITION

ACCESSION BI105452
VERSION BI105452.1 GI:11655865
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 772)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM9801 row: f column: 11
High quality sequence stop: 714.
Location/Qualifiers
1..772
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4219402"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."


```

mRNA sequence.
ACCESSION BI105452
VERSION BI105452.1 GI:14556345
SOURCE EST.
ORGANISM house mouse.
Mammalia; Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 772)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1102 row: n column: 18
High quality sequence stop: 771.
Location/Qualifiers
1..772
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DHI08"
/note="Organ: lung; Vector: pCMV-SPORT6; Site:1: Salt;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
214 a 208 c 173 g 177 t
BASE COUNT
ORIGIN

FEATURES
source
Query Match 89.1%; Score 29.4; DB 10; Length 772;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggccagccaaagtattagcaaccactacac 33
|||||
Db 136 GGCCAGCCAAAGTATTAGCAACTACCTACAC 166

RESULT 5
LOCUS BG966582
DEFINITION 602834412F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988955 5',
mRNA sequence.
ACCESSION BG966582
VERSION BG966582.1 GI:14354219
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11047 row: p column: 06
High quality sequence stop: 769.
Location/Qualifiers
1..833
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DHI08"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: Salt;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
225 a 229 c 186 g 195 t
BASE COUNT
ORIGIN

mRNA sequence.
ACCESSION BI105452
VERSION BI105452.1 GI:14556345
SOURCE EST.
ORGANISM house mouse.
Mammalia; Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 772)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1102 row: n column: 18
High quality sequence stop: 771.
Location/Qualifiers
1..772
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DHI08"
/note="Organ: lung; Vector: pCMV-SPORT6; Site:1: Salt;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
214 a 208 c 173 g 177 t
BASE COUNT
ORIGIN

FEATURES
source
Query Match 89.1%; Score 29.4; DB 10; Length 833;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggccagccaaagtattagcaaccactacac 33
|||||
Db 136 GGCCAGCCAAAGTATTAGCAACTACCTACAC 166

RESULT 6
LOCUS BI083006
DEFINITION 60287452M2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
mRNA sequence.
ACCESSION BI083006
VERSION BI083006.1 GI:14501336
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 835)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11047 row: p column: 06
High quality sequence stop: 769.
Location/Qualifiers
1..835
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DHI08"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: Salt;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
225 a 229 c 186 g 195 t
BASE COUNT
ORIGIN

mRNA sequence.
ACCESSION BG966582
VERSION BG966582.1 GI:14354219
SOURCE EST.
ORGANISM house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11047 row: p column: 06
High quality sequence stop: 769.
Location/Qualifiers
1..833
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DHI08"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: Salt;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
225 a 229 c 186 g 195 t
BASE COUNT
ORIGIN

```

```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11002 row: g column: 04
High quality sequence stop: 830.
Location/Qualifiers
1..833
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4988955"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DHI08 (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: Salt; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
227 a 227 c 186 g 193 t
BASE COUNT
ORIGIN

Query Match 89.1%; Score 29.4; DB 10; Length 833;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggccagccaaagtattagcaaccactacac 33
|||||
Db 136 GGCCAGCCAAAGTATTAGCAACTACCTACAC 166

RESULT 6
LOCUS BI083006
DEFINITION 60287452M2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
mRNA sequence.
ACCESSION BI083006
VERSION BI083006.1 GI:14501336
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 835)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11047 row: p column: 06
High quality sequence stop: 769.
Location/Qualifiers
1..835
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5006453"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DHI08"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: Salt;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
225 a 229 c 186 g 195 t
BASE COUNT
ORIGIN

```

```

Query Match      89.1%; Score 29.4; DB 10; Length 835;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaaccacctacac 33
|||||
Db 150 GGCAGCCAAAGTATTAGCAACACCTACAC 180

RESULT 7
BF579007 949 bp mRNA linear EST 12-DEC-2000
LOCUS 602096124F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224853 5',
DEFINITION mRNA sequence.
ACCESSION BF579007
VERSION BF579007.1 GI:11652719
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224853"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 278 a 241 c 210 g 220 t
ORIGIN
1. .949
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224853"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match      89.1%; Score 29.4; DB 10; Length 949;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaaccacctacac 33
|||||
Db 149 GGCAGCCAAAGTATTAGCAACACCTACAC 179

RESULT 8
BF583521 849 bp mRNA linear EST 12-DEC-2000
LOCUS 602101553F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224853 5',
DEFINITION mRNA sequence.
ACCESSION BF583521
VERSION BF583521.1 GI:11657239
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224853"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 278 a 241 c 210 g 220 t
ORIGIN
1. .949
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224853"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match      89.1%; Score 29.4; DB 10; Length 849;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaaccacctacac 33
|||||
Db 146 GGCAGCCAGAGTATTAGCAACATTACAC 176

RESULT 9
AZ928596 517 bp DNA linear GSS 01-APR-2001
LOCUS 479.dif11h11.s1 Saccharomyces kluyveri Saccharomyces kluyveri
DEFINITION genomic clone 479.dif11h11.s1, DNA sequence.
ACCESSION AZ928596
VERSION AZ928596.1 GI:13499502
KEYWORDS GSS.
SOURCE Saccharomyces kluyveri.
ORGANISM Saccharomyces kluyveri
/organism="Saccharomyces kluyveri"
/strain="NRRL Y-12651 (CBS 3082)"
/db_xref="taxon:4934"

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 849)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9815 row: 1 column: 14
High quality sequence stop: 627.
Location/Qualifiers
1. .849
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224853"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 274 a 215 c 183 g 177 t
ORIGIN
1. .849
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224853"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match      69.7%; Score 23; DB 10; Length 849;
Best Local Similarity 83.9%; Pred. No. 54;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaaccacctacac 33
|||||
Db 146 GGCAGCCAGAGTATTAGCAACATTACAC 176

RESULT 9
AZ928596 517 bp DNA linear GSS 01-APR-2001
LOCUS 479.dif11h11.s1 Saccharomyces kluyveri Saccharomyces kluyveri
DEFINITION genomic clone 479.dif11h11.s1, DNA sequence.
ACCESSION AZ928596
VERSION AZ928596.1 GI:13499502
KEYWORDS GSS.
SOURCE Saccharomyces kluyveri.
ORGANISM Saccharomyces kluyveri
/organism="Saccharomyces kluyveri"
/strain="NRRL Y-12651 (CBS 3082)"
/db_xref="taxon:4934"

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 849)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9815 row: 1 column: 14
High quality sequence stop: 627.
Location/Qualifiers
1. .849
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224853"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 274 a 215 c 183 g 177 t
ORIGIN
1. .849
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224853"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match      69.7%; Score 23; DB 10; Length 849;
Best Local Similarity 83.9%; Pred. No. 54;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaaccacctacac 33
|||||
Db 146 GGCAGCCAGAGTATTAGCAACATTACAC 176

RESULT 9
AZ928596 517 bp DNA linear GSS 01-APR-2001
LOCUS 479.dif11h11.s1 Saccharomyces kluyveri Saccharomyces kluyveri
DEFINITION genomic clone 479.dif11h11.s1, DNA sequence.
ACCESSION AZ928596
VERSION AZ928596.1 GI:13499502
KEYWORDS GSS.
SOURCE Saccharomyces kluyveri.
ORGANISM Saccharomyces kluyveri
/organism="Saccharomyces kluyveri"
/strain="NRRL Y-12651 (CBS 3082)"
/db_xref="taxon:4934"

```

```

/clone_lib="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGACACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
121 a 196 c 220 q 82 t

```

JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-CT0451-
021100-017-h04&t3=2000-11-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 239.
Location/Qualifiers
1. .239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0451"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORSTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 59 a 79 c 50 g 51 t
ORIGIN

Query Match 65.5%; Score 21.6; DB 10; Length 239;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaaccaccta 30
||||| || ||||| ||||| ||||| |||||
Db 173 GGCAGTCAGAGTATTAGCAACTACTTA 200

RESULT 14
BG058466

LOCUS BG058466 290 bp mRNA linear EST 25-JAN-2001
DEFINITION nah17g07.y1 NCI_CGAP_HN21 Homo sapiens cDNA clone IMAGE:4231477 5'
similar to SW:KV3H_HUMAN P04207 IG KAPPA CHAIN V-III REGION CLL
PRECURSOR /, mRNA sequence.
ACCESSION BG058466
VERSION BG058466.1 GI:12524992
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 290)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoimage@llnl.gov
Seq primer: -40RP from Glibco.
Location/Qualifiers
1. .290
/organism="Homo sapiens"

FEATURES
source

/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_HN21"
/tissue_type="nasopharyngeal carcinoma"
/lab_host="DH108"
/note="Organ: head/neck; Vector: pAMP1; mRNA made from head/neck tumor, cDNA made by oligo-dT priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. cDNA Library Preparation: David B. Krizman, Ph.D."
62 a 96 c 67 g 65 t
BASE COUNT 188 a 214 c 190 g 148 t
ORIGIN

Query Match 65.5%; Score 21.6; DB 10; Length 290;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 ggcacgcaaaagtattagcaaccaccta 30
||||| || ||||| ||||| |||||
Db 190 GGCACCCAGAGCTTAGCAACACCTTA 217

RESULT 15
BG397970
LOCUS 602439490F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565710 5',
DEFINITION mRNA sequence.
ACCESSION BG397970
VERSION BG397970.1 GI:13291418
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1283 row: c column: 23
High quality sequence stop: 729.
Location/Qualifiers
1..740
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4565710"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
188 a 214 c 190 g 148 t
BASE COUNT 188 a 214 c 190 g 148 t
ORIGIN

FEATURES
source
1..740
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4565710"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
188 a 214 c 190 g 148 t
BASE COUNT 188 a 214 c 190 g 148 t
ORIGIN

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 ggcacgcaaaagtattagcaaccaccta 30
||||| || ||||| ||||| |||||
Db 157 GGCACGTCAGAGTATTAGCAACTACTTA 184
Search completed: August 21, 2002, 09:56:01
Job time: 9324 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:39 ; Search time 754.01 Seconds
(without alignments)
75.142 Million cell updates/sec

Title: US-09-339-922A-107

Perfect score: 33
Sequence: 1 caggccagcacaagattagcaaccactacac 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802.*
1: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	33	AAF28237	DNA encoding enhan
2	33	100.0	39	AAV49848	LM609 grafted anti
3	33	100.0	39	AAF28204	DNA encoding LM609
4	33	100.0	321	AAV49843	LM609 antibody lig
5	33	100.0	321	AAV49821	Vitaxin antibody lig
6	33	100.0	321	AAV49823	LM609 antibody lig
7	33	100.0	321	AAH74624	DNA encoding light
8	33	100.0	321	AAH74626	DNA encoding light
9	33	100.0	321	AAF28176	Vitaxin light chal

10	33	100.0	321	22	AAF28178	Antibody LM609 lig	
11	33	100.0	321	22	AAF28199	DNA encoding light	
c	12	31	93.9	101	20	AAV71825	Alpha-v beta-3 Mab
13	31	93.9	108	20	AAV71816	Alpha-v beta-3 Mab	
14	31	93.9	315	20	AAV71803	JK gene segment.	
15	31	93.9	315	20	AAV71805	Humanised anti-aip	
16	31	93.9	321	20	AAV71800	Humanised anti-aip	
17	31	93.9	324	20	AAV71798	Murine vitronectin	
18	31	93.9	338	20	AAV71802	Vitronectin alpha-	
c	19	30	90.9	72	19	AAV49830	LM609 grafted anti
c	20	30	90.9	72	22	AAF28185	Oligonucleotide #7
c	21	30	90.9	75	19	AAV49839	LM609 grafted anti
c	22	30	90.9	75	22	AAH74633	PCR primer for lig
c	23	30	90.9	75	22	AAF28194	Grafted light chain
c	24	29.8	90.3	33	22	AAF28238	DNA encoding enhancer
c	25	29.4	89.1	128	13	AAQ26786	Oligomer jbl7 used
c	26	29.4	89.1	128	22	AAF58750	Humanised CMV5 ant
27	29.4	89.1	381	15	AAQ64167	Sequence of mouse	
28	29.4	89.1	381	22	AAF58747	Murine CMV5 antibody	
29	29.4	89.1	5238	11	AAQ04654	Plasmid pBT111 enc	
30	28.2	85.5	39	19	AAV49868	LM609 grafted anti	
31	28.2	85.5	39	22	AAF28224	DNA encoding mutant	
32	27.8	84.2	324	17	AAH73446	EGF receptor chimera	
33	27.8	84.2	342	22	AAH73446	Murine coding sequence	
34	26.2	79.4	381	21	AAZ35242	Mouse anti-verotoxin	
35	26.2	79.4	381	21	AAZ35244	Humanised anti-verotoxin	
36	24.6	74.5	651	21	AAH44346	Human secreted expression	
37	24.6	74.5	8858	20	AAH10202	Expression vector	
38	24.6	74.5	8858	24	AAH43777	Chi220 light chain	
c	39	24	72.7	114	20	AAV71817	Alpha-v beta-3 Mab
40	23	69.7	363	17	AAH38510	Light chain coding	
41	23	69.7	415	21	AAH00904	Humanised antibody	
42	23	69.7	415	21	AAH01262	Mouse monoclonal antibody	
43	21.8	66.1	9789	17	AAH41852	DNA encoding the variable	
44	20.4	61.8	321	20	AAH10203	DNA encoding the variable	
45	20.4	61.8	321	24	AAH43773	Light chain cDNA of	

ALIGNMENTS

RESULT 1
AAF28237
ID AAF28237 standard; DNA; 33 BP.
AC AAF28237;
DT 03-APR-2001 (first entry)
XX DNA encoding enhanced 6H6Lh light chain CDR1.
DE LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
XX Unidentified.
OS WO200078815-A1.
PN 28-DEC-2000.
PD 23-JUN-2000; 2000WO-US17454.
PF 24-JUN-1999; 99US-0339922.
PR (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX Huse WD, Wu H;
XX WPI; 2001-050110/06.
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -
 PS Claim 16; Page 107; 132pp; English.
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 33 BP; 12 A; 12 C; 5 G; 4 T; 0 other;
 Query Match 100.0%; Score 33; DB 22; Length 33;
 Best Local Similarity 100.0%; Pred. NO. 8.8e-05;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 caggccagccaaagtattagcaaccactacac 33
 Db 1 caggccagccaaagtattagcaaccactacac 33
 RESULT 2
 AAV49848
 ID AAV49848 standard; DNA; 39 BP.
 XX
 AC AAV49848;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-L region CDR1 DNA fragment #1.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region; ss.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 XX WPI; 1998-437472/37.
 DR P-PSDB; AAW76011.
 DR
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure; Page 40; 129pp; English.
 XX
 CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal
 CC antibody LM609 heavy and light chain variable region. LM609 and the
 CC antibody Vitaxin bind selectively to integrin alphavbeta3 and can be used
 CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 39 BP; 13 A; 12 C; 7 G; 7 T; 0 other;
 Query Match 100.0%; Score 33; DB 19; Length 39;
 Best Local Similarity 100.0%; Pred. NO. 9e-05;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 caggccagccaaagtattagcaaccactacac 33
 Db 1 caggccagccaaagtattagcaaccactacac 33
 RESULT 3
 AAF28204
 ID AAF28204 standard; DNA; 39 BP.
 XX
 AC AAF28204;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE DNA encoding LM609 VL CDR1 peptide.
 XX
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Page 40; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 39 BP; 13 A; 12 C; 7 G; 7 T; 0 other;
 Query Match 100.0%; Score 33; DB 22; Length 39;
 P-PSDB; AAW76011.

Best Local Similarity 100.0%; Pred. No. 9e-05; Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caggccagcacaagtattagcaaccactacac 33
 |||||
 Db 1 caggccagcacaagtattagcaaccactacac 33
 |||||

RESULT 4
 AAV49843
 ID AAV49843 standard; DNA; 321 BP.
 AC AAV49843;
 XX
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 antibody light chain variable region DNA grafted fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..321
 FT /tag= a
 FT /product= "LM609 grafted antibody light chain variable
 FT region"
 FT /note= "partial sequence, no start or stop codon given"
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR P-PSDB; AAW76006.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 24; Fig 7; 129pp; English.
 XX
 CC This sequence encodes a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 100.0%; Score 33; DB 19; Length 321;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caggccagcacaagtattagcaaccactacac 33
 |||||
 Db 70 caggccagcacaagtattagcaaccactacac 102
 |||||

RESULT 5
 AAV49821
 ID AAV49821 standard; DNA; 321 BP.
 AC AAV49821;
 XX
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody light chain variable region DNA.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..321
 FT /tag= a
 FT /product= "vitaxin antibody light chain variable region"
 FT /note= "partial sequence, no start or stop codon given"
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR P-PSDB; AAW76002.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 6; Fig 1b; 129pp; English.
 XX
 CC This sequence encodes the vitaxin antibody variable light chain region.
 CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Query Match 100.0%; Score 33; DB 19; Length 321;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caggccagcacaagtattagcaaccactacac 33
 |||||


```

Db      70 caggccagccaaagtattagcaaccacctacac 102

RESULT      6
AAV49823
ID      AAV49823 standard; DNA; 321 BP.
XX
XX
AC      AAV49823;
XX
XX
DT      02-NOV-1998 (first entry)
XX
XX
DE      LM609 antibody light chain variable region DNA fragment.
XX
XX
KW      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; ss.
XX
OS      Mus sp.
XX
XX
FH      Key
FT      CDS
FT      Location/Qualifiers
FT      1..321
FT      /*tag= a
FT      /transl_except= "(pos: 145..147, aa: Xaa)"
FT      /note= "Xaa is unspecified"
XX
XX
PN      W09833919-A2.
XX
XX
PD      06-AUG-1998.
XX
XX
PF      30-JAN-1998; 98MO-US01826.
XX
XX
PR      30-JAN-1997; 97US-0791391.
XX
XX
PA      (IXSY-) IXSYS INC.
XX
XX
PI      Glaser SM, Huse WD;
XX
XX
DR      WPI; 1998-437472/37.
DR      P-PSDB; AAV75004.
XX
XX
PT      Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT      integrin - and related grafted antibodies based on murine monoclonal
PT      LM609, also related nucleic acid, used to treat, prevent or diagnose
PT      angiogenesis or restenosis
XX
XX
PS      Claim 40; Fig 2b; 129pp; English.
XX
XX
CC      This sequence encodes the LM609 antibody variable light chain region.
CC      LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC      and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC      block integrin-mediated signal transduction. This is useful in the
CC      treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC      specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC      inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC      psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC      etc.). The antibodies contain non-murine framework regions so are
CC      suitable for use in humans. Enhanced types of LM609 have affinity more
CC      than 90 times greater than that of parent the parent antibody.
XX
XX
SQ      Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match      100.0%; Score 33; DB 19; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 caggccagccaaagtattagcaaccacctacac 33
      |||||
Db      70 caggccagccaaagtattagcaaccacctacac 102

RESULT      7
AAH74624
ID      AAH74624 standard; DNA; 321 BP.
XX
XX
AC      AAH74624;
XX
XX
DT      15-OCT-2001 (first entry)
XX
XX
DE      DNA encoding light chain variable region of LM609 grafted antibody.
XX
XX
KW      Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW      chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW      neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW      cancer; ss.
XX
OS      Synthetic.
OS      Mus sp.
XX
XX
FH      Key
FT      CDS
FT      Location/Qualifiers
FT      1..321
FT      /*tag= a
FT      /transl_except= "(pos: 145..147, aa: Xaa)"
FT      /note= "Xaa is unspecified"
XX
XX
PN      US2001011125-A1.
XX
XX
PD      02-AUG-2001.
XX
XX
PF      30-JAN-1997; 97US-0790540.
XX
XX
PR      30-JAN-1997; 97US-0790540.
XX
XX
PA      (HUSE/) HUSE W D.
XX
XX
PI      Huse WD;
XX
XX
DR      WPI; 2001-496171/54.
DR      P-PSDB; AAG63588.
XX
XX
PT      New LM609 grafted antibody exhibiting selective binding affinity to
PT      alphavbeta3, comprising at least one LM609 grafted heavy and light
PT      chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT      disorders or cancer -
XX
XX
PS      Claim 6; Fig 1B; 25pp; English.
XX
XX
CC      The present sequence encodes the light chain variable region of the
CC      grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC      specifically recognises the integrin alphavbeta3, and inhibits its
CC      functional activity. The LM609 grafted antibody has the
CC      complementarity determining regions (CDRs) substituted into a non-murine
CC      framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC      polypeptides and fragments are useful in diagnostic and therapeutic
CC      purposes, such as in the production of LM609 grafted antibodies and
CC      fragments having binding specificity and inhibitory activity against
CC      the integrin alphavbeta3. The antibody can be used for the diagnosis
CC      or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC      disorders, chronic articular rheumatism, psoriasis, disorders
CC      associated with inappropriate or inopportune invasion of vessels such
CC      as diabetic retinopathy, neovascular glaucoma and capillary
CC      proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC      binding activity of alphavbeta3 that are necessary for progression of
CC      an alphavbeta3-mediated disease.
XX
XX
SQ      Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match      100.0%; Score 33; DB 22; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 caggccagccaaagtattagcaaccacctacac 33
      |||||

```

```

Db      70 caggccgacaaagtattagcaaccactacac 102
RESULT  8
AAH74626
ID      AAH74626 standard; DNA; 321 BP.
XX
XX      AAH74626;
AC
XX      15-OCT-2001 (first entry)
DT
XX
XX      DNA encoding light chain variable region of LM609 antibody.
DE
XX      Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW      chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW      neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW      cancer; ss.
XX
XX      Mus sp.
OS
XX      US2001011125-A1.
PN
XX      02-AUG-2001.
PD
XX      30-JAN-1997; 97US-0790540.
PF
XX      30-JAN-1997; 97US-0790540.
PR
XX      (HUSE/) HUSE W D.
PA
XX      Huse WD;
PI
XX      WPI; 2001-496171/54.
DR      P-PSDB; AAG63590.
XX
XX      New LM609 grafted antibody exhibiting selective binding affinity to
PT      alphavbeta3, comprising at least one LM609 grafted heavy and light
PT      chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT      disorders or cancer
TX
XX      Disclosure; Fig 2B; 25pp; English.
XX
XX      The present sequence encodes the light chain variable region of the
CC      monoclonal antibody LM609. LM609 is a murine antibody which specifically
CC      recognises the integrin alphavbeta3, and inhibits its functional activity.
CC      The specification describes a LM609 grafted antibody which has the
CC      complementarity determining regions (CDRs) substituted into a non-murine
CC      framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC      polypeptides and fragments are useful in diagnostic and therapeutic
CC      purposes, such as in the production of LM609 grafted antibodies and
CC      fragments having binding specificity and inhibitory activity against
CC      the integrin alphavbeta3. The antibody can be used for the diagnosis
CC      or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC      disorders, chronic articular rheumatism, psoriasis, disorders
CC      associated with inappropriate or inopportune invasion of vessels such
CC      as diabetic retinopathy, neovascular glaucoma and capillary
CC      proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC      binding activity of alphavbeta3 that are necessary for progression of
CC      an alphavbeta3-mediated disease.
XX
XX      Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;
SQ
Query Match      100.0%; Score 33; DB 22; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 caggccgacaaagtattagcaaccactacac 33
      |||||||
Db      70 caggccgacaaagtattagcaaccactacac 102

RESULT  9
AAH74626
ID      AAH74626 standard; DNA; 321 BP.
XX
XX      AAH74626;
AC
XX      03-APR-2001 (first entry)
DT
XX
XX      Antibody LM609 light chain variable region DNA.
DE
XX      LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
KW      inflammatory; cancer; retina; restenosis; osteoporosis; ds.
KW
XX      Unidentified.
OS

```

```

AAF28176
ID      AAF28176 standard; DNA; 321 BP.
XX
XX      AAF28176;
AC
XX      03-APR-2001 (first entry)
DT
XX
XX      Vitaxin light chain variable region DNA.
DE
XX      LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
KW      inflammatory; cancer; retina; restenosis; osteoporosis; ds.
KW
XX      Unidentified.
OS
XX      WO200078815-A1.
PN
XX      28-DEC-2000.
PD
XX      23-JUN-2000; 2000WO-US17454.
PF
XX      24-JUN-1999; 99US-0339922.
PR
XX      (MOLE-) APPLIED MOLECULAR EVOLUTION.
PA
XX      Huse WD, Wu H;
PI
XX      WPI; 2001-050110/06.
DR
XX
XX      Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT      to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT      angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT      osteoporosis
TX
XX      Disclosure; Fig 1; 132pp; English.
XX
XX      The present invention relates to enhanced LM609 grafted antibodies
CC      exhibiting selective binding affinity to alphavbeta3 integrin or
CC      their functional fragments. The antibodies or their functional
CC      fragments can be used in the diagnosis and treatment of
CC      alphavbeta3-mediated diseases such as angiogenesis, inflammatory
CC      diseases (such as psoriasis and chronic articular rheumatism),
CC      disorders associated with inappropriate or inopportune invasion of
CC      vessels (such as diabetic retinopathy, neovascular glaucoma and
CC      cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC      diseases (such as macular degeneration), restenosis and
CC      osteoporosis.
XX
XX      Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
SQ
Query Match      100.0%; Score 33; DB 22; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 caggccgacaaagtattagcaaccactacac 33
      |||||||
Db      70 caggccgacaaagtattagcaaccactacac 102

RESULT  10
AAF28176
ID      AAF28176 standard; DNA; 321 BP.
XX
XX      AAF28176;
AC
XX      03-APR-2001 (first entry)
DT
XX
XX      Antibody LM609 light chain variable region DNA.
DE
XX      LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
KW      inflammatory; cancer; retina; restenosis; osteoporosis; ds.
KW
XX      Unidentified.
OS

```


PS Example 14; Page 51; 97pp; English.

XX SBA3167 is one of 4 overlapping oligonucleotides (see AAV71824-27);
 CC used to construct DNA (see AAV71805) encoding a region of the murine
 CC D12 monoclonal antibody light chain variable region (VL) that is
 CC modified in humanised D12 VL D12HZLCREI. The synthetic D12 VL
 CC gene was utilised in the construction of an expression vector for
 CC the humanised D12 VL (see AAW87455). D12 is a murine anti-human
 CC alpha-v beta-3 vitronectin receptor monoclonal antibody. Humanised
 CC D12 antibodies of the invention can be used for passive
 CC immunotherapy of disorders mediated by the alpha-v beta-3
 CC vitronectin receptor, e.g. restenosis and angiogenic-related
 CC disorders.

XX Sequence 101 BP; 21 A; 20 C; 31 G; 29 T; 0 other;

Query Match 93.9%; Score 31; DB 20; Length 101;

Best Local Similarity 100.0%; Pred. No. 0.00074;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaaccacctacac 33

Db 99 GGCACGCAAAAGTATTAGCAACCACCTACAC 69

RESULT 13

AAV71816

ID AAV71816 standard; DNA; 108 BP.

XX AAV71816;

DT 15-MAR-1999 (first entry)

XX Alpha-v beta-3 MAB D12HZHC 1-0 VL oligonucleotide SBA1327.

XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12HZHC 1-0; ss.

XX Mus sp.

OS Synthetic.

XX WO9840488-A1.

PD 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04987.

XX 12-MAR-1997; 97US-0039609.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Johanson KO, Jonak ZL, Taylor AH;

XX WPI; 1999-034590/03.

XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

XX Example 13; Page 47; 97pp; English.

XX SBA1327 is one of 4 overlapping oligonucleotides (see AAV71816-19)
 CC used to construct DNA (see AAV71802) encoding a region of the murine
 CC D12 monoclonal antibody light chain variable region (VL) that is
 CC modified in humanised D12 VL D12HZHC 1-0. The synthetic D12 VL
 CC gene was utilised in the construction of an expression vector for

CC the humanised D12 VL (see AAV71800). D12 is a murine anti-human
 CC alpha-v beta-3 vitronectin receptor monoclonal antibody. Humanised
 CC D12 antibodies of the invention can be used for passive
 CC immunotherapy of disorders mediated by the alpha-v beta-3
 CC vitronectin receptor, e.g. restenosis and angiogenic-related
 CC disorders.

XX Sequence 108 BP; 28 A; 34 C; 22 G; 24 T; 0 other;

Query Match 93.9%; Score 31; DB 20; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.00074;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaaccacctacac 33

Db 72 ggcacgcaaaagtattagcaaccacctacac 102

RESULT 14

AAV71803

ID AAV71803 standard; cDNA; 315 BP.

XX AAV71803;

DT 15-MAR-1999 (first entry)

XX Jk gene segment.

XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12HZREI; Jk gene; ds.

XX Mus sp.

OS Synthetic.

XX WO9840488-A1.

PD 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04987.

XX 12-MAR-1997; 97US-0039609.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Johanson KO, Jonak ZL, Taylor AH;

XX WPI; 1999-034590/03.

XX P-PSDB; AAW87456.

XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

XX Example 14; Page 66; 97pp; English.

XX This DNA sequence comprises a segment of the Jk gene. It was
 CC prepared from 4 overlapping synthetic oligonucleotides (see
 CC AAV71824-27) and used in the construction of an expression vector
 CC for D12HZREI humanised light chain variable region (see AAW87458)
 CC comprising a human REI framework and complementarity determining
 CC regions from the anti-human alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12. Humanised D12 antibodies can be used for
 CC passive immunotherapy of disorders mediated by the alpha-v beta-3
 CC vitronectin receptor, e.g. restenosis and angiogenic associated
 CC diseases.

XX

SQ Sequence 315 BP; 81 A; 88 C; 70 G; 76 T; 0 other;

Query Match 93.9%; Score 31; DB 20; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ggccagccaaagtatttagcaaccacctacac 33
|||||
Db 72 ggccagccaaagtatttagcaaccacctacac 102

RESULT 15

AAV71805

ID AAV71805 standard; cDNA; 315 BP.

XX AC AAV71805;

XX DT 15-MAR-1999 (first entry)

XX DE Humanised anti-alpha-v beta-3 MAb D12H2LCREI VL CDNA.

XX KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
XX KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
XX KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
XX KW angiogenesis; diabetic retinopathy; inflammation;
XX KW macular degeneration; osteoporosis; Paget's disease;
XX KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
XX KW D12H2LCREI; ds.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO9840488-A1.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US04987.

XX PR 12-MAR-1997; 97US-0039609.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Johanson KO, Jonak ZL, Taylor AH;

XX DR WPI: 1999-034590/03.

XX DR P-PSDB; AAW87458.

XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
XX PT immunotherapeutic treatment of e.g. diabetic retinopathy,
XX PT inflammatory disorders, atherosclerosis, restenosis, cancers or
XX PT osteoporosis

PS Example 14; Page 68-69; 97pp; English.

XX CC This DNA sequence codes for the light chain variable region (VL,
XX CC see AAW87458) of humanised anti-alpha-v beta-3 vitronectin receptor
XX CC monoclonal antibody D12H2LCREI. It is based on a synthetic
XX CC humanised kappa chain based on a modified human REI kappa
XX CC framework and complementarity determining regions from the murine
XX CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
XX CC D12 (see AAW84094). Humanised antibodies of the invention can be used
XX CC for passive immunotherapy of a disorder mediated by the alpha-v
XX CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
XX CC related disorders, such as angiogenesis associated with diabetic
XX CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
XX CC disorders, macular degeneration, rheumatoid arthritis and cancer,
XX CC e.g. solid tumour metastasis, and diseases where bone resorption is
XX CC associated with pathology such as osteoporosis, hyperparathyroidism,
XX CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
XX CC produced by bone metastasis, bone loss due to immobilisation or sex
XX CC hormone deficiency. They can also be used for targeted drug
XX CC therapy, and for detection and diagnosis.

XX SQ Sequence 315 BP; 81 A; 88 C; 70 G; 76 T; 0 other;

Query Match 93.9%; Score 31; DB 20; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ggccagccaaagtatttagcaaccacctacac 33
|||||
Db 72 ggccagccaaagtatttagcaaccacctacac 102

Search completed: August 21, 2002, 10:08:40
Job time: 10058 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:19 ; Search time 174.26 Seconds
(without alignments)
46.516 Million cell updates/sec

Title: US-09-339-922A-107
Perfect score: 33
Sequence: 1 caggccagccaaagtatttagcaaccctacac 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	29.4	89.1	128	1	US-07-634-278-91
C 2	29.4	89.1	128	1	US-08-477-728-91
C 3	29.4	89.1	128	1	US-08-474-040-91
C 4	29.4	89.1	128	1	US-08-487-200-91
C 5	29.4	89.1	128	4	US-08-484-537-91
C 6	29.4	89.1	381	1	US-07-634-278-82
7	29.4	89.1	381	1	US-08-477-728-82
8	29.4	89.1	381	1	US-08-474-040-82
9	29.4	89.1	381	1	US-08-487-200-82
10	29.4	89.1	381	4	US-08-484-537-82
11	29.4	89.1	424	1	US-08-436-463-3
12	29.4	89.1	5238	6	5453363-1
13	24.6	74.5	324	4	US-09-247-352-14
14	24.6	74.5	8858	4	US-09-247-352-6
15	23	69.7	324	4	US-08-737-560A-13
16	23	69.7	363	2	US-08-737-560A-8
17	20.4	61.8	321	4	US-09-247-352-7
18	20.4	61.8	321	4	US-09-247-352-11
19	18.4	55.8	812	1	US-08-053-131-178
20	18.4	55.8	812	1	US-08-096-762-178
21	18.4	55.8	812	4	US-09-042-353-41
22	18.4	55.8	812	4	US-08-758-417A-306
23	18.2	55.2	322	2	US-08-476-176B-3
24	18.2	55.2	322	3	US-08-127-721A-3
25	18.2	55.2	322	3	US-08-485-246A-3
26	18.2	55.2	424	2	US-08-476-176B-5
27	18.2	55.2	424	2	US-08-476-176B-7

28	18.2	55.2	424	2	US-08-476-176B-9	Sequence 9, Appli
29	18.2	55.2	424	3	US-08-127-721A-5	Sequence 5, Appli
30	18.2	55.2	424	3	US-08-127-721A-7	Sequence 7, Appli
31	18.2	55.2	424	3	US-08-127-721A-9	Sequence 9, Appli
32	18.2	55.2	424	3	US-08-485-246A-5	Sequence 5, Appli
33	18.2	55.2	424	3	US-08-485-246A-7	Sequence 7, Appli
34	18.2	55.2	424	3	US-08-485-246A-9	Sequence 9, Appli
C 35	18.2	55.2	4800	5	PCT-US94-07779-1	Sequence 1, Appli
C 36	18.2	55.2	7083	4	US-09-198-839-1	Sequence 1, Appli
C 37	18.2	55.2	7294	1	US-08-440-787A-1	Sequence 1, Appli
C 38	18.2	55.2	7294	1	US-08-440-787A-5	Sequence 5, Appli
C 39	18.2	55.2	7294	4	US-08-367-685-1	Sequence 1, Appli
C 40	18.2	55.2	7294	4	US-08-367-685-5	Sequence 5, Appli
C 41	18.2	55.2	7294	5	PCT-US91-071141-1	Sequence 1, Appli
C 42	18.2	55.2	7294	5	PCT-US91-071141-5	Sequence 5, Appli
C 43	18.2	55.2	7317	1	US-08-464-136-2	Sequence 2, Appli
C 44	18.2	55.2	7317	2	US-08-349-131-2	Sequence 2, Appli
C 45	18.2	55.2	7317	3	US-08-470-297A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-07-634-278-91/c
; Sequence 91, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-07-634-278-91

Query Match 89.1%; Score 29.4; DB 1; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.00019;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggcagcgaagattattagcaaacctacac 33
|||||
Db 95 GGCAGCAGCAAGTATTAGCAACAACCTACAC 65

RESULT 2
US-08-477-728-91/c
Sequence 91, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)

US-08-477-728-91
Query Match 89.1%; Score 29.4; DB 1; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.00019;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggcagcgaagattattagcaaacctacac 33
|||||
Db 95 GGCAGCAGCAAGTATTAGCAACAACCTACAC 65

Qy 3 ggcagcgaagattattagcaaacctacac 33
|||||
Db 95 GGCAGCAGCAAGTATTAGCAACAACCTACAC 65

RESULT 3
US-08-474-040-91/c
Sequence 91, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)

US-08-474-040-91
Query Match 89.1%; Score 29.4; DB 1; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.00019;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggcagcgaagattattagcaaacctacac 33
|||||
Db 95 GGCAGCAGCAAGTATTAGCAACAACCTACAC 65

RESULT 4
US-08-487-200-91/c

```
; Sequence 91, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-487-200-91

Query Match      89.1%; Score 29.4; DB 1; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.00019;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaaccacctacac 33
   |||||||||||||||||||
DB 95 GCCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 5
US-08-484-537-91/c
; Sequence 91, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
```

```
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-484-537-91

Query Match      89.1%; Score 29.4; DB 4; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.00019;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaaccacctacac 33
   |||||||||||||||||||
DB 95 GCCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 6
US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
```


Query Match 89.1%; Score 29.4; DB 1; Length 381;
Best Local Similarity 96.8%; Pred. No. 0.00024;
Matches 30; Conservative 0; Mismatches 1; Indels

Qy 3 gccagcaagtagtagcaaccacacac 33
 |||
 pb 132 ggccagcccaagtagtagcaaccacacac 162

RESULT 8
US-08-474-040-82
; Sequence 82, Application US/08474040
; Patent No. 5693761

?
? GUNNING LINE ORGANIZATION.
?
? APPLICANT: QUEEN, Cary L.
?
? APPLICANT: CO, Man Sung
?
? APPLICANT: SCHNEIDER, William P.
?
? APPLICANT: LANDOLFI, Nicholas F.
?
? APPLICANT: COELINGH, Kathleen L.
?
? APPLICANT: SELICK, Harold E.
?
? TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBULINS
?
? NUMBER OF SEQUENCES: 113
?
? CORRESPONDENCE ADDRESS:
?
? ADDRESSEE: Townsend and Townsend Khourie and Crew
?
? STREET: 379 Lyttton Avenue
?
? CITY: Palo Alto
?
? STATE: California
?
? COUNTRY: US
?
? ZIP: 94301
?
? COMPUTER READABLE FORM:
?
? MEDIUM TYPE: Floppy disk
?
? COMPUTER: IBM PC compatible
?
? OPERATING SYSTEM: PC-DOS/VMS-POS
?
? SOFTWARE: Patent In Release #1.0, Version #1.25
?
? CURRENT APPLICATION DATA:
?
? APPLICATION NUMBER: US/08/474.040

:
:

```
;
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
;
US-08-474-040-82

Query Match 89.1%; Score 29.4; DB 1; Length 381;
Best Local Similarity 96.8%; Pred. No. 0.00024;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gccagcagcaaaagtattagcaaccacctacac 33
|||||
DB 132 GCCAGCCCAAGTATTAGCAACACCTACAC 162

RESULT 9
US-08-487-200-82
; Sequence 82, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
```

```
;
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
;
US-08-487-200-82

Query Match 89.1%; Score 29.4; DB 1; Length 381;
Best Local Similarity 96.8%; Pred. No. 0.00024;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gccagcagcaaaagtattagcaaccacctacac 33
|||||
DB 132 GCCAGCCCAAGTATTAGCAACACCTACAC 162

RESULT 10
US-08-484-537-82
; Sequence 82, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-484-537-82

Query Match      89.1%; Score 29.4; DB 4; Length 381;
Best Local Similarity 96.8%; Pred. No. 0.00024;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ggcagccaaagtattagcaaccacctacac 33
Db      132 GCCAGCCAAAGTATTAGCAACACCTACAC 162

RESULT 11
US-08-436-463-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
```

```
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..403
US-08-436-463-3

Query Match      89.1%; Score 29.4; DB 1; Length 424;
Best Local Similarity 96.8%; Pred. No. 0.00025;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ggcagccaaagtattagcaaccacctacac 33
Db      154 GCCAGCCAAAGTATTAGCAACACCTACAC 184

RESULT 12
5453363-1
; Patent No. 5453363
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
; ING AFTER GENETIC EXPRESSION IN PROKARYOTES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,044
; FILING DATE: 02-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 942,370
; FILING DATE: 09-SEP-1992
; APPLICATION NUMBER: 498,500
; FILING DATE: 23-MAR-1990
; APPLICATION NUMBER: 76,207
; FILING DATE: 23-OCT-1986
; SEQ ID NO:1:
; LENGTH: 5238
5453363-1

Query Match      89.1%; Score 29.4; DB 6; Length 5238;
Best Local Similarity 96.8%; Pred. No. 0.00042;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ggcagccaaagtattagcaaccacctacac 33
Db      78 ggcagccaaagtattagcaaccacctacac 108

RESULT 13
US-09-247-352-14
; Sequence 14, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Sladak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19
```

; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Human and Mouse
US-09-247-352-14

Query Match 74.5%; Score 24.6; DB 4; Length 324;
Best Local Similarity 87.1%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 gcccagccaaagtattagcaaccactacac 33
||||||| ||||||| || |||||
Db 72 gcccagccagagtattagcgactactacac 102

RESULT 14

US-09-247-352-6
; Sequence 6, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Sladak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Rajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8858
; TYPE: DNA
; ORGANISM: Human and Mouse
US-09-247-352-6

Query Match 74.5%; Score 24.6; DB 4; Length 8858;
Best Local Similarity 87.1%; Pred. No. 0.061;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 gcccagccaaagtattagcaaccactacac 33
||||||| ||||||| || |||||
Db 1136 gcccagccagagtattagcgactactacac 1166

RESULT 15

US-08-737-560A-13
; Sequence 13, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuil
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea

; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1
; OTHER INFORMATION: light chain variable region
US-08-737-560A-13

Query Match 69.7%; Score 23; DB 2; Length 324;
Best Local Similarity 83.9%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 gcccagccaaagtattagcaaccactacac 33
||||||| ||||||| || |||||
Db 72 GCCCAGCCAGACTATTAGCGACTACTTACAC 102

Search completed: August 21, 2002, 10:52:20
Job time: 9660 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: August 21, 2002, 10:49:57 ; Search time 2408.76 Seconds
(without alignments)
286.693 Million cell updates/sec

Title: US-09-339-922A-109
Perfect score: 33
Sequence: 1 caggccgcaaaagtattagcaacttctacac 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:

2: gb_hgtg:

3: gb_in:

4: gb_om:

5: gb_ov:

6: gb_pat:

7: gb_ph:

8: gb_pl:

9: gb_pr:

10: gb_ro:

11: gb_sts:

12: gb_sy:

13: gb_un:

14: gb_vl:

15: em_ba:

16: em_fun:

17: em_in:

18: em_mu:

19: em_om:

20: em_or:

21: em_ov:

22: em_pat:

23: em_ph:

24: em_pl:

25: em_ro:

26: em_sts:

27: em_sy:

28: em_un:

29: em_vl:

30: em_hgtg_hum:

31: em_hgtg_inv:

32: em_hgtg_other:

33: em_hgtg_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
--------	-------	-------	-------	--------	----	-------------

RESULT 1

AX060888

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

AX060888

Sequence 109 from Patent WO0078815.

AX060888

AX060888.1

GI:12406266

synthetic construct.

synthetic construct

artificial sequence.

1 (bases 1 to 33)

Huse, W.D. and Wu, H.

Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids

encoding same and methods of use

Patent: WO 0078815-A 109 28-DEC-2000;

Applied Molecular Evolution (US)

Location/Qualifiers

1..33

/organism="synthetic construct"

/db_xref="taxon:32630"

<1..>33

/note="Mutated complementarity determining region (CDR)"

/codon_start=1

ALIGNMENTS

33 bp DNA

linear PAT 22-JAN-2001

1	33	100.0	33	6	AX060888	AX060888 Sequence
2	31.4	95.2	39	6	AX060860	AX060860 Sequence
3	28.8	90.3	33	6	AX060886	AX060886 Sequence
4	29.8	90.3	39	6	AX060820	AX060820 Sequence
5	29.8	90.3	321	6	AX060782	AX060782 Sequence
6	29.8	90.3	321	6	AX060786	AX060786 Sequence
7	29.8	90.3	321	6	AX060810	AX060810 Sequence
8	29.4	89.1	243	10	MMU19309	U19309 Mus musculus
9	28.4	89.1	285	10	AF139842	AF139842 Mus muscu
10	29.4	89.1	303	10	S60864	S60864 Ab2 kappa c
11	29.4	89.1	324	10	MMU16184	U16184 Mus muscu
12	29.4	89.1	330	10	MUSIGL2VK	L78684 Mus muscu
13	29.4	89.1	348	10	MMY16070	Y16070 Mus muscu
14	29.4	89.1	370	10	MUSIGXD	M93959 Mouse Ig ac
15	28.4	89.1	845	10	MMU235976	AJ235976 Mus muscu
16	29.4	89.1	56168	2	AC101339	AC101339 Mus muscu
17	27.8	84.2	128	6	ARI26867	ARI26867 Sequence
18	27.8	84.2	128	6	I31962	I31962 Sequence 91
19	27.8	84.2	128	6	I78574	I78574 Sequence 91
20	27.8	84.2	128	6	I78629	I78629 Sequence 91
21	27.8	84.2	276	10	MMU19328	U19328 Mus muscu
22	27.8	84.2	286	10	AF139843	AF139843 Mus muscu
23	27.8	84.2	297	10	AF137617	AF137617 Mus muscu
24	27.8	84.2	300	10	MUSIGKABJ	M34528 Mouse Ig ka
25	27.8	84.2	303	10	S66242	S66242 anti-myelin
26	27.8	84.2	306	10	MMIGIT91	X59211 Mouse immun
27	27.8	84.2	306	10	MMVL3E6	X86546 M.musculus
28	27.8	84.2	315	10	MMU88691	U88691 Mus muscu
29	27.8	84.2	317	10	MMIGIKL3	X02555 Mouse mrna
30	27.8	84.2	317	10	MMIGIKL4	X02556 Mouse mrna
31	27.8	84.2	318	10	MMIGKVR4	X02234 Mouse mrna
32	27.8	84.2	318	10	MMU88689	U88689 Mus muscu
33	27.8	84.2	321	10	AF087030	AF087030 Mus muscu
34	27.8	84.2	321	10	AF113242	AF113242 Mus muscu
35	27.8	84.2	321	10	AF113243	AF113243 Mus muscu
36	27.8	84.2	321	10	AF163757	AF163757 Mus muscu
37	27.8	84.2	321	10	MMALCVR26	X90901 M.musculus
38	27.8	84.2	321	10	MMU277215	AJ277215 Mus muscu
39	27.8	84.2	321	10	MUSCWVF	M95943 Mouse mrna
40	27.8	84.2	321	10	MUSCWVH	M95945 Mouse mrna
41	27.8	84.2	323	10	MUSANTDNF	L08211 Mouse anti-
42	27.8	84.2	324	6	A43800	A43800 Sequence 4
43	27.8	84.2	324	6	A57187	A57187 Sequence 4
44	27.8	84.2	324	10	AF087031	AF087031 Mus muscu
45	27.8	84.2	324	10	AF139844	AF139844 Mus muscu

```

/translation="QASQISNPLH"
BASE COUNT      11 a      11 c      5 g      6 t
ORIGIN
Query Match      100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttctctacac 33
    |||
Db 1 CAGGCCAGCCAAAGTATTAGCAACTTCTCTACAC 33

RESULT 2
LOCUS      AX060860      39 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 81 from Patent WO0078815.
ACCESSION AX060860
VERSION   AX060860.1 GI:12406238
KEYWORDS  synthetic construct.
SOURCE    synthetic construct.
ORGANISM  artificial sequence.
REFERENCE 1 (bases 1 to 39)
AUTHORS   Huse,W.D. and Wu,H.
TITLE     Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
          encoding same and methods of use
JOURNAL   Patent: WO 0078815-A 81 28-DEC-2000;
          Applied Molecular Evolution (US)
FEATURES   Location/Qualifiers
            source          1..39
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
            CDS              <1..>39
                        /note="Mutated complementarity determining region (CDR)"
                        /codon_start=1
                        /translation="QASQISNPLH"
                        /protein_id="CAC24916.1"
                        /db_xref="GI:12406239"
BASE COUNT      12 a      10 c      7 g      10 t
ORIGIN
Query Match      95.2%; Score 31.4; DB 6; Length 39;
Best Local Similarity 97.0%; Pred. No. 0.00095;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttctctacac 33
    |||
Db 1 CAGGCCAGCCAAAGTATTAGCAACTTCTCTACAC 33

RESULT 3
LOCUS      AX060886      33 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 107 from Patent WO0078815.
ACCESSION AX060886
VERSION   AX060886.1 GI:12406264
KEYWORDS  synthetic construct.
SOURCE    synthetic construct.
ORGANISM  artificial sequence.
REFERENCE 1 (bases 1 to 33)
AUTHORS   Huse,W.D. and Wu,H.
TITLE     Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
          encoding same and methods of use
JOURNAL   Patent: WO 0078815-A 107 28-DEC-2000;
          Applied Molecular Evolution (US)
FEATURES   Location/Qualifiers
            source          1..33
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
            CDS              <1..>33
                        /note="Mutated complementarity determining region (CDR)"
                        /codon_start=1
                        /translation="QASQISNPLH"
                        /protein_id="CAC24916.1"
                        /db_xref="GI:12406239"
BASE COUNT      12 a      10 c      7 g      10 t
ORIGIN
Query Match      90.3%; Score 29.8; DB 6; Length 39;
Best Local Similarity 93.9%; Pred. No. 0.0053;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttctctacac 33
    |||
Db 1 CAGGCCAGCCAAAGTATTAGCAACTTCTCTACAC 33

RESULT 4
LOCUS      AX060820      39 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 41 from Patent WO0078815.
ACCESSION AX060820
VERSION   AX060820.1 GI:12406198
KEYWORDS  house mouse.
SOURCE    Mus musculus
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 39)
AUTHORS   Huse,W.D. and Wu,H.
TITLE     Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
          encoding same and methods of use
JOURNAL   Patent: WO 0078815-A 41 28-DEC-2000;
          Applied Molecular Evolution (US)
FEATURES   Location/Qualifiers
            source          1..39
                        /organism="Mus musculus"
                        /db_xref="taxon:10090"
                        <1..>39
                        /note="unnamed protein product"
                        /codon_start=1
                        /protein_id="CAC24896.1"
                        /db_xref="GI:12406199"
                        /translation="QASQISNHLHW"
BASE COUNT      13 a      12 c      7 g      7 t
ORIGIN
Query Match      90.3%; Score 29.8; DB 6; Length 39;
Best Local Similarity 93.9%; Pred. No. 0.0053;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttctctacac 33
    |||
Db 1 CAGGCCAGCCAAAGTATTAGCAACTTCTCTACAC 33

RESULT 5
LOCUS      AX060782      321 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 3 from Patent WO0078815.
ACCESSION AX060782
VERSION   AX060782.1 GI:12406162
KEYWORDS  synthetic construct.
SOURCE    synthetic construct.
ORGANISM  synthetic construct.

```

artificial sequence.
1 (bases 1 to 321)
Huse,W.D. and Wu,H.
Anti-g(a) v7-g(b)j3? recombinant human antibodies, nucleic acids
encoding same and methods of use
Patent: WO 0078815-A 3 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
1..321
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>321
/note="grafted antibody variable region"
/codon_start=1
/transl_table=11
/protein_id="CAC24899.1"
/db_xref="GI:12406163"
/translation="EIVLTQSPATLSLSPGERATLSCQASQTSNHLHWYQORPGQAP
RLLIYRSQISGIPARFSGSGGTDFTLTISLSEDFAVYYCQSGSWPHTFGGT
KVEIK"

BASE COUNT 78 a 93 c 79 g 71 t
ORIGIN

Query Match 90.3%; Score 29.8; DB 6; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0052; Mismatches 0; Indels 0; Gaps 0;
Matches 31; Conservative 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33
|||||
Db 70 CAGGCCAGCCAAAGTATTAGCACACCCTACAC 102

RESULT 6
AX060786
LOCUS
DEFINITION
Sequence 7 from Patent WO0078815.
ACCESSION
AX060786
VERSION
AX060786.1 GI:12406166
KEYWORDS
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 321)
Huse,W.D. and Wu,H.
Anti-g(a) v7-g(b)j3? recombinant human antibodies, nucleic acids
encoding same and methods of use
Patent: WO 0078815-A 7 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
1..321
/organism="Mus musculus"
/db_xref="taxon:10090"
<1..>321
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC24899.1"
/db_xref="GI:12406167"
/translation="DIVLTQSPATLSVTPGDVSLSCQASQTSNHLHWYQOKSHESP
RLLIYRSQISGIPARFSGSGGTDFALNSVETDFGMFCQSGSWPHTFGGT
KLEIK"

BASE COUNT 83 a 83 c 77 g 78 t
ORIGIN

Query Match 90.3%; Score 29.8; DB 6; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0052; Mismatches 0; Indels 0; Gaps 0;
Matches 31; Conservative 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33
|||||
Db 70 CAGGCCAGCCAAAGTATTAGCACACCCTACAC 102

RESULT 7
AX060810
LOCUS
DEFINITION
Sequence 31 from Patent WO0078815.
ACCESSION
AX060810
VERSION
AX060810.1 GI:12406189
KEYWORDS
synthetic construct.
SOURCE
synthetic construct
artificial sequence.
1 (bases 1 to 321)
Huse,W.D. and Wu,H.
Anti-g(a) v7-g(b)j3? recombinant human antibodies, nucleic acids
encoding same and methods of use
Patent: WO 0078815-A 31 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
1..321
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="grafted antibody variable region"
145..147
/note="NNN-CGT OR ATG"
BASE COUNT 76 a 93 c 78 g 71 t 3 others
ORIGIN

Query Match 90.3%; Score 29.8; DB 6; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0052; Mismatches 2; Indels 0; Gaps 0;
Matches 31; Conservative 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33
|||||
Db 70 CAGGCCAGCCAAAGTATTAGCACACCCTACAC 102

RESULT 8
MMU19309
LOCUS
DEFINITION
Mus musculus immunoglobulin kappa light chain variable region mRNA,
clone MRL1-17, partial cds.
ACCESSION
U19309
VERSION
U19309.1 GI:619954
KEYWORDS
house mouse.
SOURCE
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 243)
Roark,J.H., Kuntz,C.L., Nguyen,K.A., Caton,A.J. and Erikson,J.
Breakdown of B cell tolerance in a mouse model of systemic lupus
erythematosus
J. Exp. Med. 181 (3), 1157-1167 (1995)
95173583
2. (bases 1 to 243)
Roark,J.H.
Direct Submission
Submitted (02-JAN-1995) Jessica H. Roark, Wistar Institute, 3601
Spruce St., Philadelphia, PA 19104, USA
Location/Qualifiers
1..243
/organism="Mus musculus"
/strain="MRL-lpr/lpr"
/db_xref="taxon:10090"
/clone="MRL1-17"
/cell_type="splenic B cell hybridoma"
/tissue_type="spleen"
/dev_stage="adult"
<1..>243
/codon_start=1
/product="immunoglobulin kappa light chain variable

```

region"
/protein_id="AA68563.1"
/db_xref="GI:619955"
/translation="ACRASQISINYLHWYQOKSHESPRLLIKVQASISGIPSRFSGS
GSGTFTLINSVETDFGMYFCQQSNSPHFGSGT"
BASE COUNT      65 a   52 c   56 g   60 t
ORIGIN

Query Match      89.1%; Score 29.4; DB 10; Length 243;
Best Local Similarity 96.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttctacac 33
|||||
Db 9 GGCAGCCAAAGTATTAGCAACTACCTACAC 39

RESULT 9
AF139842
LOCUS      AF139842      285 bp      DNA      linear      ROD 04-NOV-1999
DEFINITION Mus musculus clone G11 immunoglobulin kappa light chain variable
region V $\kappa$ 23 (Ig) gene, partial cds.
ACCESSION  AF139842
VERSION     AF139842.1 GI:4732148
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 285)
AUTHORS    Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE      Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
J. Exp. Med. 190 (5), 691-704 (1999)
JOURNAL    99406777
MEDLINE    10477553
PUBMED     2 (bases 1 to 285)
AUTHORS     Brard,F. and Weigert,M.
DIRECT SUBMISSION
TITLE      Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
JOURNAL
FEATURES    source
            1..285
            /organism="Mus musculus"
            /strain="MRL/Mp-lpr/lpr"
            /db_xref="taxon:10090"
            /chromosome="6"
            /clone="G11"
            /tissue_type="tail"
            /germline
            /gene="Ig"
            /note="variable region"
            <1..>285
            /codon_start=1
            /product="immunoglobulin kappa light chain variable region
            V $\kappa$ 23"
            /protein_id="AAD28629.1"
            /db_xref="GI:4732149"
            /translation="DIVLTQSPATLSVTPGDRVLSCRASQISINYLHWYQOKSHESP
            RLLIKVQASISGIPSRFSGSGTFTLINSVETDFGMYFCQQSNSWP"
            70..105
            /gene="Ig"
            /note="CDR1; complementarity determining region 1"
            148..168
            /gene="Ig"
            /note="CDR2; complementarity determining region 2"
            75 a   73 c   63 g   74 t
BASE COUNT
ORIGIN

```

```

Query Match      89.1%; Score 29.4; DB 10; Length 285;
Best Local Similarity 96.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttctacac 33
|||||
Db 72 GCCAGCCAAAGTATTAGCAACTACCTACAC 102

RESULT 10
S60864
LOCUS      S60864      303 bp      mRNA      linear      ROD 15-APR-1996
DEFINITION Ab2 kappa chain V region/mab p168 [V/J junction] [mice,
MLR-lpr/lpr, mRNA Partial, 303 nt].
ACCESSION  S60864
VERSION     S60864.1 GI:235110
KEYWORDS   Mus sp. MLR-lpr/lpr.
SOURCE     Mus sp.
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 303)
AUTHORS    Kolzumi,T., Puccetti,A., Migliorini,P., Barrett,K.J. and
Schwartz,R.S.
TITLE      Molecular heterogeneity of auto-anti-idiotypic antibodies in
MLR-lpr/lpr mice
Eur. J. Immunol. 21 (9), 2185-2193 (1991)
JOURNAL    91364791
MEDLINE
REMARK     GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 60864] from the original journal article.
This sequence comes from Fig.6.
FEATURES    source
            1..303
            /organism="Mus sp."
            /db_xref="taxon:10095"
            1..303
            /gene="Ab2 kappa chain V region/mab p168"
            77 a   80 c   66 g   80 t
BASE COUNT
ORIGIN

Query Match      89.1%; Score 29.4; DB 10; Length 303;
Best Local Similarity 96.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttctacac 33
|||||
Db 72 GCCAGCCAAAGTATTAGCAACTACCTACAC 102

RESULT 11
MMU16184
LOCUS      MMU16184      324 bp      mRNA      linear      ROD 03-FEB-2000
DEFINITION Mus musculus anti-cardiolipin antibody CAR Ig light chain mRNA,
partial cds.
ACCESSION  U16184
VERSION     U16184.1 GI:604311
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 324)
AUTHORS    Blank M., Waisman,A., Mozes,E., Koike,T. and Shoenfeld,Y.
TITLE      Characteristics and pathogenic role of anti-beta2-glycoprotein I
single-chain Fv domains: induction of experimental antiphospholipid
syndrome
Int. Immunol. 11 (12), 1917-1926 (1999)
JOURNAL    20059391
MEDLINE    10590257
PUBMED     2 (bases 1 to 324)
AUTHORS     Blank,M., Waisman,A., Mozes,E. and Shoenfeld,Y.
TITLE      Pathogenic and nonpathogenic anti-cardiolipin antibodies: Binding

```



```

JOURNAL      properties and V gene analysis
REFERENCE    Unpublished
AUTHORS      3 (bases 1 to 324)
TITLE       Blank.M.
JOURNAL      Direct Submission
SUBMITTED    (20-OCT-1994) Miri Blank, Research Unit of Autoimmune
DISEASES     Diseases, Shiba Medical Center, Tel Hashomer, 52621, Israel
FEATURES     Location/Qualifiers
source       1..324
              /organism="Mus musculus"
              /strain="BALB/c"
              /db_xref="taxon:10090"
              <1..>324
              /note="monoclonal antibody is called CARK"
              /codon_start=1
              /product="Ig light chain"
              /protein_id="AA57511.1"
              /db_xref="GI:604312"
              /translation="DIVLTSPATLSVTPGDRVSLSCRASOSISNFWYQOKSHESP
              RLLIKYQSISIGIPSRFSGSGTDFTLINSVDTEDFGMYFCQNSWPHRFSGSI
              KLEIKS"
BASE COUNT   86 a 81 c 71 g 86 t
ORIGIN
Query Match  89.1%; Score 29.4; DB 10; Length 324;
Best Local Similarity 96.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3  ggccagccaaagtattagcaacttcctacac 33
      ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  72  GGCTAGCCAAAGTATTAGCAACTTCCTACAC 102

RESULT 12
MUSIGL2VK
LOCUS      MUSIGL2VK
DEFINITION Mus musculus (isolate 3D7.2VK) DNA linear ROD 17-JUN-1996
            chain, partial variable region.
ACCESSION  L78684
VERSION    1
KEYWORDS   Mus musculus
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 330)
AUTHORS    Gillespie, G.S., Lefkowitz, J.B. and Di Valerio, R.
TITLE      Murine glomerulotropic monoclonal antibodies are highly
            oligoclonal and exhibit distinctive molecular features
JOURNAL    J. Immunol. (1996) In press
FEATURES   Location/Qualifiers
source     1..330
            /organism="Mus musculus"
            /strain="MRL-LPR/LPR"
            /isolate="3D7.2VK"
            /db_xref="taxon:10090"
            <1..>330
            /gene="Igl-v"
            /product="immunoglobulin light chain"
            1..330
            /gene="Igl-v"
            <1..>330
            /note="This CDS feature is included to show the
            translation of the corresponding V_region. Presently
            translation qualifiers on V_region features are illegal."
            /codon_start=1
            /protein_id="AA802668.1"
            /db_xref="GI:1374936"
            /translation="DIVLTQSPATLSVTPGDRVSLSCRASOSISNFWYQOKSHESP
            RLLIKYQSISIGIPSRFSGSGTDFTLINSVDTEDFGMYFCQNSWPHYFGSGT
            KLEIKRAD"

```

```

BASE COUNT   89 a 80 c 77 g 84 t
ORIGIN
Query Match  89.1%; Score 29.4; DB 10; Length 330;
Best Local Similarity 96.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3  ggccagccaaagtattagcaacttcctacac 33
      ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  72  GGCCAGCCAAAGTATTAGCAACTACCTACAC 102

RESULT 13
MMY16070
LOCUS      MMY16070
DEFINITION Mus musculus mRNA for immunoglobulin kappa chain variable region.
ACCESSION  Y16070
VERSION    Y16070.1
KEYWORDS   IgG1; immunoglobulin light chain variable region; kappa chain.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 348)
AUTHORS    Mousli, M., Goyffon, M. and Billiald, P.
TITLE      Production and characterization of a bivalent single chain
            Fv/alkaline phosphatase conjugate specific for the hemocyanin of
            the scorpion Androctonus australis
JOURNAL    Biochim. Biophys. Acta 1425 (2), 348-360 (1998)
MEDLINE    99013722
REFERENCE  2 (bases 1 to 348)
AUTHORS    Billiald, P.
TITLE      Direct Submission
JOURNAL    Submitted (30-DEC-1997) P. Billiald, Leraï - MNHN, Museum National
            D'Histoire Nat., 57 rue Cuvier, 75231 Paris, Cedex 05, FRANCE
COMMENT    Related sequences: M16162, M93959.
FEATURES   Location/Qualifiers
source     1..348
            /organism="Mus musculus"
            /strain="Bp"
            /db_xref="taxon:10090"
            /cell_line="splenic lymphocyte + sp2-0-Ag14"
            /cell_line="hybridoma Al02"
            /cell_type="hybridoma"
            <1..>339
            /gene="IgG1"
            /product="immunoglobulin light chain, variable region"
            1..339
            /gene="IgG1"
            <1..>339
            /gene="IgG1"
            /note="anti-scorpian hemocyanin"
            /codon_start=1
            /product="immunoglobulin light chain, variable region"
            /protein_id="CAA76036.1"
            /db_xref="GI:2760535"
            /translation="DIVMTQAPATLSVTPGDRVSLSCRASOSISNFWYQOKSHESP
            RLLIKYASQISIGIPSRFSGSGTDFTLINSVDTEDFGMYFCQNSWPTFGGTT
            KLEIKRADAAP"
BASE COUNT   91 a 89 c 85 g 83 t
ORIGIN
Query Match  89.1%; Score 29.4; DB 10; Length 348;
Best Local Similarity 96.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3  ggccagccaaagtattagcaacttcctacac 33
      ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  72  GGCCAGCCAAAGTATTAGCAACTACCTACAC 102

```

RESULT 14

MUSIGKXD
 LOCUS MUSIGKXD 370 bp mRNA linear ROD 27-APR-1993
 DEFINITION Mouse Ig active kappa-chain V-region, partial cds.
 ACCESSION M93959
 VERSION M93959.1 GI:197572
 KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.
 SOURCE Mus musculus CDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 370)
 AUTHORS Takeda Y., Wise, K.S. and Hoffman, R.W.
 TITLE Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a monoclonal autoantibody specific for a unique set of small nuclear ribonucleoprotein complexes
 JOURNAL Nucleic Acids Res. 20, 4099-4099 (1992)
 MEDLINE 92375706
 FEATURES
 Location/Qualifiers
 1..370
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /map="6"
 1..370
 /gene="Igk"
 1..370
 /partial
 /gene="Igk"
 /function="variable region"
 /note="putative"
 /codon_start=1
 /product="immunoglobulin kappa-chain"
 /protein_id="AAA39079.1"
 /db_xref="GI:554148"
 /translation="GLMFWISASRGDIVLTQSPATLSVTPCDKVSILSCASOSISNYLHWYQKSHESPRLLIKYVSQSIGIPSRFSGSGTFTLSINSVETEDFGMYFCQQSNSWPHTFGSGTKLEIKRADA"

BASE COUNT 96 a 90 c 86 g 98 t
 ORIGIN
 Query Match 89.1%; Score 29.4; DB 10; Length 370;
 Best Local Similarity 96.8%; Pred. No. 0.008;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ggcacgcaaaagtattagcaacttctctacac 33
 |||||
 Db 108 GCCACGCAAAAGTATTAGCAACTACCTACAC 138

BASE COUNT 96 a 90 c 86 g 98 t
 ORIGIN

Query Match 89.1%; Score 29.4; DB 10; Length 370;
 Best Local Similarity 96.8%; Pred. No. 0.008;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ggcacgcaaaagtattagcaacttctctacac 33
 |||||
 Db 108 GCCACGCAAAAGTATTAGCAACTACCTACAC 138

RESULT 15

MMU235976
 LOCUS MMU235976 845 bp DNA linear ROD 03-AUG-1999
 DEFINITION Mus musculus IgV kappa fp23r gene.
 ACCESSION AJ235976
 VERSION AJ235976.1 GI:5327168
 KEYWORDS IgV kappa gene; immunoglobulin; kappa light chain; variable region.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 845)
 AUTHORS Schaeble, K.F., Thiele, R., Bensch, A., Brensing-Kueppers, J., Heim, V., Kirschbaum, T., Lamm, R., Ohnrich, M., Pourrajabi, S., Roeschenthaler, F., Schwendinger, J., Wichelhaus, D. and Zocher, H.G.
 TITLE Characteristics of the immunoglobulin V kappa genes, pseudogenes, relics and orphans in the mouse genome
 JOURNAL Eur. J. Immunol. 29 (7), 2082-2086 (1999)
 MEDLINE 99354924
 REFERENCE 2 (bases 1 to 845)
 AUTHORS Kirschbaum, T.

TITLE Direct Submission
 JOURNAL Submitted (23-DEC-1998) T. Kirschbaum, Adolf-Butenandt-Institut fuer, Physiologische Chemie, Schillerstr. 44, D-80336 Muenchen, FRG
 FEATURES
 Location/Qualifiers
 1..845
 /organism="Mus musculus"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /chromosome="6"
 /clone="FEYH4"
 /sub_clone="cosmid F10"
 /haplotype="c"
 /tissue_type="kidney"
 /clone_lib="Princeton Mouse YAC library"
 21..28
 /gene="fp23r"
 /note="octamer regulatory sequence"
 21..388
 /gene="fp23r"
 68..73
 /gene="fp23r"
 join(<130..178,387..>388)
 /gene="fp23r"
 /note="insertion of A in codon 39 leads to a frameshift compared to other V kappa 23 genes; the homology ends with codon 61"
 /codon_start=1
 /product="immunoglobulin light chain variable region"
 /protein_id="CAB4631.1"
 /db_xref="GI:5327169"
 /translation="MVFAPQILGFLLLWISA"
 130..178
 /gene="fp23r"
 /number=1
 join(<130..178,387..>388)
 /gene="fp23r"
 /product="variable region of immunoglobulin kappa light chain"
 387..>388
 /gene="fp23r"
 /number=2
 BASE COUNT 246 a 173 c 157 g 269 t
 ORIGIN
 Query Match 89.1%; Score 29.4; DB 10; Length 845;
 Best Local Similarity 96.8%; Pred. No. 0.008;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ggcacgcaaaagtattagcaacttctctacac 33
 |||||
 Db 469 GCCACGCAAAAGTATTAGCAACTACCTACAC 499

Search completed: August 21, 2002, 10:49:58
 Job time: 9813 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 09:56:01 ; Search time 6260.2 seconds
(without alignments)
71.148 Million cell updates/sec

Title: US-09-339-922A-109
Perfect score: 33
Sequence: 1 caggccagcaagattagcaacttctacac 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estnu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hc:*
 - 9: gb_esti:*
 - 10: gb_est2:*
 - 11: gb_hc:*
 - 12: gb_gss:*
 - 13: em_gss_hum:*
 - 14: em_gss_inv:*
 - 15: em_gss_pln:*
 - 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	ID Description
c	1 29.4	89.1	517 12 A2846516
	2 29.4	89.1	772 10 B1105452
	3 27.8	84.2	202 10 BG144658
	4 27.8	84.2	738 10 BF582153
	5 27.8	84.2	833 10 BG966582
	6 27.8	84.2	835 10 B1083006
	7 27.8	84.2	949 10 BF579007
c	9 22.4	67.9	371 10 T27081
	10 22.4	67.9	391 10 W81641
c	11 22.4	67.9	414 9 AA569320
	12 22.4	67.9	478 10 R51067
c	13 22.4	67.9	519 10 B518335
	14 22.4	67.9	520 9 AU158038
	15 21.6	65.5	674 10 BG198873
	16 21.6	65.5	239 10 BF756995
17	21.6	65.5	740 10 BG397970
	21.6	65.5	823 10 BG686045

18	20.8	63.0	549	9	AW642646	
19	20.8	63.0	556	10	BM004705	
20	20.6	62.4	459	9	BB852173	
c	21	20.6	470	10	BE848989	
	22	20.6	62.4	639	10	BE382000
23	20.6	62.4	648	9	BB620078	
24	20.6	62.4	662	9	BB630699	
c	25	20.6	745	10	BG975083	
	26	20.4	61.8	343	10	BE815288
27	20.4	61.8	406	10	R41697	
c	28	20.4	61.8	591	9	AV756066
	29	20.4	61.8	653	9	BB626942
c	30	20.2	61.2	168	10	BG737726
	31	20.2	61.2	202	9	AI010320
32	20.2	61.2	213	12	A2660650	
33	20.2	61.2	532	10	BF838031	
c	34	20.2	61.2	878	10	BF786148
	35	20.2	61.2	1005	12	CNS048VJ
36	20	60.6	208	9	BB575049	
37	20	60.6	250	10	BG231232	
38	20	60.6	290	10	BG058466	
39	20	60.6	311	9	AW405931	
40	20	60.6	324	9	AV693705	
41	20	60.6	352	9	AV690753	
42	20	60.6	367	9	AV694860	
43	20	60.6	374	9	AV695931	
44	20	60.6	398	10	M89293	
45	20	60.6	413	9	AW406440	

ALIGNMENTS

RESULT 1
AZ846516/c

LOCUS 2M0146D17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0146D17 R, DNA sequence.

DEFINITION 2M0146D17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0146D17 R, DNA sequence.

ACCESSION AZ846516

VERSION AZ846516.1 GI:13016424

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 517)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: D column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 517.
Location/Qualifiers
1. 517
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0146D17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 159 a 99 c 118 g 141 t
 ORIGIN

Query Match 89.1%; Score 29.4; DB 12; Length 517;
 Best Local Similarity 96.8%; Pred. No. 0.059; Mismatches 0; Gaps 0;
 Matches 30; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaactctctacac 33
 |||||
 Db 370 GCCCAGCCAAAGTATTAGCAACTACCTACAC 340

RESULT 2

BI105452 772 bp mRNA linear EST 26-JUN-2001
 LOCUS 602891971F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5037137 5',
 DEFINITION mRNA sequence.

ACCESSION BI105452
 VERSION BI105452.1 GI:14556345
 KEYWORDS EST.
 SOURCE house mouse.

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 772)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Place: LLAM1102 row: n column: 18
 High quality sequence stop: 771.
 Location/Qualifiers

FEATURES source

1. .772
 /organism="Mus musculus"
 /strain="CZECH II (fetal)"
 /db_xref="taxon:10090"
 /clone="IMAGE:5037137"
 /clone_lib="NCI_CGAP_Lu29"
 /tissue_type="spontaneous tumor, metastatic to mammary.
 Stem cell origin."
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"
 BASE COUNT 214 a 208 c 173 g 177 t
 ORIGIN

Query Match 89.1%; Score 29.4; DB 10; Length 772;
 Best Local Similarity 96.8%; Pred. No. 0.066; Mismatches 0; Gaps 0;
 Matches 30; Conservative 0; Indels 1; Indels 0; Gaps 0;
 QY 3 ggcagccaaagtattagcaactctctacac 33
 |||||
 Db 136 GCCCAGCCAAAGTATTAGCAACTACCTACAC 166

RESULT 3

BI144658 202 bp mRNA linear EST 01-FEB-2001
 LOCUS ut73a01.y1 Soares_mouse_NMGB_bcell Mus musculus cDNA clone
 DEFINITION IMAGE:3333385 5' similar to SW:KV51_MOUSE F01642 IG KAPPA CHAIN V-V
 REGION L7 PRECURSOR ;, mRNA sequence.

ACCESSION BI144658
 VERSION BI144658.1 GI:12648058
 KEYWORDS EST.
 SOURCE house mouse.

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 202)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1077549

Trace considered overall poor quality
 Seq primer: -40RP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES source

1. .202
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:3333385"
 /clone_lib="Soares_mouse_NMGB_bcell"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: germinal B-cell; Vector: p7T73D-Pac
 (Pharmacia) with a modified polylinker; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 TGTTCACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT7T3 vector.
 Library is normalized; constructed by Bento Soares and
 M. Fatima Bonaldo."

BASE COUNT 53 a 61 c 45 g 43 t
 ORIGIN

Query Match 84.2%; Score 27.8; DB 10; Length 202;
 Best Local Similarity 93.5%; Pred. No. 0.21; Mismatches 0; Gaps 0;
 Matches 29; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaactctctacac 33
 |||||
 Db 40 GCCCAGCCAAAGTATTAGCAACACCTACAC 70

RESULT 4

BF582153

```

LOCUS      BF582153      738 bp      mRNA      linear      EST 12-DEC-2000
DEFINITION 602099743F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219402 5',
            mRNA sequence.
ACCESSION   BF582153
VERSION     BF582153.1 GI:11655865
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 738)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tissue Procurement: Jeffrey E. Green, M.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9801 row: f column: 11
            High quality sequence stop: 714.
            Location/Qualifiers
                1..738
                /organism="Mus musculus"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:4219402"
                /clone_lib="NCI_CGAP_Co24"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.6 kb. Constructed by Life
                Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      210 a      189 c      172 g      167 t
ORIGIN
source
Query Match      84.2%; Score 27.8; DB 10; Length 738;
Best Local Similarity 93.5%; Pred. No. 0.3;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gccacgccaagattagcaactctctacac 33
|||||
Db 144 gccacgccaagattagcaacacctacac 174

RESULT 5
BG966582
LOCUS      BG966582      833 bp      mRNA      linear      EST 12-JUN-2001
DEFINITION 602834412F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988955 5',
            mRNA sequence.
ACCESSION   BG966582
VERSION     BG966582.1 GI:14354219
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 833)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11047 row: p column: 06
            High quality sequence stop: 769.
            Location/Qualifiers
                1..835
                /organism="Mus musculus"
                /strain="FVB/N-3"
                /db_xref="taxon:10090"
                /clone="IMAGE:5006453"
                /clone_lib="NCI_CGAP_Mam2"
                /tissue_type="tumor, biopsy sample"
                /dev_stage="5 months"
                /lab_host="DH10B"
                /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"

BASE COUNT      225 a      229 c      186 g      195 t
ORIGIN
source
Query Match      84.2%; Score 27.8; DB 10; Length 833;
Best Local Similarity 93.5%; Pred. No. 0.31;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gccacgccaagattagcaactctctacac 33
|||||
Db 136 gccacgccaagattagcaacacctacac 166

RESULT 6
BI083006
LOCUS      BI083006      835 bp      mRNA      linear      EST 20-JUN-2001
DEFINITION 602874524F2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
            mRNA sequence.
ACCESSION   BI083006
VERSION     BI083006.1 GI:14501336
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 835)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11002 row: q column: 04
            High quality sequence stop: 830.
            Location/Qualifiers
                1..833
                /organism="Mus musculus"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:4988955"
                /clone_lib="NCI_CGAP_Co24"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.6 kb. Constructed by Life
                Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      227 a      227 c      186 g      193 t
ORIGIN
source
Query Match      84.2%; Score 27.8; DB 10; Length 833;
Best Local Similarity 93.5%; Pred. No. 0.31;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gccacgccaagattagcaactctctacac 33
|||||
Db 136 gccacgccaagattagcaacacctacac 166

RESULT 6
BI083006
LOCUS      BI083006      835 bp      mRNA      linear      EST 20-JUN-2001
DEFINITION 602874524F2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
            mRNA sequence.
ACCESSION   BI083006
VERSION     BI083006.1 GI:14501336
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 835)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11047 row: p column: 06
            High quality sequence stop: 769.
            Location/Qualifiers
                1..835
                /organism="Mus musculus"
                /strain="FVB/N-3"
                /db_xref="taxon:10090"
                /clone="IMAGE:5006453"
                /clone_lib="NCI_CGAP_Mam2"
                /tissue_type="tumor, biopsy sample"
                /dev_stage="5 months"
                /lab_host="DH10B"
                /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"

BASE COUNT      225 a      229 c      186 g      195 t
ORIGIN
source

```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11002 row: q column: 04
High quality sequence stop: 830.

FEATURES

Location/Qualifiers
1..833
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4988955"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 227 a 227 c 186 g 193 t
ORIGIN

Query Match 84.2%; Score 27.8; DB 10; Length 833;
Best Local Similarity 93.5%; Pred. No. 0.31;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gccacgccaagattagcaactctctacac 33
|||||
Db 136 gccacgccaagattagcaacacctacac 166

RESULT

BI083006
LOCUS BI083006 835 bp mRNA linear EST 20-JUN-2001
DEFINITION 602874524F2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
mRNA sequence.
ACCESSION BI083006
VERSION BI083006.1 GI:14501336
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 835)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM11047 row: p column: 06
High quality sequence stop: 769.
Location/Qualifiers

FEATURES

Location/Qualifiers
1..835
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5006453"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 225 a 229 c 186 g 195 t
ORIGIN

BF582153 738 bp mRNA linear EST 12-DEC-2000
DEFINITION 602099743F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219402 5',
mRNA sequence.
ACCESSION BF582153
VERSION BF582153.1 GI:11655865
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 738)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9801 row: f column: 11
High quality sequence stop: 714.
Location/Qualifiers

FEATURES

Location/Qualifiers
1..738
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4219402"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 210 a 189 c 172 g 167 t
ORIGIN

Query Match 84.2%; Score 27.8; DB 10; Length 738;
Best Local Similarity 93.5%; Pred. No. 0.3;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gccacgccaagattagcaactctctacac 33
|||||
Db 144 gccacgccaagattagcaacacctacac 174

RESULT

BG966582
LOCUS BG966582 833 bp mRNA linear EST 12-JUN-2001
DEFINITION 602834412F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988955 5',
mRNA sequence.
ACCESSION BG966582
VERSION BG966582.1 GI:14354219
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 833)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

```

Query Match      84.2%; Score 27.8; DB 10; Length 835;
Best Local Similarity 93.5%; Pred. No. 0.31; 2; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttctacac 33
|||||
Db 150 GGCCAGCCAAAGTATTAGCAACACCTACAC 180

RESULT 7
BF579007
LOCUS BF579007 949 bp mRNA linear EST 12-DEC-2000
DEFINITION 602096124F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4216180 5',
mRNA sequence.
ACCESSION BF579007
VERSION BF579007.1 GI:11652719
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 949)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9792 row: p column: 05
High quality sequence start: 9
High quality sequence stop: 730.
Location/Qualifiers
1. .949
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4216180"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 278 a 241 c 210 g 220 t
ORIGIN

Query Match      84.2%; Score 27.8; DB 10; Length 949;
Best Local Similarity 93.5%; Pred. No. 0.32; 2; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttctacac 33
|||||
Db 149 GGCCAGCCAAAGTATTAGCAACACCTACAC 179

RESULT 8
T27081
LOCUS T27081 371 bp mRNA linear EST 25-JUL-1996
DEFINITION NIBT258G01 Infant brain, LLNL array of Dr. M. Soares INIB Homo
sapiens cDNA clone LLAB258G01 3'end, mRNA sequence.
ACCESSION T27081
VERSION T27081.1 GI:774123
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 371)
AUTHORS Sikela, J.M.
TITLE Human cDNAs from infant brain
JOURNAL Unpublished (1993)
COMMENT Contact: Sikela JM
Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Fax: 3032707097
Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal.
Location/Qualifiers
1. .371
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LLAB258G01"
/clone_lib="Infant brain, LLNL array of Dr. M. Soares
INIB"
/note="vector: lafmid BA; Site_1: HindIII; Site_2: NotI;
Normalized infant brain cDNA library made by Dr. M. Soares
(Columbia University), oligo-dt primed and directionally
cloned between HindIII (5') and NotI (3') sites "

BASE COUNT 101 a 72 c 90 g 104 t 4 others
ORIGIN

Query Match      67.9%; Score 22.4; DB 10; Length 371;
Best Local Similarity 81.2%; Pred. No. 42;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 cagccagccaaagtattagcaacttctaca 32
|||||
Db 241 CAGCGAGCAAATTTAATAGCAACTTCTCCA 272

RESULT 9
W81641/c
LOCUS W81641 391 bp mRNA linear EST 17-OCT-1996
DEFINITION zd88e04.r1 Soares fetal heart_NBH19W Homo sapiens cDNA clone
IMAGE:347742 5' similar to PIR:S22934 S22934 testis-specific
protein ;, mRNA sequence.
ACCESSION W81641
VERSION W81641.1 GI:1392680
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 391)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
R., Williamson, A., Wohlmann, P., and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 479 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 373.
Location/Qualifiers
1. .391
/organism="Homo sapiens"
/db_xref="GDB:1273117"

```

Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."

BASE COUNT 118 a 99 c 87 g 110 t
ORIGIN

Query Match 67.9%; Score 22.4; DB 9; Length 414;
Best Local Similarity 81.2%; Pred. No. 43;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 caggcagccaaagtattagcaacttccata 32
||||| ||| || || ||||| ||||| ||
DB 224 CAGCGAGCAAAATTAAATAGCAACTTCCTCCA 193

RESULT 11

R51067
LOCUS R51067 478 bp mRNA linear EST 18-MAY-1995
DEFINITION Y964D01.sl Soares infant brain lNIB Homo sapiens cDNA clone
IMAGE:37385 3' similar to SP:S22934 S22934 TESTIS-SPECIFIC PROTEIN
;; mRNA sequence.

ACCESSION R51067
VERSION R51067.1 GI:812969
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1133
High quality sequence steps: 384 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1133 Std Error: 0.00
Seq primer: Promega -2iml3
High quality sequence stop: 384.
Location/Qualifiers
1. .478
/organism="Homo sapiens"
/db_xref="GDB:409886"
/db_xref="taxon:9606"
/clone="IMAGE:37385"
/clone_lib="Soares infant brain lNIB"
/sex="female"
/rev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lfamid BA; Site_1: Not
I; Site_2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5'
ACTGGAACAATTCGGCGCGCAGGAATTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bonaldo."

BASE COUNT 115 a 95 c 124 g 137 t 7 others
ORIGIN

Query Match 67.9%; Score 22.4; DB 10; Length 478;
Best Local Similarity 81.2%; Pred. No. 45;

```

Matches 26; Conservative 0; Mismatches. 6; Indels 0; Gaps 0;

QY 1 caggccagcgaagatttagcaactctctaca 32
||||| ||| || || ||||| ||||| ||
Db 251 CAGCGGAGCAAAATTTAATAGCAACTTCTCTCCA 282

RESULT 12
BI518335
LOCUS
DEFINITION
ACCESSION BI518335
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 519)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1455 row: n column: 05
High quality sequence start: 30
High quality sequence stop: 519.

FEATURES
source
Location/Qualifiers
1..519
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182660"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT 127 a 125 c 144 g 123 t
ORIGIN

Query Match 67.9%; Score 22.4; DB 10; Length 519;
Best Local Similarity 81.2%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 caggccagcgaagatttagcaactctctaca 32
||||| ||| || || ||||| ||||| ||
Db 201 CAGCGGAGCAAAATTTAATAGCAACTTCTCTCCA 232

RESULT 13
AU158038
LOCUS
DEFINITION
ACCESSION AU158038
VERSION AU158038.1 GI:11019559
sequence.
AU158038
AU158038.1 GI:11019559

```

```

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 520)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano
,S. and Isogai,T.).
HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S.,
Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura
,Y., Nagai,T., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
source
Location/Qualifiers
1..520
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1010661"
/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pWE18SF13"

BASE COUNT 132 a 124 c 115 g 133 t 16 others
ORIGIN

Query Match 67.9%; Score 22.4; DB 9; Length 520;
Best Local Similarity 81.2%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 caggccagcgaagatttagcaactctctaca 32
||||| ||| || || ||||| ||||| ||
Db 245 CAGCGGAGCAAAATTTAATAGCAACTTCTCTCCA 276

RESULT 14
BG198873/c
LOCUS
DEFINITION BG198873
ACCESSION BG198873
VERSION BG198873.1 GI:13720560
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 674)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 674.

```


FEATURES

source

Location/Qualifiers

1. .674
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athensys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
 175 a 187 c 147 g 164 t 1 others

BASE COUNT
 ORIGIN

Query Match 67.9%; Score 22.4; DB 10; Length 674;
 Best Local Similarity 81.2%; Pred. No. 49;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 caggccagccaaagtattagcaacttctctaca 32
 ||||| ||| || || ||||| ||||| ||
 Db 358 CAGGCGGCAAAATTAAATAGCAACTTCTCTCCA 327

RESULT 15

BF756995

LOCUS BF756995 239 bp mRNA linear EST 12-JAN-2001
 DEFINITION MR0-CT0451-021100-017-h04 CT0451 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF756995

VERSION

BF756995.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 239)

Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,

Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,

Goldman G.H., Carvalho A.F., Matsukuma A., Baia G.S., Simpson D.H.,

Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare

M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and

Simpson A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-CT0451-

021100-017-h04&t3=2000-11-02&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 11

High quality sequence stop: 239.

Location/Qualifiers

1. .239

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="CT0451"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site: 1; SmaI; Site 2;

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the puc 18 vector. Reverse transcription of tissue

FEATURES

source

BASE COUNT 59 a 79 c 50 g 51 t
 ORIGIN

Query Match 65.5%; Score 21.6; DB 10; Length 239;
 Best Local Similarity 85.7%; Pred. No. 78;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 3 ggccagccaaagtattagcaacttctcta 30
 ||||| || ||||| ||||| ||
 Db 173 GCCCAGTCAGAGTATTAGCAACTACTTA 200

Search completed: August 21, 2002, 09:56:05
 Job time: 9328 sec

Location/Qualifiers

1. .674
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athensys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
 175 a 187 c 147 g 164 t 1 others

BASE COUNT
 ORIGIN

Query Match 67.9%; Score 22.4; DB 10; Length 674;
 Best Local Similarity 81.2%; Pred. No. 49;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 caggccagccaaagtattagcaacttctctaca 32
 ||||| ||| || || ||||| ||||| ||
 Db 358 CAGGCGGCAAAATTAAATAGCAACTTCTCTCCA 327

RESULT 15

BF756995

LOCUS BF756995 239 bp mRNA linear EST 12-JAN-2001
 DEFINITION MR0-CT0451-021100-017-h04 CT0451 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF756995

VERSION

BF756995.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 239)

Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,

Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,

Goldman G.H., Carvalho A.F., Matsukuma A., Baia G.S., Simpson D.H.,

Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare

M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and

Simpson A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-CT0451-

021100-017-h04&t3=2000-11-02&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 11

High quality sequence stop: 239.

Location/Qualifiers

1. .239

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="CT0451"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site: 1; SmaI; Site 2;

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the puc 18 vector. Reverse transcription of tissue

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:40 ; Search time 754.01 Seconds
(without alignments)
75.142 Million cell updates/sec

Title: US-09-339-922a-109
Perfect score: 33
Sequence: 1 cagccgcgcaaaagtattagcaacttctctacac 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	33	22	AAF28238
2	31.4	95.2	39	19	AAV49868
3	31.4	95.2	39	22	AAF28224
4	29.8	90.3	33	22	AAF28237
5	29.8	90.3	39	19	AAV49848
6	29.8	90.3	39	22	AAF28204
7	29.8	90.3	321	19	AAV49843
8	29.8	90.3	321	19	AAV49821
9	29.8	90.3	321	19	AAV49823

10	29.8	90.3	321	22	AAH74624	DNA encoding light
11	29.8	90.3	321	22	AAH74626	DNA encoding light
12	29.8	90.3	321	22	AAF28176	Vitaxin light chain
13	29.8	90.3	321	22	AAF28178	Antibody LM609 lig
14	29.8	90.3	321	22	AAF28199	DNA encoding light
15	27.8	84.2	101	20	AAV71825	Alpha-v beta-3 Mab
16	27.8	84.2	108	20	AAV71816	Alpha-v beta-3 Mab
17	27.8	84.2	128	13	AAQ26786	Oligomer jbi7 used
18	27.8	84.2	128	22	AAF56750	Humanised CMV5 ant
19	27.8	84.2	315	20	AAV71803	Jk gene segment.
20	27.8	84.2	315	20	AAV71805	Humanised anti-alp
21	27.8	84.2	321	20	AAV71800	Humanised anti-alp
22	27.8	84.2	324	17	AAV33446	ESF receptor chime
23	27.8	84.2	324	20	AAV71798	Murine vitronectin
24	27.8	84.2	338	20	AAV71802	Vitronectin alpha-
25	27.8	84.2	381	15	AAQ64167	Sequence of mouse
26	27.8	84.2	381	22	AAF58747	Murine CMV5 antibo
27	27.8	84.2	5238	11	AAQ04654	Plasmid pBT111 enc
28	26.8	81.2	72	19	AAV49830	LM609 grafted anti
29	26.8	81.2	72	22	AAF28185	Oligonucleotide #7
30	26.8	81.2	75	19	AAV49839	LM609 grafted anti
31	26.8	81.2	75	22	AAH74633	PCR primer for lig
32	26.8	81.2	75	22	AAF28194	Grafted light chain
33	26.2	79.4	342	22	AAH27466	Murine coding sequ
34	24.6	74.5	381	21	AAZ55242	Mouse anti-verotox
35	24.6	74.5	381	21	AAZ35244	Humanised anti-ver
36	24.6	74.5	651	21	AAA44346	Human secreted exp
37	24.6	74.5	8858	20	AAZ10202	Expression vector
38	24.6	74.5	8858	24	AAH43777	Chi220 light chain
39	23	69.7	363	17	AAV38510	Light chain coding
40	23	69.7	415	21	AAV00904	Humanised antibody
41	23	69.7	415	21	AAV01262	Mouse monoclonal a
42	22.4	67.9	520	22	AAH13081	Human CDNA clone (
43	22.4	67.9	1585	22	AAH15219	Human CDNA sequenc
44	22.4	67.9	1864	22	AAI58470	Human polynucleoti
45	22.4	67.9	1900	22	AAH15178	Human CDNA sequenc

ALIGNMENTS

RESULT 1
AAF28238
ID AAF28238 standard; DNA; 33 BP.
XX
AC AAF28238;
XX
XX
DT 03-APR-2001 (first entry)
XX
DE DNA encoding enhanced LM609 VH CDR1 peptide.
XX
KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
XX inflammatory; cancer; retina; restenosis; osteoporosis; SS.
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -
 XX
 PS Claim 14; Page 45; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 33 BP; 11 A; 11 C; 5 G; 6 T; 0 other;
 Query Match 100.0%; Score 33; DB 22; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 caggccagccaaagtattagcaacttctacac 33
 Db 1 caggccagccaaagtattagcaacttctacac 33
 RESULT 2
 AAV49868
 ID AAV49868 standard; DNA; 39 BP.
 XX
 AC AAV49868;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-L region CDR1 DNA fragment #2.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region; ss.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR P-PSDB; AAW76031.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure; Page 42; 129pp; English.
 XX
 CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal
 CC antibody LM609 heavy and light chain variable region. LM609 and the
 CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used
 CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 39 BP; 12 A; 10 C; 7 G; 10 T; 0 other;
 Query Match 95.2%; Score 31.4; DB 19; Length 39;
 Best Local Similarity 97.0%; Pred. No. 0.00014;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 caggccagccaaagtattagcaacttctacac 33
 Db 1 caggccagccaaagtattagcaacttctacac 33
 RESULT 3
 AAF28224
 ID AAF28224 standard; DNA; 39 BP.
 XX
 AC AAF28224;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE DNA encoding mutant VL CDR1 peptide.
 XX
 KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Page 42; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 39 BP; 12 A; 10 C; 7 G; 10 T; 0 other;
 Query Match 95.2%; Score 31.4; DB 22; Length 39;

Best Local Similarity 97.0%; Pred. No. 0.00014;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 caggccagcacaagattagcaacttctctacac 33
 Db 1 caggccagcacaagattagcaacttctctacac 33
 |||||

RESULT 4
 AAF28237
 ID AAF28237 standard; DNA; 33 BP.
 XX
 AC AAF28237;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE DNA encoding enhanced 6H6Lh light chain CDR1.
 XX
 KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT osteoporosis -
 XX
 PS Claim 16; Page 107; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 33 BP; 12 A; 12 C; 5 G; 4 T; 0 other;

Query Match 90.3%; Score 29.8; DB 22; Length 33;
 Best Local Similarity 93.9%; Pred. No. 0.0007; 2; Indels 0; Gaps 0;
 Matches 31; Conservative 0; Mismatches 2;

QY 1 caggccagcacaagattagcaacttctctacac 33
 Db 1 caggccagcacaagattagcaacttctctacac 33
 |||||

RESULT 5
 AAV49848
 ID AAV49848 standard; DNA; 39 BP.
 XX
 AC AAV49848;

XX 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-L region CDR1 DNA fragment #1.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region; ss.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR P-PSDB; AAW76011.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure; Page 40; 129pp; English.
 XX
 CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal
 CC antibody LM609 heavy and light chain variable region. LM609 and the
 CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used
 CC to inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 39 BP; 13 A; 12 C; 7 G; 7 T; 0 other;

Query Match 90.3%; Score 29.8; DB 19; Length 39;
 Best Local Similarity 93.9%; Pred. No. 0.00072;
 Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagcacaagattagcaacttctctacac 33.
 Db 1 caggccagcacaagattagcaacttctctacac 33
 |||||

RESULT 6
 AAF28204
 ID AAF28204 standard; DNA; 39 BP.
 XX
 AC AAF28204;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE DNA encoding LM609 VL CDR1 peptide.
 XX
 KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

```

XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX WPI; 2001-050110/06.
XX DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis -
XX PS Disclosure; Page 40; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphaVbeta3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX SQ Sequence 39 BP; 13 A; 12 C; 7 G; 7 T; 0 other;

Query Match 90.3%; Score 29.8; DB 22; Length 39;
Best Local Similarity 93.9%; Pred. No. 0.00072;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagcacaagtattagcaacttctacac 33
   |||||||
Db 1 caggccagcacaagtattagcaaccctacac 33

RESULT 7
AAV49843
ID AAV49843 standard; DNA; 321 BP.
XX AC
XX AC AAV49843;
XX DT 02-NOV-1998 (first entry)
XX DE
XX DE LM609 antibody light chain variable region DNA grafted fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 1..321
XX FT /*tag= a
XX FT /product= "LM609 grafted antibody light chain variable
XX FT region"
XX FT /note= "partial sequence, no start or stop codon given"
XX FT
XX FT
XX FT

```

```

PN WO9833919-A2.
XX 06-AUG-1998.
XX 30-JAN-1998; 98WO-US01826.
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX P-PSDB; AAW76006.
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX PS Claim 24; Fig 7; 129pp; English.
XX CC This sequence encodes a LM609 grafted antibody variable light chain
XX CC region. LM609 and the antibody vitaxin bind selectively to integrin
XX CC alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand
XX CC and thus block integrin-mediated signal transduction. This is useful in
XX CC the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
XX CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX CC etc.). The antibodies contain non-murine framework regions so are
XX CC suitable for use in humans. Enhanced types of LM609 have affinity more
XX CC than 90 times greater than that of parent the parent antibody.
XX SQ Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 90.3%; Score 29.8; DB 19; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagcacaagtattagcaacttctacac 33
   |||||||
Db 70 caggccagcacaagtattagcaaccctacac 102

RESULT 8
AAV49821
ID AAV49821 standard; DNA; 321 BP.
XX AC
XX AC AAV49821;
XX DT 02-NOV-1998 (first entry)
XX DE
XX DE Vitaxin antibody light chain variable region DNA.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 1..321
XX FT /*tag= a
XX FT /product= "vitaxin antibody light chain variable region"
XX FT /note= "partial sequence, no start or stop codon given"
XX FT
XX FT
XX FT
XX WO9833919-A2.
XX 06-AUG-1998.

```

```

XX PF 30-JAN-1998; 98WO-US01826.
XX PR
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX DR WPI: 1998-437472/37.
XX DR P-PSDB; AAW76002.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX
XX Claim 6; Fig 1b; 129pp; English.
XX
XX This sequence encodes the vitaxin antibody variable light chain region.
XX CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
XX CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX CC block integrin-mediated signal transduction. This is useful in the
XX CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX CC etc.). The antibodies contain non-murine framework regions so are
XX CC suitable for use in humans. Enhanced types of LM609 have affinity more
XX CC than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Query Match 90.3%; Score 29.8; DB 19; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagcgaagtagtagcaacttcctacac 33
Db 70 caggccagcgaagtagtagcaaccctacac 102

RESULT 9
AAV49823
ID AAV49823 standard; DNA; 321 BP.
XX
XX AAV49823;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 antibody light chain variable region DNA fragment.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..321
XX /tag= a
XX /product= "LM609 antibody light chain variable region"
XX /note= "partial sequence, no start or stop codon given"
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX

```

```

PR 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX DR WPI: 1998-437472/37.
XX DR P-PSDB; AAW75004.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX
XX Claim 40; Fig 2b; 129pp; English.
XX
XX This sequence encodes the LM609 antibody variable light chain region.
XX CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
XX CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX CC block integrin-mediated signal transduction. This is useful in the
XX CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX CC etc.). The antibodies contain non-murine framework regions so are
XX CC suitable for use in humans. Enhanced types of LM609 have affinity more
XX CC than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 90.3%; Score 29.8; DB 19; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagcgaagtagtagcaacttcctacac 33
Db 70 caggccagcgaagtagtagcaaccctacac 102

RESULT 10
AAH74624
ID AAH74624 standard; DNA; 321 BP.
XX
XX AAH74624;
XX
XX 15-OCT-2001 (first entry)
XX
XX DNA encoding light chain variable region of LM609 grafted antibody.
XX
XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
XX chronic articular rheumatism; psoriasis; diabetic retinopathy;
XX neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
XX cancer; ss.
XX
XX Synthetic.
XX OS Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..321
XX /tag= a
XX /transl_except= "(pos: 145..147, aa: Xaa)"
XX /note= "Xaa is unspecified"
XX
XX US2001011125-A1.
XX
XX 02-AUG-2001.
XX
XX 30-JAN-1997; 97US-0790540.
XX
XX 30-JAN-1997; 97US-0790540.
XX
XX (HUSE/) HUSE W D.

```

XX PI Huse WD;

XX WPI; 2001-496171/54.

DR P-PSDB; AAG63588.

XX New LM609 grafted antibody exhibiting selective binding affinity to

PT alphavbeta3, comprising at least one LM609 grafted heavy and light

PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory

PT disorders or cancer

XX Claim 6; Fig 1B; 25pp; English.

XX The present sequence encodes the light chain variable region of the

CC grafted monoclonal antibody LM609. LM609 is a murine antibody which

CC specifically recognises the integrin alphavbeta3, and inhibits its

CC functional activity. The LM609 grafted antibody has the

CC complementarity determining regions (CDRs) substituted into a non-murine

CC framework. Nucleic acids encoding LM609 grafted heavy and light chain

CC polypeptides and fragments are useful in diagnostic and therapeutic

CC purposes, such as in the production of LM609 grafted antibodies and

CC fragments having binding specificity and inhibitory activity against

CC the integrin alphavbeta3. The antibody can be used for the diagnosis

CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory

CC disorders, chronic articular rheumatism, psoriasis, disorders

CC associated with inappropriate or inopportune invasion of vessels such

CC as diabetic retinopathy, neovascular glaucoma and capillary

CC proliferation in atherosclerotic plaques, or cancers), and to inhibit

CC binding activity of alphavbeta3 that are necessary for progression of

CC an alphavbeta3-mediated disease.

XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

SQ

Query Match 90.3%; Score 29.8; DB 22; Length 321;

Best Local Similarity 93.9%; Pred. No. 0.0011;

Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagcgaagattattagcaacttctctacac 33

|||||

Db 70 caggccagcgaagattattagcaaccctctacac 102

RESULT 11

AAH74626

ID AAH74626 standard; DNA; 321 BP.

XX AC AAH74626;

XX 15-OCT-2001 (first entry)

DE DNA encoding light chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;

KW chronic articular rheumatism; psoriasis; diabetic retinopathy;

KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;

KW cancer; ss.

XX Mus sp.

XX US2001011125-A1.

PN 02-AUG-2001.

PD 30-JAN-1997; 97US-0790540.

PF 30-JAN-1997; 97US-0790540.

PR (HUSE/) HUSE W D.

PA Huse WD;

XX WPI; 2001-496171/54.

DR

DR P-PSDB; AAG63590.

XX New LM609 grafted antibody exhibiting selective binding affinity to

PT alphavbeta3, comprising at least one LM609 grafted heavy and light

PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory

PT disorders or cancer

XX Disclosure; Fig 2B; 25pp; English.

PS The present sequence encodes the light chain variable region of the

XX monoclonal antibody LM609. LM609 is a murine antibody which specifically

CC recognises the integrin alphavbeta3, and inhibits its functional activity.

CC The specification describes a LM609 grafted antibody which has the

CC complementarity determining regions (CDRs) substituted into a non-murine

CC framework. Nucleic acids encoding LM609 grafted heavy and light chain

CC polypeptides and fragments are useful in diagnostic and therapeutic

CC purposes, such as in the production of LM609 grafted antibodies and

CC fragments having binding specificity and inhibitory activity against

CC the integrin alphavbeta3. The antibody can be used for the diagnosis

CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory

CC disorders, chronic articular rheumatism, psoriasis, disorders

CC associated with inappropriate or inopportune invasion of vessels such

CC as diabetic retinopathy, neovascular glaucoma and capillary

CC proliferation in atherosclerotic plaques, or cancers), and to inhibit

CC binding activity of alphavbeta3 that are necessary for progression of

CC an alphavbeta3-mediated disease.

XX Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

SQ

Query Match 90.3%; Score 29.8; DB 22; Length 321;

Best Local Similarity 93.9%; Pred. No. 0.0011;

Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagcgaagattattagcaacttctctacac 33

|||||

Db 70 caggccagcgaagattattagcaaccctctacac 102

RESULT 12

AAF28176

ID AAF28176 standard; DNA; 321 BP.

XX AC AAF28176;

XX 03-APR-2001 (first entry)

DE Vitaxin light chain variable region DNA.

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

XX Unidentified.

XX WO200078815-A1.

PN 28-DEC-2000.

PD 23-JUN-2000; 2000WO-US17454.

PF 24-JUN-1999; 99US-0339922.

PR (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis

XX

```
PS Disclosure; Fig 1; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Query Match          90.3%; Score 29.8; DB 22; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaacttctacac 33
   |||||||||||||||||||
Db 70 caggccagccaaagtattagcaaccctacac 102

RESULT 13
AAF28178
ID AAF28178 standard; DNA; 321 BP.
XX
AC AAF28178;
XX
DT 03-APR-2001 (first entry)
XX
DE Antbody LM609 light chain variable region DNA.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PS Disclosure; Fig 2; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Query Match          90.3%; Score 29.8; DB 22; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaacttctacac 33
   |||||||||||||||||||
Db 70 caggccagccaaagtattagcaaccctacac 102

RESULT 14
AAF28199
ID AAF28199 standard; DNA; 321 BP.
XX
AC AAF28199;
XX
DT 03-APR-2001 (first entry)
XX
DE DNA encoding light chain variable region of LM609.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Fig 7; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match          90.3%; Score 29.8; DB 22; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaacttctacac 33
   |||||||||||||||||||
Db 70 caggccagccaaagtattagcaaccctacac 102
```



```

RESULT 15
AAV71825/c
ID AAV71825 standard; DNA; 101 BP.
XX
XX AAV71825;
XX
XX DT 15-MAR-1999 (first entry)
XX
XX DE Alpha-v beta-3 MAb D12HZLCREI VL oligonucleotide SBA3167.
XX
XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12HZLCREI; ss.
XX
XX OS Mus sp.
XX OS Synthetic.
XX
XX PN WO9840488-A1.
XX
XX PD 17-SEP-1998.
XX
XX PF 12-MAR-1998; 98WO-US04987.
XX
XX PR 12-MAR-1997; 97US-0039609.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX PI Johanson KO, Jonak ZL, Taylor AH;
XX
XX DR WPI; 1999-034590/03.
XX
XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis
XX
XX PS Example 14; Page 51; 97pp; English.
XX
XX CC SBA3167 is one of 4 overlapping oligonucleotides (see AAV71824-27)
CC used to construct DNA (see AAV71805) encoding a region of the murine
CC D12 monoclonal antibody light chain variable region (VL) that is
CC modified in humanised D12 VL D12HZLCREI. The synthetic D12 VL
CC gene was utilised in the construction of an expression vector for
CC the humanised D12 VL (see AAW87455). D12 is a murine anti-human
CC alpha-v beta-3 vitronectin receptor monoclonal antibody. Humanised
CC D12 antibodies of the invention can be used for passive
CC immunotherapy of disorders mediated by the alpha-v beta-3
CC vitronectin receptor, e.g. restenosis and angiogenic-related
CC disorders.
XX
XX SQ Sequence 101 BP; 21 A; 20 C; 31 G; 29 T; 0 other;

```

Query Match 84.2%; Score 27.8; DB 20; Length 101;
Best Local Similarity 93.5%; Pred. No. 0.0067; 2; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 3 ggccagccaaagtattagcaacttcctacac 33
   |||||
Db 99 GCCCAGCCCAAGTATTAGCAACCACTACAC 69

```

Search completed: August 21, 2002, 10:08:40
Job time: 10058 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:20 ; Search time 174.26 Seconds
(without alignments)
46.516 Million cell updates/sec

Title: US-09-339-922A-109
Perfect score: 33
Sequence: 1 caggccagcaaaagtattagcaacttctctacac 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27.8	84.2	128	1	US-07-634-278-91
C 2	27.8	84.2	128	1	US-08-477-728-91
C 3	27.8	84.2	128	1	US-08-474-040-91
C 4	27.8	84.2	128	1	US-08-487-200-91
C 5	27.8	84.2	128	4	US-08-484-537-91
6	27.8	84.2	381	1	US-07-634-278-82
7	27.8	84.2	381	1	US-08-477-728-82
8	27.8	84.2	381	1	US-08-474-040-82
9	27.8	84.2	381	1	US-08-487-200-82
10	27.8	84.2	381	4	US-08-484-537-82
11	27.8	84.2	424	1	US-08-436-463-3
12	27.8	84.2	5238	6	5453363-1
13	24.6	74.5	324	4	US-09-247-352-14
14	24.6	74.5	8858	4	US-09-247-352-6
15	23	69.7	324	2	US-08-737-560A-13
16	23	69.7	363	2	US-08-737-560A-8
17	20.4	61.8	321	4	US-09-247-352-7
18	20.4	61.8	321	4	US-09-247-352-11
C 19	19.4	58.8	1568	4	US-08-858-207A-105
C 20	18.6	56.4	1266	2	US-08-659-984A-2
C 21	18.6	56.4	1266	4	US-08-659-984A-2
C 22	18.6	56.4	1335	2	US-08-660-531-2
C 23	18.6	56.4	1335	2	US-08-659-984A-4
C 24	18.4	55.8	812	1	US-08-660-531-4
25	18.4	55.8	812	1	US-08-053-131-178
26	18.4	55.8	812	1	US-08-096-762-178
27	18.4	55.8	812	4	US-09-042-353-41
27	18.4	55.8	812	4	US-08-758-417A-306

C 28	18.2	55.2	4800	5	PCT-US94-07779-1	Sequence 1, Appli
C 29	18.2	55.2	7083	4	US-09-198-839-1	Sequence 1, Appli
C 30	18.2	55.2	7294	1	US-08-440-787A-1	Sequence 1, Appli
C 31	18.2	55.2	7294	1	US-08-440-787A-5	Sequence 5, Appli
C 32	18.2	55.2	7294	4	US-08-367-685-1	Sequence 1, Appli
C 33	18.2	55.2	7294	4	US-08-367-685-5	Sequence 5, Appli
C 34	18.2	55.2	7294	5	PCT-US91-07141-1	Sequence 1, Appli
C 35	18.2	55.2	7294	5	PCT-US91-07141-5	Sequence 5, Appli
C 36	18.2	55.2	7317	1	US-08-464-136-2	Sequence 2, Appli
C 37	18.2	55.2	7317	2	US-08-349-131-2	Sequence 2, Appli
C 38	18.2	55.2	7317	3	US-08-470-297A-2	Sequence 2, Appli
C 39	18.2	55.2	7317	5	PCT-US91-07149-2	Sequence 2, Appli
C 40	18.2	55.2	7320	1	US-08-440-787A-2	Sequence 2, Appli
C 41	18.2	55.2	7320	4	US-08-367-685-2	Sequence 2, Appli
C 42	18.2	55.2	7320	5	PCT-US91-07141-2	Sequence 2, Appli
C 43	18.2	55.2	7394	1	US-08-440-787A-6	Sequence 6, Appli
C 44	18.2	55.2	7394	4	US-08-367-685-6	Sequence 6, Appli
C 45	18.2	55.2	7394	5	PCT-US91-07141-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-07-634-278-91/C
; Sequence 91, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-07-634-278-91

Query Match 84.2%; Score 27.8; DB 1; Length 128;
Best Local Similarity 93.5%; Pred. No. 0.00041;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ggcagcccaagattagcaacttctctacac 33
|||||
Db 95 GGCACCCAAAGTATTAGCACACCTACAC 65

RESULT 2
US-08-477-728-91/c
; Sequence 91, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)

US-08-477-728-91

Query Match 84.2%; Score 27.8; DB 1; Length 128;
Best Local Similarity 93.5%; Pred. No. 0.00041;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ggcagcccaagattagcaacttctctacac 33
|||||
Db 95 GGCACCCAAAGTATTAGCACACCTACAC 65

RESULT 4
US-08-487-200-91/c

Qy 3 ggcagcccaagattagcaacttctctacac 33
|||||
Db 95 GGCACCCAAAGTATTAGCACACCTACAC 65

RESULT 3
US-08-474-040-91/c
; Sequence 91, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990

; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)

US-08-474-040-91

Query Match 84.2%; Score 27.8; DB 1; Length 128;
Best Local Similarity 93.5%; Pred. No. 0.00041;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ggcagcccaagattagcaacttctctacac 33
|||||
Db 95 GGCACCCAAAGTATTAGCACACCTACAC 65

RESULT 4
US-08-487-200-91/c

```
; Sequence 91, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-487-200-91

Query Match      84.2%; Score 27.8; DB 1; Length 128;
Best Local Similarity 93.5%; Pred. No. 0.00041;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcagcaagattaggcaacttcctacac 33
   |||||||||||||||||||
DB 95 GGCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 5
US-08-484-537-91/c
; Sequence 91, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
```

```
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-484-537-91

Query Match      84.2%; Score 27.8; DB 4; Length 128;
Best Local Similarity 93.5%; Pred. No. 0.00041;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcagcaagattaggcaacttcctacac 33
   |||||||||||||||||||
DB 95 GGCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 6
US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
```

STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-07-634-278-82

Query Match 84.2%; Score 27.8; DB 1; Length 381;
Best Local Similarity 93.5%; Pred. No. 0.00054;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gccacgcaaaagtattagcaactctctacac 33
|||||
Db 132 GCCACGCCAAAGTATTAGCAACACCTACAC 162

RESULT 7
US-08-477-728-82
Sequence 82, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-477-728-82

Query Match 84.2%; Score 27.8; DB 1; Length 381;
Best Local Similarity 93.5%; Pred. No. 0.00054;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gccacgcaaaagtattagcaactctctacac 33
|||||
Db 132 GCCACGCCAAAGTATTAGCAACACCTACAC 162

RESULT 8
US-08-474-040-82
Sequence 82, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040

; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-474-040-82

Query Match 84.2%; Score 27.8; DB 1; Length 381;
Best Local Similarity 93.5%; Pred. No. 0.00054;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 gcccagccaaagtattagcaactctctacac 33
|||||
DB 132 GCCCAGCCAAAGTATTAGCAACACCTACAC 162

RESULT 9
US-08-487-200-82
; Sequence 82, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278

; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-487-200-82

Query Match 84.2%; Score 27.8; DB 1; Length 381;
Best Local Similarity 93.5%; Pred. No. 0.00054;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 gcccagccaaagtattagcaactctctacac 33
|||||
DB 132 GCCCAGCCAAAGTATTAGCAACACCTACAC 162

RESULT 10
US-08-484-537-82
; Sequence 82, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-484-537-82

Query Match 84.2%; Score 27.8; DB 4; Length 381;
Best Local Similarity 93.5%; Pred. No. 0.00054;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcgaagattagcaactctctacac 33
|||||
Db 132 GCCAGCCAAAGTATTAGCAACACCTACAC 162

RESULT 11
US-08-436-463-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..403
US-08-436-463-3

Query Match 84.2%; Score 27.8; DB 1; Length 424;
Best Local Similarity 93.5%; Pred. No. 0.00056;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcgaagattagcaactctctacac 33
|||||
Db 154 GCCAGCCAAAGTATTAGCAACACCTACAC 184

RESULT 12
5453363-1
; Patent No. 5453363
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
; ING AFTER GENETIC EXPRESSION IN PROKARYOTES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,044
; FILING DATE: 02-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 942,370
; FILING DATE: 09-SEP-1992
; APPLICATION NUMBER: 498,500
; FILING DATE: 23-MAR-1990
; APPLICATION NUMBER: 76,207
; FILING DATE: 23-OCT-1986
; SEQ ID NO: 1:
; LENGTH: 5238
5453363-1

Query Match 84.2%; Score 27.8; DB 6; Length 5238;
Best Local Similarity 93.5%; Pred. No. 0.0011;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcgaagattagcaactctctacac 33
|||||
Db 78 ggcagcgaagattagcaacacacacac 108

RESULT 13
US-09-247-352-14
; Sequence 14, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19

; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Human and Mouse
US-09-247-352-14

Query Match 74.5%; Score 24.6; DB 4; Length 324;
Best Local Similarity 87.1%; Pred. No. 0.015;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ggcacgccaagattaggcaacttcctacac 33
||||| ||||| ||||| ||| |||||
Db 72 ggcacgccaagattaggcactactacac 102

RESULT 14
US-09-247-352-6
; Sequence 6, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Sladak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Rajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8858
; TYPE: DNA
; ORGANISM: Human and Mouse
US-09-247-352-6

Query Match 74.5%; Score 24.6; DB 4; Length 8858;
Best Local Similarity 87.1%; Pred. No. 0.037;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ggcacgccaagattaggcaacttcctacac 33
||||| ||||| ||||| ||| |||||
Db 1136 ggcacgccaagattaggcactactacac 1166

RESULT 15
US-08-737-560A-13
; Sequence 13, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuul
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuul
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea

; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1
; OTHER INFORMATION: light chain variable region
US-08-737-560A-13

Query Match 69.7%; Score 23; DB 2; Length 324;
Best Local Similarity 83.9%; Pred. No. 0.084;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ggcacgccaagattaggcaacttcctacac 33
||||| ||||| ||||| ||| |||||
Db 72 ggcacgccaagattaggcactactacac 102

Search completed: August 21, 2002, 10:52:21
Job time: 9661 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:49:58 ; Search time 2408.76 Seconds
(without alignments)
182.441 Million cell updates/sec

Title: US-09-339-922A-111
Perfect score: 21
Sequence: 1 tatcgtccacagtcacatctct 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg_hum.*

31: em.htg_inv.*

32: em.htg_other.*

33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
--------	-------	-------	-------	--------	----	-------------

RESULT 1
AX060890
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
CDS

AX060890 Sequence
AX060822 Sequence
AX060795 Sequence
AX060804 Sequence
AX060782 Sequence
AX060786 Sequence
AX060810 Sequence
AL671173 Mus muscu
AL671173 Mus muscu
AL627345 Mus muscu
AX060862 Sequence
22072 M.domesticu
U19309 Mus musculu
U19328 Mus musculu
U19328 Mus musculu
AF139842 Mus muscu
AF139843 Mus muscu
AF137617 Mus muscu
M34528 Mouse Ig ka
S60864 Ab2 kappa c
S66242 anti-myeelin
X59211 Mouse immu
X86546 M.musculus
AF139235 Mus muscu
L09019 Mus musculu
L09021 Mus musculu
X02556 Mouse mrna
X02234 Mouse mrna
AF087030 Mus muscu
AF163757 Mus muscu
X0901 M.musculus
U16181 Mus musculu
AJ277215 Mus muscu
AJ277216 Mus muscu
M95941 Mouse mrna
M95943 Mouse mrna
M95945 Mouse mrna
M35667 Mouse lysoz
L08211 Mouse anti-
A43800 Sequence 4
A57187 Sequence 4
AF139845 Mus muscu
AF139846 Mus muscu
AF139847 Mus muscu
AF139848 Mus muscu
AF139849 Mus muscu
U16184 Mus musculu

21 bp DNA linear PAT 22-JAN-2001

Sequence 111 from Patent WO0078815.
AX060890
AX060890.1 GI:12406268
synthetic construct.
synthetic construct.
artificial sequence.
1 (bases 1 to 21)
Huse,W.D. and Wu,H.
Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
Patent: WO 0078815-A 111 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
1. .21
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>21
/note="Mutated complementarity determining region (CDR)"
/codon_start=1

AX060890
Sequence 111 from Patent WO0078815.
AX060890
AX060890.1 GI:12406268
synthetic construct.
synthetic construct.
artificial sequence.
1 (bases 1 to 21)
Huse,W.D. and Wu,H.
Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
Patent: WO 0078815-A 111 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
1. .21
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>21
/note="Mutated complementarity determining region (CDR)"
/codon_start=1

```

/transl_table=11
/protein_id="CAC24931.1"
/db_xref="GI:12406269"
/translation="YRSQIS"
      3 a      8 c      2 g      8 t
BASE COUNT
ORIGIN

Query Match      100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccagtcctctct 21
   |||||
Db 1 TATCGTTCCAGTCCATCTCT 21

RESULT 2
LOCUS AX060822 33 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 43 from Patent WO0078815.
ACCESSION AX060822
VERSION AX060822.1 GI:12406200
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 33)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 43 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
Source 1..33
/organism="Mus musculus"
/db_xref="taxon:10090"
<1..>33
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAC24897.1"
/db_xref="GI:12406201"
/translation="LLIRYSQIS"
      4 a      13 c      3 g      13 t
BASE COUNT
ORIGIN

Query Match      100.0%; Score 21; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccagtcctctct 21
   |||||
Db 13 TATCGTTCCAGTCCATCTCT 33

RESULT 3
LOCUS AX060795 84 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 16 from Patent WO0078815.
ACCESSION AX060795
VERSION AX060795.1 GI:12406175
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 84)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 16 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
Source 1..33
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>321
/notes="oligonucleotide"
      17 a      25 c      20 g      22 t
BASE COUNT
ORIGIN

Query Match      100.0%; Score 21; DB 6; Length 84;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccagtcctctct 21
   |||||
Db 19 TATCGTTCCAGTCCATCTCT 39

RESULT 4
LOCUS AX060804 84 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 25 from Patent WO0078815.
ACCESSION AX060804
VERSION AX060804.1 GI:12406184
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 84)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 25 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
Source 1..84
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>321
/notes="oligonucleotide"
      17 a      25 c      20 g      22 t
BASE COUNT
ORIGIN

Query Match      100.0%; Score 21; DB 6; Length 84;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccagtcctctct 21
   |||||
Db 19 TATCGTTCCAGTCCATCTCT 39

RESULT 5
LOCUS AX060782 321 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 3 from Patent WO0078815.
ACCESSION AX060782
VERSION AX060782.1 GI:12406162
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 321)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 3 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
Source 1..321
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>321
/notes="oligonucleotide"

```

```

/note="grafted antibody variable region"
/codon_start=1
/transl_table=11
/protein_id="CAC24899.1"
/db_xref="GI:12406163"
/translations="EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAP
RLIKYRSQISGIPARFSGSGSTDTLTLSISLEPEFAVYYCQSGSWPHTFGGTT
KLEIK"
BASE COUNT      78 a   93 c   79 g   71 t
ORIGIN
      1 tatcgttcccgagtcctctct 21
      148 TATCGTTCCCGAGTCCATCTCT 168

Query Match      100.0%; Score 21; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatcgttcccgagtcctctct 21
      148 TATCGTTCCCGAGTCCATCTCT 168

Db 148 TATCGTTCCCGAGTCCATCTCT 168

RESULT 6
LOCUS      AX060786          321 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION      Sequence 7 from Patent WO0078815.
ACCESSION      AX060786
VERSION      AX060786.1 GI:12406166
KEYWORDS
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Huse,W.D. and Wu,H.
TITLE      Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL      Patent: WO 0078815-A 7 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source      1..321
/organism="synthetic construct"
/db_xref="taxon:10090"
variation      145..147
/note="grafted antibody variable region"
BASE COUNT      76 a   93 c   78 g   71 t   3 others
ORIGIN
      1 tatcgttcccgagtcctctct 21
      148 TATCGTTCCCGAGTCCATCTCT 168

Query Match      100.0%; Score 21; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatcgttcccgagtcctctct 21
      148 TATCGTTCCCGAGTCCATCTCT 168

Db 148 TATCGTTCCCGAGTCCATCTCT 168

RESULT 8
LOCUS      AL671173/c      199080 bp      DNA      linear      HTG 08-FEB-2002
DEFINITION      Mus musculus chromosome 4 clone RP23-426N4, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION      AL671173
VERSION      AL671173.3 GI:18643846
KEYWORDS      HTG; HTGS_PHASE1.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Plumb,B.
TITLE      Direct Submission
JOURNAL      Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 10, 2002 this sequence version replaced gi:18477144.
COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bm426N4
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 74% of reads
Chemistry: Dye-terminator; 25% of reads
Consensus quality: 196691 bases at least Q40
Consensus quality: 197461 bases at least Q30
Consensus quality: 197868 bases at least Q20
Insert size: 198280; sum-of-contigs
Insert size: 205652; 5.0% error; agarose-fp
Quality coverage: 7.13x in Q20 bases; sum-of-contigs Quality
coverage: 7.00x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
FEATURES
source      1..199080
/organism="Mus musculus"
/db_xref="taxon:10090"

```

```

/note="grafted antibody variable region"
/codon_start=1
/transl_table=11
/protein_id="CAC24899.1"
/db_xref="GI:12406163"
/translations="EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAP
RLIKYRSQISGIPARFSGSGSTDTLTLSISLEPEFAVYYCQSGSWPHTFGGTT
KLEIK"
BASE COUNT      78 a   93 c   79 g   71 t
ORIGIN
      1 tatcgttcccgagtcctctct 21
      148 TATCGTTCCCGAGTCCATCTCT 168

Query Match      100.0%; Score 21; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatcgttcccgagtcctctct 21
      148 TATCGTTCCCGAGTCCATCTCT 168

Db 148 TATCGTTCCCGAGTCCATCTCT 168

RESULT 6
LOCUS      AX060786          321 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION      Sequence 7 from Patent WO0078815.
ACCESSION      AX060786
VERSION      AX060786.1 GI:12406166
KEYWORDS
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Huse,W.D. and Wu,H.
TITLE      Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL      Patent: WO 0078815-A 7 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source      1..321
/organism="Mus musculus"
/db_xref="taxon:10090"
<1..>321
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC24899.1"
/db_xref="GI:12406167"
/translations="DIVLTQSPATLSVTPGDVSVLSQAQSQISNHLHWYQOKSHESP
RLIKYRSQISGIPARFSGSGSTDTLTLSISLEPEFAVYYCQSGSWPHTFGGTT
KLEIK"
BASE COUNT      83 a   83 c   77 g   78 t
ORIGIN
      1 tatcgttcccgagtcctctct 21
      148 TATCGTTCCCGAGTCCATCTCT 168

Query Match      100.0%; Score 21; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatcgttcccgagtcctctct 21
      148 TATCGTTCCCGAGTCCATCTCT 168

Db 148 TATCGTTCCCGAGTCCATCTCT 168

RESULT 7
LOCUS      AX060810          321 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION      Sequence 31 from Patent WO0078815.
ACCESSION      AX060810
VERSION      AX060810.1 GI:12406189
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      synthetic construct
artificial sequence.

```

```

/chromosome="4"
/clone="RP23-426N4"
/clone_lib="RPC1-23"
1. .3299
/feature="assembly_fragment:00717"
fragment_chain:1"
3400. .46221
/note="assembly_fragment:00198"
fragment_chain:1"
46322. .84635
/note="assembly_fragment:01999"
fragment_chain:1"
84736. .94486
/note="assembly_fragment:02694"
fragment_chain:1"
94587. .96789
/note="assembly_fragment:01661"
fragment_chain:1"
96890. .119792
/note="assembly_fragment:00161"
fragment_chain:2"
119893. .125701
/note="assembly_fragment:00140"
fragment_chain:2"
125802. .196306
/note="assembly_fragment:00002"
196407. .199080
/note="assembly_fragment:01500"
815 others

BASE COUNT 52895 a 47980 c 46823 g 50567 t
ORIGIN

Query Match 85.7%; Score 18; DB 2; Length 199080;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgttcacagtcacatctct 21
|||||
Db 123307 CGTTCACAGTCACATCTCT 123290

RESULT 9
AL627345/c
LOCUS
DEFINITION Mus musculus chromosome 4 clone RP23-169E7, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION AL627345
VERSION AL627345.4 GI:16596763
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Burton, J.
Direct Submission
TITLE Submitted (30-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Nov 2, 2001 this sequence version replaced gi:16596752.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM169E7
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 1% of reads
Sequencing vector: plasmid; L08752; 98% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 208062 bases at least Q40

```

Consensus quality: 209911 bases at least Q30
Consensus quality: 211313 bases at least Q20
Insert size: 212988; sum-of-contigs
Insert size: 237457; 1.8% error; agarose-fp
Quality coverage: 7.10x in Q20 bases; sum-of-contigs Quality
coverage: 6.79x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
Location/Qualifiers
1. .216188
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-169E7"
/clone_lib="RPC1-23"
1. .13211
/note="assembly_fragment:04054"
clone_end:SP6
vector_side:left"
13312. .37041
/note="assembly_fragment:05232"
fragment_chain:1"
37142. .39300
/note="assembly_fragment:02127"
fragment_chain:1"
39401. .45603
/note="assembly_fragment:01795"
fragment_chain:1"
45704. .48389
/note="assembly_fragment:05387"
fragment_chain:1"
48490. .51610
/note="assembly_fragment:05684"
fragment_chain:1"
51711. .57795
/note="assembly_fragment:00041"
fragment_chain:1"
57896. .62317
/note="assembly_fragment:05227"
fragment_chain:1"
62418. .66250
/note="assembly_fragment:00195"
fragment_chain:1"
66351. .72994
/note="assembly_fragment:02274"
fragment_chain:1"
73095. .76869
/note="assembly_fragment:05274"
fragment_chain:1"
76970. .81417
/note="assembly_fragment:03583"
fragment_chain:2"
81518. .95713
/note="assembly_fragment:01196"
fragment_chain:2"
95814. .108724
/note="assembly_fragment:05397"
fragment_chain:2"
108825. .114591
/note="assembly_fragment:05157"
fragment_chain:2"
114692. .119312
/note="assembly_fragment:01061"
fragment_chain:2"
119413. .122148
/note="assembly_fragment:02286"
fragment_chain:3"
12249. .124750
/note="assembly_fragment:02147"
fragment_chain:3"

BASE COUNT

/db_xref="taxon:10090"
 /chromosome="6"
 /clone="GL1"
 /tissue_type="tail"
 /germline
 <l..>285
 /gene="Ig"
 /note="variable region"
 <l..>285

gene

CDS
 /gene="Ig"
 /codon_start=1
 /product="immunoglobulin kappa light chain variable region
 Vk23"
 /protein_id="AAD28629.1"
 /db_xref="GI:4732149"
 /translation="DIVLTQSPATLSVTPGDRVSLSCRASQISNYLHWYQKSHESP
 RLLIKYASQISGIPSRFSGSGTDTLSINSVETEDFGMYFCQSNWP"
 70..105
 /gene="Ig"
 /note="CDR1; complementarity determining region 1"
 148..168
 /gene="Ig"
 /note="CDR2; complementarity determining region 2"
 73 c 63 g 74 t

misc_feature

misc_feature

BASE COUNT 75 a 73 c 63 g 74 t
 ORIGIN

Query Match 84.8%; Score 17.8; DB 10; Length 285;
 Best Local Similarity 90.5%; Pred. No. 1.4e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgtccagtcctctct 21
 ||| |||||
 Db 148 TATGCTTCCAGTCCATCTCT 168

RESULT 15

AF139843
 LOCUS AF139843 286 bp DNA linear ROD 04-NOV-1999
 DEFINITION Mus musculus clone GL2 immunoglobulin kappa light chain variable
 region Vk23 (Ig) gene, partial cds.

ACCESSION AF139843
 VERSION AF139843.1 GI:4732150

KEYWORDS
 SOURCE house mouse.

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 286)
 Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.

AUTHORS Somatic mutation and light chain rearrangement generate
 TITLE autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
 J. Exp. Med. 190 (5), 691-704 (1999)

JOURNAL

MEDLINE

PUBMED

10477553

2 (bases 1 to 286)

Brard,F. and Weigert,M.

AUTHORS

Direct Submission

TITLE

Submitted (01-APR-1999) Molecular Biology, Princeton University,

JOURNAL

Washington Road, Room 401, Princeton, NJ 08544, USA

FEATURES

Location/Qualifiers

1..286

/organism="Mus musculus"

/strain="MRL/Mp-lpr/lpr"

/db_xref="taxon:10090"

/chromosome="6"

/clone="GL2"

/tissue_type="tail"

/germline

<l..>286

/gene="Ig"

/note="variable region"

<l..>286

gene

CDS

/gene="Ig"
 /codon_start=1
 /product="immunoglobulin kappa light chain variable region
 Vk23"
 /protein_id="AAD28630.1"
 /db_xref="GI:4732151"
 /translation="DIVLTQSPATLSVTPGDSVSLSCRASQISNNLHWYQKSHESP
 RLLIKYASQISGIPSRFSGSGTDTLSINSVETEDFGMYFCQSNWP"
 70..105
 /gene="Ig"
 /note="CDR1; complementarity determining region 1"
 148..168
 /gene="Ig"
 /note="CDR2; complementarity determining region 2"
 75 a 75 c 62 g 74 t

misc_feature

misc_feature

BASE COUNT 75 a 75 c 62 g 74 t
 ORIGIN

Query Match 84.8%; Score 17.8; DB 10; Length 286;
 Best Local Similarity 90.5%; Pred. No. 1.4e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgtccagtcctctct 21

||| |||||
 Db 148 TATGCTTCCAGTCCATCTCT 168

Search completed: August 21, 2002, 10:50:08
 Job time: 9823 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 09:56:05 ; Search time 6260.2 seconds
(without alignments)
45.276 Million cell updates/sec

Title: US-09-339-922A-111

Perfect score: 21

Sequence: 1 tatcgttccagtcctctct 21

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hc:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_hc:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.8	84.8	236	10	BG089048
c	17.8	84.8	369	12	AQ138719
3	17.8	84.8	738	10	BF582153
4	17.8	84.8	833	10	BG966582
5	17.8	84.8	835	10	BI083006
c	16.8	80.0	320	9	AI452179
c	16.8	80.0	388	10	BE688887
8	16.8	80.0	397	9	AU062862
c	16.8	80.0	455	10	BF15275
10	16.8	80.0	460	9	AW179330
11	16.8	80.0	461	9	AI530706
12	16.8	80.0	470	9	AI120431
13	16.8	80.0	474	9	AI007215
c	16.8	80.0	545	10	BI509406
c	16.8	80.0	625	12	BH319848
c	16.8	80.0	634	10	BG923521
c	16.8	80.0	637	12	BH037505

18	16.8	80.0	655	10	BF228627
c	16.8	80.0	656	12	AZ371833
20	16.8	80.0	668	10	BE866105
21	16.8	80.0	709	9	BB272460
c	16.8	80.0	736	12	BH277625
c	16.8	80.0	829	10	BI254403
23	16.8	80.0	901	12	BI2211494
24	16.8	80.0	901	12	AV243452
25	16.4	78.1	232	9	AV243452
26	16.4	78.1	298	9	BB286013
c	16.4	78.1	386	9	AW145423
28	16.4	78.1	452	9	BB795741
29	16.4	78.1	555	10	BF253052
c	16.4	78.1	595	9	AW857225
30	16.4	78.1	738	10	BM050606
c	16.4	78.1	738	10	BM050606
32	16.2	77.1	240	9	AA676203
c	16.2	77.1	250	9	AW810350
33	16.2	77.1	285	9	BB308305
34	16.2	77.1	291	9	AA676202
35	16.2	77.1	291	9	AA676202
c	16.2	77.1	309	9	AW848100
c	16.2	77.1	314	12	BH009715
37	16.2	77.1	346	9	AA676200
c	16.2	77.1	360	10	C47045
39	16.2	77.1	363	10	BM177637
40	16.2	77.1	367	12	B85305
41	16.2	77.1	394	12	AQ430140
c	16.2	77.1	394	12	AQ430140
42	16.2	77.1	400	12	AZ754750
43	16.2	77.1	400	12	AZ754750
44	16.2	77.1	408	12	AZ788388
45	16.2	77.1	415	9	AW756096

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

BG089048 236 bp mRNA linear EST 26-JAN-2001
ut61b10.y1 Soares_mouse.NMGB_bcell Mus musculus cDNA clone
IMAGE:3332299.5' similar to SW:KVSI_MOUSE P01642 IG KAPPA CHAIN V-V
REGION L7 PRECURSOR ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:1076463

Seq primer: -40RP from Gibco.

Location/Qualifiers

1. .236

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:3332299"

/lab_host="PH10B (phage-resistant)"

/note="Organ: germinal B-cell; Vector: pT7T3D-Pac

(Pharmacia) with a modified polylinker; Site.1: Not I;

Site.2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5'

TGTACCAATCTGAAGTGGAGCCGCCCTGTTTTTTTTTTTTTTTTTTTTTTTTTTT

T 3'; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

Library is normalized; constructed by Bento Soares and


```

BASE COUNT      66 a      54 c      58 g      58 t
ORIGIN
M.Fatima Bonaldo."

Query Match      84.8%; Score 17.8; DB 10; Length 236;
Best Local Similarity 90.5%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttcccgagtcctctct 21
   ||| ||||| ||||| |||||
Db 55 TATGCTTCCCGAGTCCTCTCT 75

RESULT 2
AQ138719/c
LOCUS
DEFINITION
HS_3073_A2_G11_MR_CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate-3073 Col-22 Row=M, DNA sequence.
ACCESSION
AQ138719
VERSION
AQ138719.1 GI:3529372
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 369)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3073 row: M column: 22
Class: BAC ends
High quality sequence stop: 369.
Location/Qualifiers
1. .369
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT      152 a      55 c      125 g      37 t
ORIGIN

Query Match      84.8%; Score 17.8; DB 12; Length 369;
Best Local Similarity 90.5%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttcccgagtcctctct 21
   |||| | ||||| |||||
Db 285 TATCGGTCTCAGTCCTCTCT 265

RESULT 3
BF582153
LOCUS
DEFINITION-- 602099743F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219402 5',
mRNA sequence.
ACCESSION
BF582153
EST 12-DEC-2000

```

```

VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 738)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9801 row: f column: 11
High quality sequence stop: 714.
Location/Qualifiers
1. 738
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4219402"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      210 a      189 c      172 g      167 t
ORIGIN

Query Match      84.8%; Score 17.8; DB 10; Length 738;
Best Local Similarity 90.5%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttcccgagtcctctct 21
   ||| ||||| ||||| |||||
Db 220 TATGCTTCCCGAGTCCTCTCT 240

RESULT 4
BG966582
LOCUS
DEFINITION
602834412F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:498955 5',
mRNA sequence.
ACCESSION
BG966582
VERSION
BG966582.1 GI:14354219
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1002 row: g column: 04
High quality sequence stop: 830.

```

QY	1	tatcgttccccagtcacatctct 21
Db	226	TATGCTTCCCAGTCACATCTCT 246
RESULT	6	
AI452179/c		
LOCUS		320 bp mRNA linear EST 09-MAR-1999
DEFINITION		mp82gll.xl Soares_thymus_2NDMT Mus musculus cDNA clone IMAGE:575780 3', mRNA sequence.
ACCESSION		AI452179
VERSION		AI452179
KEYWORDS		EST.
SOURCE		house mouse.
ORGANISM		Mus musculus
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 320)
AUTHORS		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE		National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL		Unpublished (1997)
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgapsr@mail.nih.gov This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this new data is from the 3' end High quality sequence stop: 319.
FEATURES		Location/Qualifiers
source		1..320
		/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="IMAGE:575780"
		/glone_lib="Soares_thymus_2NbMT"
		/sex="male"
		/tissue.type="Thymus"
		/dev_stage="4 weeks"
		/lab_host="DH10B"
		/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCGAAGTCGGACGCCGGCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	83 a	65 c 68 g 104 t
ORIGIN		
Query Match	80.0%;	Score 16.8; DB 9; Length 320;
Best Local Similarity	90.0%;	Pred. No. 1.3e+03;
Matches	18; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	2	atcgttccccagtcacatctct 21
Db	179	ATCTGCCAGTCACATCTCT 160
RESULT	7	
BE688887/c		
LOCUS		388 bp mRNA linear EST 11-SEP-2000
DEFINITION		uw39d03.xl Soares_thymus_2NDMT Mus musculus cDNA clone IMAGE:3419045 3', mRNA sequence.
ACCESSION		BE688887
VERSION		BE688887
KEYWORDS		EST.
SOURCE		house mouse.

```

ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 388)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Other_ESTs: uw39d03.y1
              Contact: Robert Strausberg, Ph.D.
              Email: cgaps-remail.nih.gov
              This clone is available royalty-free through LLNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:1094857
              High quality sequence stop: 351.

FEATURES      source
              Location/Qualifiers
                1..388
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:3419045"
                /clone_lib="Soares_thymus_2NdbMT"
                /sex="male"
                /tissue_type="thymus"
                /dev_stage="4 weeks"
                /lab_host="DH10B"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was primed with a Not I - oligo(dT) primer [5',
                TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGT
                3']; double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT7T3 vector. RNA
                provided by Dr. Bertrand Jordan. Library went through two
                rounds of normalization, and was constructed by Bento
                Soares and M.Fatima Bonaldo."
BASE COUNT    93 a 88 c 84 g 123 t
ORIGIN
Query Match   80.0%; Score 16.8; DB 10; Length 388;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcgtcccgagtcctctct 21
||||| ||||| ||||| |||||
Db 179 ATCTTCCCGCAGTCCATCTCT 160

RESULT 8
AU062862
LOCUS      AU062862 Rice callus Oryza sativa cDNA clone C51207_1A, mRNA
DEFINITION AU062862 sequence.
ACCESSION  AU062862
VERSION    AU062862.1 GI:4878563
KEYWORDS   EST.
SOURCE     Oryza sativa.
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 397)
AUTHORS    Sasaki, T. and Minobe, Y.
TITLE      Rice cDNA from callus
JOURNAL    Unpublished (1994)
COMMENT    Contact: Takuji Sasaki
              National Institute of Agrobiological Resources
              Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
              305-8602, Japan
              Tel: 81-298-38-7441
              Fax: 81-298-38-7468
              Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 397)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Other_ESTs: uw39d03.y1
              Contact: Robert Strausberg, Ph.D.
              Email: cgaps-remail.nih.gov
              This clone is available royalty-free through LLNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:1094857
              High quality sequence stop: 351.

FEATURES      source
              Location/Qualifiers
                1..388
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:3419045"
                /clone_lib="Soares_thymus_2NdbMT"
                /sex="male"
                /tissue_type="thymus"
                /dev_stage="4 weeks"
                /lab_host="DH10B"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was primed with a Not I - oligo(dT) primer [5',
                TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGT
                3']; double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT7T3 vector. RNA
                provided by Dr. Bertrand Jordan. Library went through two
                rounds of normalization, and was constructed by Bento
                Soares and M.Fatima Bonaldo."
BASE COUNT    93 a 88 c 84 g 123 t
ORIGIN
Query Match   80.0%; Score 16.8; DB 10; Length 388;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcgtcccgagtcctctct 21
||||| ||||| ||||| |||||
Db 179 ATCTTCCCGCAGTCCATCTCT 160

PROJECT = 'RGP'
Location/Qualifiers
1..397
/organism="Oryza sativa"
/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="C51207_1A"
/clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid."
BASE COUNT    70 a 94 c 101 g 124 t
ORIGIN
Query Match   80.0%; Score 16.8; DB 9; Length 397;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tatcgtcccgagtcctctct 21
||||| ||||| ||||| |||||
Db 122 TATCTTTCCATCCATCTCT 142

RESULT 9
BF715275/c
LOCUS      BF715275 455 bp mRNA linear EST 02-JAN-2001
DEFINITION mab06f07 x1 Soares_thymus_2NdbMT Mus musculus cDNA clone
IMAGE:3825564 3', mRNA sequence.
ACCESSION  BF715275
VERSION    BF715275.1 GI:12014547
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 455)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgaps-remail.nih.gov
              This clone is available royalty-free through LLNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:1461916.

FEATURES      Location/Qualifiers
              1..455
              /organism="Mus musculus"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="IMAGE:3825564"
              /clone_lib="Soares_thymus_2NdbMT"
              /sex="male"
              /tissue_type="Thymus"
              /dev_stage="4 weeks"
              /lab_host="DH10B"
              /note="vector: pT7T3D-Pac (Pharmacia) with a modified
              polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
              was primed with a Not I - oligo(dT) primer [5',
              TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGT
              3']; double-stranded cDNA was ligated to Eco RI adaptors
              (Pharmacia), digested with Not I and cloned into the Not I
              and Eco RI sites of the modified pT7T3 vector. RNA
              provided by Dr. Bertrand Jordan. Library went through two
              rounds of normalization, and was constructed by Bento
              Soares and M.Fatima Bonaldo."
BASE COUNT    106 a 111 c 99 g 139 t
ORIGIN
Query Match   80.0%; Score 16.8; DB 10; Length 455;

```

```

Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atggttccaggtccatctct 21
    ||| | ||||| |||||
Db 179 ATCTTGGCCAGTCCATCTCT 160

```

[illegible]

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1. (bases 1 to 460)
AUTHORS	HCGP http://www.ludwig.org.br/ORESTES .
TITLE	The FAPESP/LICR Human Cancer Genome Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM4st2-PM4-ST0120-100999-001-c09&t3=1999-09-10&t4=1) Seq primer: puc 18 forward High quality sequence stop: 229.

```

FEATURES
source
1. .460
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="SR0120"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
116 a 125 c 104 g 115 t
BASE COUNT

```

BASE COUNT	116 a	125 c	104 g	115 t
ORIGIN				
Query Match		80.0%	Score 16.8;	DB 9;
Best Local Similarity		90.0%	Pred. No. 1.5e+03;	Length 460;
Matches 18;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps 0;				

Qy	1	tatcgttccccagtcctcatc	20
Dδ	212	TATGTTCCCAgTCCATCTC	231

RESULT	11
AI530706	
LOCUS	
DEFINITION	AI530706 461 bp mRNA linear EST 18-MAR-1999 mp82q11.v1 Soares_thymus_2NbMt Mus musculus cDNA clone IMAGE:575780 5'.. mRNA sequence.
ACCESSION	AI530706
VERSION	AI530706.1 GI:4444841
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
-------------------------------	--------------------

	FEATURES	SOURCE
1.	100% Pure Cotton	USA
2.	Machine Washable	India
3.	Soft & Comfortable	Bangladesh
4.	Durable & Long Lasting	Pakistan
5.	Eco-Friendly	Vietnam
6.	Available in Multiple Colors	Thailand
7.	Lightweight & Breathable	Philippines
8.	Easy to Fold & Store	Malaysia
9.	Hypoallergenic	Singapore
10.	Perfect for Travel	Indonesia

BASE COUNT ORIGIN	BASE COUNT ORIGIN
0	0
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100
101	101
102	102
103	103
104	104
105	105
106	106
107	107
108	108
109	109
110	110
111	111
112	112
113	113
114	114
115	115
116	116
117	117
118	118
119	119
120	120
121	121
122	122
123	123
124	124
125	125
126	126
127	127
128	128
129	129
130	130
131	131
132	132
133	133
134	134
135	135
136	136
137	137
138	138
139	139
140	140
141	141
142	142
143	143
144	144
145	145
146	146
147	147
148	148
149	149
150	150
151	151
152	152
153	153
154	154
155	155
156	156
157	157
158	158
159	159
160	160
161	161
162	162
163	163
164	164
165	165
166	166
167	167
168	168
169	169
170	170

Query Match	2	a	1	A
Best Local				
Matches				
Qy				
Db			379	A

RESULT	12
AA120431	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

TITLE	JOURNAL	COMMENT
REFERENCE		AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 461)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
This read is a SEQUENCE of a previously sequenced mouse clone.
This read has been verified (found to hit its original self in the correct orientation)

```

Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .461
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:575780"
/cloned_lib="Soares_thymus_2NDMT"
/sex="male"
/tissue_type="Thymus"
/lab_stage="4 weeks"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TCTTACCAATCGAATGGAGCCGCCGGCTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
107 a 110 c 129 g 115 t

```

```

      ch      80.0%; Score 16.8; DB 9; Length 461;
      11 Similarity 90.0%; Pred. No. 1.5e+03;
      18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

      cggtcccgagtcacatctct 21
      ||| ||||| |||||
      TCCTGCCAGTCCATCTCT 398

```

AA120431 470 bp mRNA linear EST 17-FEB-1997
mp82g11.r1 Soares_thymus_2NbWT Mus musculus cDNA clone IMAGE:575780
5', mRNA sequence.

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 470)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Willson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

FEATURES
source

Location/Qualifiers
1. .545
/organism="Apis mellifera"
/strain="mixed strains of European bees, predominantly
A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB170016A20C04"
/clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; This BB17 cDNA library was generated by
subtraction of the BB16 library with 4000 previously
sequenced clones. The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."

BASE COUNT
ORIGIN

173 a 133 c 111 g 128 t

Query Match 80.0%; Score 16.8; DB 10; Length 545;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcggtcccgagtcctctct 21

|||||

Db 195 ACCTTCCCGAGTCCATCTCT 176

RESULT 15
BH319848/c

LOCUS

BH319848 625 bp DNA linear GSS 03-DEC-2001
CH230-63K4.TVB CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-63K4, DNA sequence.

ACCESSION

VERSION

BH319848.1 GI:17250562

KEYWORDS

SOURCE

Norway rat.

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

AUTHORS

Zhao S., Shetty J., Shatsman S., Tsegaye G., Geer K., Shvartsbeyn
A., Gebregorgis E., Overton L., Russell D., Chen D., Riggs F., de
Jong P. and Fraser C.M.

TITLE

JOURNAL

COMMENT

Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.choi.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/orering_information.htm). BAC end

plate: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html

Seq primer: T7

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1. .625

/organism="Rattus norvegicus"

/strain="BN/SSNHsd/MCW"

/db_xref="taxon:10116"

/clone="CH230-63K4"

/clone_lib="CHORI-230 Segment 1"

/sex="Female"

/cell_type="Brain"

/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

BASE COUNT 156 a 151 c 169 g 149 t

ORIGIN

Query Match 80.0%; Score 16.8; DB 12; Length 625;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcggtcccgagtcctctct 21

|||||

Db 56 ATCTCTCCCGAGTCCATCTCT 37

Search completed: August 21, 2002, 09:56:12
Job time: 9335 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:40 ; Search time 754.01 seconds
(without alignments)
47.818 Million cell updates/sec

Title: US-09-339-922A-111

Perfect score: 21

Sequence: 1 tatcgttccagtcctctct 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_032802.*
1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	22	AAV49843
2	21	100.0	33	19	AAV49849
3	21	100.0	33	22	AAV28205
4	21	100.0	84	19	AAV49840
5	21	100.0	84	19	AAV49831
6	21	100.0	84	22	AAH74634
7	21	100.0	84	22	AAV28186
8	21	100.0	84	22	AAV28195
9	21	100.0	321	19	AAV49843

10	21	100.0	321	19	AAV49821
11	21	100.0	321	19	AAV49823
12	21	100.0	321	22	AAH74624
13	21	100.0	321	22	AAH74626
14	21	100.0	321	22	AAH74626
15	21	100.0	321	22	AAH74626
16	21	100.0	321	22	AAH74626
17	17.8	84.8	33	19	AAV49869
18	17.8	84.8	33	22	AAV49869
19	17.8	84.8	33	22	AAV49869
20	17.8	84.8	33	22	AAV49869
21	17.8	84.8	315	20	AAV71803
22	17.8	84.8	315	20	AAV71803
23	17.8	84.8	321	17	AAV71800
24	17.8	84.8	324	17	AAV71800
25	17.8	84.8	324	20	AAV71798
26	17.8	84.8	338	20	AAV71802
27	17.8	84.8	342	22	AAH27466
28	17.8	84.8	381	15	AAQ64167
29	17.8	84.8	381	22	AAV58747
30	16.8	80.0	5238	11	AAQ04654
31	16.8	80.0	101	20	AAV71825
32	16.8	80.0	308	22	AAK49560
33	16.8	80.0	384	21	AAZ39321
34	16.8	80.0	573	22	AAK36602
35	16.8	80.0	753	21	AAK38914
36	16.2	77.1	1632	21	AAK50082
37	16.2	77.1	363	17	AAV38510
38	16.2	77.1	381	21	AAZ35242
39	16.2	77.1	381	21	AAZ35244
40	16.2	77.1	415	21	AAZ00904
41	16.2	77.1	415	21	AAZ00906
42	16.2	77.1	415	21	AAZ01262
43	16.2	77.1	465	21	AAZ48877
44	16.2	77.1	510	23	AAZ76374
45	16.2	77.1	651	21	AAZ44346
			8858	20	AAZ10202

ALIGNMENTS

RESULT 1

AAV28239

ID AAV28239 standard; DNA; 21 BP.

XX AAV28239;

XX 03-APR-2001 (first entry)

XX DNA encoding enhanced 6H6LH light chain CDR2.

XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
XX inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

Vitaxin antibody 1
LM609 antibody lig
DNA encoding light
DNA encoding light
Vitaxin light chain
Antibody LM609 lig
DNA encoding light
LM609 grafted anti
DNA encoding mutan
Alpha-v beta-3 MAb
JK gene segment.
Humanised anti-
Humanised anti-
EGF receptor chime
Murine vitronectin
Vitronectin alpha-
Murine coding sequ
Sequence of mouse
Murine CMV5 antibo
Plasmid pBT11 enc
Alpha-v beta-3 MAb
Human bone marrow
Nucleotide sequenc
Human bone marrow
Arabidopsis thalia
Arabidopsis thalia
Light chain coding
Mouse anti-verotox
Humanised anti-ver
Humanised antibody
Humanised antibody
Mouse monoclonal a
DNA encoding the k
DNA encoding novel
Human secreted exp
Expression vector

PT osteoporosis -
 PS Claim 16; Page 107; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 21 BP; 3 A; 8 C; 2 G; 8 T; 0 other;
 Query Match 100.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 tatcgttccagtcacatctct 21
 Db 1 tatcgttccagtcacatctct 21
 RESULT 2
 AAV49849
 ID AAV49849 standard; DNA; 33 BP.
 XX
 AC AAV49849;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-L region CDR2 DNA fragment #1.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region; ss.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure; Page 40; 129pp; English.
 XX
 CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal
 CC antibody LM609 heavy and light chain variable region. LM609 and the
 CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used
 CC to inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 33 BP; 4 A; 13 C; 3 G; 13 T; 0 other;
 Query Match 100.0%; Score 21; DB 19; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 tatcgttccagtcacatctct 21
 Db 13 tatcgttccagtcacatctct 33
 RESULT 3
 AAF28205
 ID AAF28205 standard; DNA; 33 BP.
 XX
 AC AAF28205;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE DNA encoding LM609 VL CDR2 peptide.
 XX
 KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 XX
 OS Unidentified.
 XX
 PN WO200078615-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity.
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Page 40; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 33 BP; 4 A; 13 C; 3 G; 13 T; 0 other;
 Query Match 100.0%; Score 21; DB 22; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.45;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcgttcccagtcctctct 21
 |||||
 Db 13 tctcgttcccagtcctctct 33

RESULT 4

AAV49840
 ID AAV49840 standard; DNA; 84 BP.
 XX
 AC AAV49840;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody light chain variable region oligonucleotide #3.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Example 5; Page 80; 129pp; English.
 XX
 CC AAV49838-V49842 are oligonucleotides used in the construction of grafted
 CC LM609 monoclonal antibody light chain variable regions. LM609 and the
 CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be
 CC used to inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 84 BP; 17 A; 25 C; 20 G; 22 T; 0 other;

Query Match 100.0%; Score 21; DB 19; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcgttcccagtcctctct 21
 |||||
 Db 19 tctcgttcccagtcctctct 39

RESULT 5

AAV49831
 ID AAV49831 standard; DNA; 84 BP.
 XX
 AC AAV49831;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody variable region oligonucleotide #8.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Example 2; Page 65; 129pp; English.
 XX
 CC AAV49824-V49833 are oligonucleotides used in the construction of grafted
 CC LM609 monoclonal antibody heavy and light chain variable regions. LM609
 CC and the antibody vitaxin bind selectively to integrin alphavbeta3 and
 CC can be used to inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 XX
 SQ Sequence 84 BP; 16 A; 25 C; 20 G; 21 T; 2 other;

Query Match 100.0%; Score 21; DB 19; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcgttcccagtcctctct 21
 |||||
 Db 19 tctcgttcccagtcctctct 39

RESULT 6

AAH74634
 ID AAH74634 standard; DNA; 84 BP.
 XX
 AC AAH74634;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE PCR primer for light chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer; PCR primer; ss.
 XX Mus sp.
 OS
 XX US2001011125-A1.
 PN
 XX
 PD 02-AUG-2001.
 XX
 XX 30-JAN-1997; 97US-0790540.
 PF
 XX 30-JAN-1997; 97US-0790540.
 PR
 XX (HUSE/) HUSE W D.
 PA
 XX Huse WD;
 PI
 XX WPI; 2001-496171/54.
 DR
 XX New LM609 grafted antibody exhibiting selective binding affinity to
 XX alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -
 PT
 XX
 PS Example 2; Page 17; 25pp; English.
 CC PCR primers AAH74632-36 were used to amplify DNA encoding fragments
 CC of the light chain variable region of the monoclonal antibody LM609.
 CC LM609 is a murine antibody which specifically recognises the integrin
 CC alphavbeta3, and inhibits its functional activity. The specification
 CC describes a LM609 grafted antibody which has the complementarity
 CC determining regions (CDRs) substituted into a non-murine framework.
 CC Nucleic acids encoding LM609 grafted heavy and light chain polypeptides
 CC and fragments are useful in diagnostic and therapeutic purposes, such
 CC as in the production of LM609 grafted antibodies and fragments having
 CC binding specificity and inhibitory activity against the integrin
 CC alphavbeta3. The antibody can be used for the diagnosis or treatment
 CC of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic
 CC articular rheumatism, psoriasis, disorders associated with inappropriate
 CC or inopportune invasion of vessels such as diabetic retinopathy,
 CC neovascular glaucoma and capillary proliferation in atherosclerotic
 CC plaques, or cancers), and to inhibit binding activity of alphavbeta3
 CC that are necessary for progression of an alphavbeta3-mediated disease.
 XX
 XX Sequence 84 BP; 17 A; 25 C; 20 G; 22 T; 0 other;
 SQ
 Query Match 100.0%; Score 21; DB 22; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 tatcgttccagtcctctct 21
 Db 19 tatcgttccagtcctctct 39
 RESULT 7
 AAF28186
 ID AAF28186 standard; DNA; 84 BP.
 XX
 AC AAF28186;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Grafted light chain variable region oligonucleotide #8.
 DE
 XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 KW
 OS Unidentified.

XX WO200078815-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 23-JUN-2000; 2000WO-US17454.
 PF
 XX 24-JUN-1999; 99US-0339922.
 PR
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA
 XX Huse WD, Wu H;
 PI
 XX WPI; 2001-050110/06.
 DR
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 PT
 XX
 PS Example 2; Page 67; 132pp; English.
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 XX Sequence 84 BP; 16 A; 25 C; 20 G; 21 T; 2 other;
 SQ
 Query Match 100.0%; Score 21; DB 22; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 tatcgttccagtcctctct 21
 Db 19 tatcgttccagtcctctct 39
 RESULT 8
 AAF28195
 ID AAF28195 standard; DNA; 84 BP.
 XX
 AC AAF28195;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Grafted light chain variable region oligonucleotide #3.
 DE
 XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.
 KW
 OS Unidentified.
 OS
 XX WO200078815-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 23-JUN-2000; 2000WO-US17454.
 PF
 XX 24-JUN-1999; 99US-0339922.
 PR
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA
 XX Huse WD, Wu H;
 PI
 XX

DR WPI; 2001-0501110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 XX
 PS Example 4; Page 81; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 84 BP; 17 A; 25 C; 20 G; 22 T; 0 other;
 Query Match 100.0%; Score 21; DB 22; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.49; 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 tatcgtccagtcacatctct 21
 |||||
 Db 19 tatcgtccagtcacatctct 39
 |||||
 RESULT 9
 AAV49843
 ID AAV49843 standard; DNA; 321 BP.
 XX
 AC AAV49843;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 antibody light chain variable region DNA grafted fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..321
 FT /tag= a
 FT /product= "LM609 grafted antibody light chain variable
 FT region"
 FT /note= "partial sequence, no start or stop codon given"
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR P-PSDB; AAW76006.
 XX

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 24; Fig 7; 129pp; English.
 XX
 CC This sequence encodes a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
 Query Match 100.0%; Score 21; DB 19; Length 321;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 tatcgtccagtcacatctct 21
 |||||
 Db 148 tatcgtccagtcacatctct 168
 |||||
 RESULT 10
 AAV49821
 ID AAV49821 standard; DNA; 321 BP.
 XX
 AC AAV49821;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody light chain variable region DNA.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..321
 FT /tag= a
 FT /product= "vitaxin antibody light chain variable region"
 FT /note= "partial sequence, no start or stop codon given"
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR P-PSDB; AAW76002.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT anglogenesis or restenosis
 XX Claim 6; Fig 1b; 129pp; English.
 XX This sequence encodes the vitaxin antibody variable light chain region.
 CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
 SQ

Query Match 100.0%; Score 21; DB 19; Length 321;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccgatccatctct 21
 |||||
 Db 148 tatcgttcccgatccatctct 168

RESULT 11
 AAV49823
 ID AAV49823 standard; DNA; 321 BP.
 XX
 AC AAV49823;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 antibody light chain variable region DNA fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..321
 FT /*tag= a
 FT /product= "LM609 antibody light chain variable region"
 FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-0501826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR P-PSDB; AAV75004.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT anglogenesis or restenosis
 XX
 PS Claim 40; Fig 2b; 129pp; English.

XX This sequence encodes the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;
 SQ

Query Match 100.0%; Score 21; DB 19; Length 321;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccgatccatctct 21
 |||||
 Db 148 tatcgttcccgatccatctct 168

RESULT 12
 AAH74624
 ID AAH74624 standard; DNA; 321 BP.
 XX
 AC AAH74624;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE DNA encoding light chain variable region of LM609 grafted antibody.
 XX
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..321
 FT /*tag= a
 FT /transl_except= "(pos: 145..147, aa: Xaa)"
 FT /note= "Xaa is unspecified"

XX US2001011125-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 30-JAN-1997; 97US-0790540.
 XX
 PR 30-JAN-1997; 97US-0790540.
 XX
 PA (HUSE/) HUSE W D.
 XX
 PI Huse WD;
 XX
 DR WPI; 2001-496171/54.
 DR P-PSDB; AAG63588.
 XX
 PT New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer
 XX
 PS Claim 6; Fig 1B; 25pp; English.
 XX
 CC The present sequence encodes the light chain variable region of the
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which

CC specifically recognises the integrin alphavbeta3, and inhibits its
 CC functional activity. The LM609 grafted antibody has the
 CC complementarily determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
 CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 100.0%; Score 21; DB 22; Length 321;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgtcccgagtcacatctct 21
 Db 148 tatcgtcccgagtcacatctct 168

RESULT 13
 AAH74626
 ID AAH74626 standard; DNA; 321 BP.

XX AC AAH74626;

DT 15-OCT-2001 (first entry)

DE DNA encoding light chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
 KW cancer; ss.

OS Mus sp.

XX US2001011125-A1.

XX PD 02-AUG-2001.

XX PF 30-JAN-1997; 97US-0790540.

XX PR 30-JAN-1997; 97US-0790540.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX WPI; 2001-496171/54.

DR P-PSDB; AAG63590.

XX New LM609 grafted antibody exhibiting selective binding affinity to
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
 PT disorders or cancer -

PS Disclosure; Fig 2B; 25pp; English.

XX The present sequence encodes the light chain variable region of the
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.
 CC The specification describes a LM609 grafted antibody which has the
 CC complementarity determining regions (CDRs) substituted into a non-murine
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain

CC polypeptides and fragments are useful in diagnostic and therapeutic
 CC purposes, such as in the production of LM609 grafted antibodies and
 CC fragments having binding specificity and inhibitory activity against
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
 CC disorders, chronic articular rheumatism, psoriasis, disorders
 CC associated with inappropriate or inopportune invasion of vessels such
 CC as diabetic retinopathy, neovascular glaucoma and capillary
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
 CC binding activity of alphavbeta3 that are necessary for progression of
 CC an alphavbeta3-mediated disease.

XX Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 321;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgtcccgagtcacatctct 21
 Db 148 tatcgtcccgagtcacatctct 168

RESULT 14

AAH28176

ID AAF28176 standard; DNA; 321 BP.

XX AC AAF28176;

DT 03-APR-2001 (first entry)

DE Vitaxin light chain variable region DNA.

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

PS Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Job time: 10059 sec

Query Match 100.0%; Score 21; DB 22; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tatcgttccagtcctctct 21
 |||||
Db 148 tatcgttccagtcctctct 168

RESULT 15
AAF28178
ID AAF28178 standard; DNA; 321 BP.
XX
AC AAF28178;
XX
DT 03-APR-2001 (first entry)
XX
DE Antibody LM609 light chain variable region DNA.
XX
KW LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
XX inflammatory; cancer; retina; restenosis; osteoporosis; ds.
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 200WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Fig 2; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tatcgttccagtcctctct 21
 |||||
Db 148 tatcgttccagtcctctct 168

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:21 ; Search time 174.26 Seconds
(without alignments)
29.601 Million cell updates/sec

Title: US-09-339-922A-111

Perfect score: 21

Sequence: 1 tatcgtccagtcacatctct 21

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 303533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.8	84.8	381	1 US-07-634-278-82	Sequence 82, Appl
2	17.8	84.8	381	1 US-08-477-728-82	Sequence 82, Appl
3	17.8	84.8	381	1 US-08-474-040-82	Sequence 82, Appl
4	17.8	84.8	381	1 US-08-487-200-82	Sequence 82, Appl
5	17.8	84.8	381	4 US-08-484-537-82	Sequence 82, Appl
6	17.8	84.8	424	1 US-08-436-463-3	Sequence 3, Appli
7	17.8	84.8	5238	6 5453363-1	Patent No. 5453363
8	16.2	77.1	324	2 US-08-737-560A-13	Sequence 13, Appl
9	16.2	77.1	324	4 US-09-247-352-14	Sequence 14, Appl
10	16.2	77.1	363	2 US-08-737-560A-8	Sequence 8, Appli
11	16.2	77.1	8858	4 US-09-247-352-6	Sequence 6, Appli
12	15.8	75.2	1100	3 US-09-094-103-3	Sequence 3, Appli
13	15.8	75.2	1172	3 US-09-094-103-1	Sequence 1, Appli
14	15.2	72.4	80161	3 US-09-036-987A-1	Sequence 1, Appli
15	15.2	72.4	80161	4 US-09-370-700-1	Sequence 1, Appli
16	15	71.4	113	1 US-07-634-278-92	Sequence 92, Appl
17	15	71.4	113	1 US-08-477-728-92	Sequence 92, Appl
18	15	71.4	113	1 US-08-474-040-92	Sequence 92, Appl
19	15	71.4	113	1 US-08-487-200-92	Sequence 92, Appl
20	15	71.4	113	4 US-08-484-537-92	Sequence 92, Appl
21	14.6	69.5	49	2 US-08-980-071-74	Sequence 74, Appl
22	14.6	69.5	49	3 US-09-314-093-74	Sequence 74, Appl
23	14.6	69.5	49	4 US-09-337-635-74	Sequence 74, Appl
24	14.6	69.5	703	4 US-08-998-416-828	Sequence 828, App
25	14.6	69.5	966	3 US-08-748-506-5	Sequence 5, Appli
26	14.6	69.5	966	3 US-08-748-506-7	Sequence 7, Appli
27	14.6	69.5	966	3 US-08-748-506-8	Sequence 8, Appli

28	14.6	69.5	3441	2 US-08-525-864A-1	Sequence 1, Appli
29	14.6	69.5	3907	3 US-08-475-742-1	Sequence 1, Appli
30	14.6	69.5	7379	4 US-09-341-587-5	Sequence 5, Appli
31	14.4	68.6	445	3 US-09-188-930-233	Sequence 233, App
32	14.4	68.6	2622	4 US-09-130-616-170	Sequence 170, App
33	14.4	68.6	3111	2 US-09-014-969-12	Sequence 12, Appl
34	14.4	68.6	5049	1 US-08-336-345-1	Sequence 1, Appli
35	14.4	68.6	5049	1 US-08-336-345-2	Sequence 2, Appli
36	14.4	68.6	5049	2 US-08-647-655-1	Sequence 1, Appli
37	14.4	68.6	5049	2 US-08-647-655-2	Sequence 2, Appli
38	14.4	68.6	35081	2 US-08-752-760A-1	Sequence 1, Appli
39	14.2	67.6	540	1 US-08-117-083-18	Sequence 18, Appl
40	14.2	67.6	642	4 US-09-385-982-386	Sequence 386, App
41	14.2	67.6	789	1 US-08-436-748-4	Sequence 4, Appli
42	14.2	67.6	789	3 US-08-483-857-3	Sequence 3, Appli
43	14.2	67.6	1237	1 US-08-197-792-40	Sequence 40, Appl
44	14.2	67.6	1237	1 US-08-459-850-40	Sequence 40, Appl
45	14.2	67.6	1237	1 US-08-459-214-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-07-634-278-82

Query Match 84.8%; Score 17.8; DB 1; Length 381;
Best Local Similarity 90.5%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgtcccgagtcacatctct 21
||| ||||||||||||||||
Db 208 TATGCTTCCCGAGTCACATCTCT 228

RESULT 2
US-08-477-728-82
; Sequence 82, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-477-728-82

Query Match 84.8%; Score 17.8; DB 1; Length 381;
Best Local Similarity 90.5%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgtcccgagtcacatctct 21
||| ||||||||||||||||
Db 208 TATGCTTCCCGAGTCACATCTCT 228

RESULT 3
US-08-474-040-82
; Sequence 82, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLEFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-474-040-82

Query Match 84.8%; Score 17.8; DB 1; Length 381;
Best Local Similarity 90.5%; Pred. No. 4;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21
Db 208 TATGCTTCCAGTCCATCTCT 228

RESULT 4
US-08-487-200-82
; Sequence 82, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-487-200-82

Query Match 84.8%; Score 17.8; DB 1; Length 381;
Best Local Similarity 90.5%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21

Db 208 TATGCTTCCAGTCCATCTCT 228

RESULT 5
US-08-484-537-82
; Sequence 82, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-484-537-82

Query Match 84.8%; Score 17.8; DB 4; Length 381;
Best Local Similarity 90.5%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21
Db 208 TATGCTTCCAGTCCATCTCT 228

```
RESULT 6
US-08-436-463-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-PELVINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..403
; US-08-436-463-3

Query Match 84.8%; Score 17.8; DB 1; Length 424;
Best Local Similarity 90.5%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgttccagtcacatctct 21
   ||| ||||| ||||| |||||
Db 230 TATGCTTCCAGTCACATCTCT 250

RESULT 7
5453363-1
; Patent No. 5453363
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
; ING AFTER GENETIC EXPRESSION IN PROKARYOTES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,044
; FILING DATE: 02-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 942,370
; FILING DATE: 09-SEP-1992
```

```
; APPLICATION NUMBER: 498,500
; FILING DATE: 23-MAR-1990
; APPLICATION NUMBER: 76,207
; FILING DATE: 23-OCT-1986
; SEQ ID NO:1:
; LENGTH: 5238
5453363-1

Query Match 84.8%; Score 17.8; DB 6; Length 5238;
Best Local Similarity 90.5%; Pred. No. 5.2;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgttccagtcacatctct 21
   ||| ||||| ||||| |||||
Db 154 tatcgttccagtcacatctct 174

RESULT 8
US-08-737-560A-13
; Sequence 13, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuul
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuul
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1
; OTHER INFORMATION: light chain variable region
; US-08-737-560A-13
```

Query Match 77.1%; Score 16.2; DB 2; Length 324;
 Best Local Similarity 85.7%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21
 ||| ||||| ||||| |||||
 Db 148 TATGCTTCCCAATCCATCTCT 168

RESULT 9
 US-09-247-352-14
 ; Sequence 14, Application US/09247352
 ; Patent No. 6312693
 ; GENERAL INFORMATION:
 ; APPLICANT: Aruffo, Alejandro A.
 ; APPLICANT: Siadak, Anthony W.
 ; APPLICANT: Berry, Karen K.
 ; APPLICANT: Harris, Linda
 ; APPLICANT: Thorne, Barbara A.
 ; APPLICANT: Bajorath, Jurgen
 ; APPLICANT: Huse, William D.
 ; APPLICANT: Wu, Herren
 ; APPLICANT: Watkins, Jeffry D.
 ; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
 ; FILE REFERENCE: DB2a SEQUENCE
 ; CURRENT APPLICATION NUMBER: US/09/247,352
 ; EARLIER FILING DATE: 1999-02-10
 ; EARLIER FILING DATE: 1998-02-19
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 324
 ; TYPE: DNA
 ; ORGANISM: Human and Mouse
 US-09-247-352-14

Query Match 77.1%; Score 16.2; DB 4; Length 324;
 Best Local Similarity 85.7%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21
 ||| ||||| ||||| |||||
 Db 148 tatcgttccagtcctctct 168

RESULT 10
 US-08-737-560A-8
 ; Sequence 8, Application US/08737560A
 ; Patent No. 5928893
 ; GENERAL INFORMATION:
 ; APPLICANT: KANG, Chang-Yuill
 ; APPLICANT: KIM, Joong-Gon
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
 ; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: KANG, Chang-Yuill
 ; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
 ; STREET: Kwanak-gu
 ; CITY: Seoul
 ; STATE: Seoul
 ; COUNTRY: Republic of Korea
 ; ZIP: 151-057
 ; ADDRESSEE: KIM, Joong-Gon
 ; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
 ; CITY: Seoul
 ; STATE: Seoul
 ; COUNTRY: Republic of Korea
 ; ZIP: 135-110
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
 ; COMPUTER: IBM PC/AT
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/737,560A
 ; FILING DATE: 13-NOV-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: KR 95-8176
 ; FILING DATE: 08-APR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME:
 ; REGISTRATION NUMBER:
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE:
 ; TELEFAX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 363 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; FEATURE:
 ; OTHER INFORMATION: 1 to 324 bp 4B4-1-1 light chain
 ; OTHER INFORMATION: variable region
 ; OTHER INFORMATION: 70 to 102 bp hypervariable region CDR1
 ; OTHER INFORMATION: 148 to 168 bp hypervariable region CDR2
 ; OTHER INFORMATION: 265 to 291 bp hypervariable region CDR3
 ; OTHER INFORMATION: 325 to 363 bp 4B4-1-1 light chain constant region
 US-08-737-560A-8

Query Match 77.1%; Score 16.2; DB 2; Length 363;
 Best Local Similarity 85.7%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21
 ||| ||||| ||||| |||||
 Db 148 TATGCTTCCCAATCCATCTCT 168

RESULT 11
 US-09-247-352-6
 ; Sequence 6, Application US/09247352
 ; Patent No. 6312693
 ; GENERAL INFORMATION:
 ; APPLICANT: Aruffo, Alejandro A.
 ; APPLICANT: Siadak, Anthony W.
 ; APPLICANT: Berry, Karen K.
 ; APPLICANT: Harris, Linda
 ; APPLICANT: Thorne, Barbara A.
 ; APPLICANT: Bajorath, Jurgen
 ; APPLICANT: Huse, William D.
 ; APPLICANT: Wu, Herren
 ; APPLICANT: Watkins, Jeffry D.
 ; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
 ; FILE REFERENCE: DB2a SEQUENCE
 ; CURRENT APPLICATION NUMBER: US/09/247,352
 ; CURRENT FILING DATE: 1999-02-10
 ; EARLIER FILING DATE: 1998-02-19
 ; EARLIER FILING DATE: 1998-02-19
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 8858
 ; TYPE: DNA
 ; ORGANISM: Human and Mouse
 US-09-247-352-6

Query Match 77.1%; Score 16.2; DB 4; Length 8858;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tatcgttccagtcacatct 21
||| ||||| ||||| |||||
Db 1212 tatcgttccagtcacatct 1232

RESULT 12
US-09-094-103-3/c
; Sequence 3, Application US/09094103
; Patent No. 6140061
; GENERAL INFORMATION:
; APPLICANT: Wallis, Nicola G.
; APPLICANT: Zalacain, Magdalena
; APPLICANT: Throup, John
; APPLICANT: Biswas, Sanjoy
; TITLE OF INVENTION: Response regulator
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,103
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,332
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-09-094-103-3
Query Match 75.2%; Score 15.8; DB 3; Length 1100;
Best Local Similarity 89.5%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgttccagtcacatct 19
||| | ||| ||||| |||||
Db 45 TATCGCTTCAGTCCATCT 27

RESULT 13
US-09-094-103-1/c
; Sequence 1, Application US/09094103
; Patent No. 6140061
; GENERAL INFORMATION:
; APPLICANT: Wallis, Nicola G.
; APPLICANT: Zalacain, Magdalena
; APPLICANT: Throup, John

; APPLICANT: Biswas, Sanjoy
; TITLE OF INVENTION: Response regulator
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,103
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,332
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1172 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-09-094-103-1
Query Match 75.2%; Score 15.8; DB 3; Length 1172;
Best Local Similarity 89.5%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgttccagtcacatct 19
||| | ||| ||||| |||||
Db 117 TATCGCTTCAGTCCATCT 99

RESULT 14
US-09-036-987A-1/c
; Sequence 1, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences LLC Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

US-09-094-103-1
Query Match 75.2%; Score 15.8; DB 3; Length 1100;
Best Local Similarity 89.5%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgttccagtcacatct 19
||| | ||| ||||| |||||
Db 45 TATCGCTTCAGTCCATCT 27

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-036-987A-1

Query Match 72.4%; Score 15.2; DB 3; Length 80161;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 atcgctcccgagtcacatctct 21
||||| ||||| ||||| |||||
Db 59135 ATCGCTCCGAGTCCACATCT 59116

RESULT 15
US-09-370-700-1/c
; Sequence 1, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; EARLIER FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 80161
; TYPE: DNA
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-1

Query Match 72.4%; Score 15.2; DB 4; Length 80161;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 atcgctcccgagtcacatctct 21
||||| ||||| ||||| |||||
Db 59135 ATCGCTCCGAGTCCACATCT 59116

Search completed: August 21, 2002, 10:52:27
Job time: 9667 sec